774

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Minimum
Maximum
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                                                                                                                                         Database
                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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DB
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seq length: 2000000000
 A_Geneseq_21:*
1: geneseqp1980
2: geneseqp2000
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4: geneseqp2001
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6: geneseqp2003
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8: geneseqp2003
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538
1 MAADPESTAALPDG
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geneseqp1980s:*
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(c) 1993 - 2006
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Biocceleration Ltd
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score and is Pred. No. re greater than is derived by a 18 the number of results predicted by chance to have a r than or equal to the score of the result being printed. ed by analysis of the total score distribution.

# SUMMARIES

24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	<sub>U</sub>	4	ω	N	_	Reguit	•
99	99	104	105	105	105	112.5	123.5	127.5	127.5	128.5	131.5	132	185	266.5	266.5	266.5	423	449	485	531	533	534	534	Score	
18.4	18.4	19.3	19.5	19.5	19.5	20.9	23.0	23.7	23.7	23.9	24.4	24.5	34.4	49.5	49.5	49.5	78.6	83.5	90.1	98.7	99.1	99.3	99.3	Match	
1088	1088	539	1041	1041	1040	1080	1067	1185	1185	1035	1065	1091	1103	1063	1054	1052	1059	1061	1045	108	107	1041	1041	Query Match Length	
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AAY00892	AAY00891	AAY37205	ADC34773	AAY56782	AAW97216	ADM26293	AAB96257	ABM39522	AAU43003	ABU24074	ADN46385	ABU48588	ABP66334	ADD13268 .	AAG92098	ABU26087	ABU35902	ABU34060	AAW57448	AAY21902	AAW72885	ABU36647	ABU34693	ID	
Aay00892 Isoleucyl	Aay00891 Isoleucyl	Aay37205 Protein i	Adc34773 Chlamydia	Aay56782 C. tracho		Adm26293 Hyperther	Aab96257 Putative	Abm39522 Propionib	Aau43003 Propionib	Abu24074 Protein e	Adn46385 Thermococ	Abu48588 Protein e	Abp66334 Bifidobac		Aag92098 C glutami		Abu35902 Protein e	Abu34060 Protein e	Aaw57448 M. tuberc	Aay21902 Amino aci	Aaw72885 Mycobacte	Abu36647 Protein e	Abu34693 Protein e	Description	

WPI; 2003-029926/02. N-PSDB; ACA38563.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 62617; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
78.5	78.5	79	80.5	80.5	80.5	80.5	82.5	82.5	82.5	82.5	86	87	89	93	96	96	97	97	97.5	98
14.6	14.6	14.7	15.0	15.0	15.0	15.0	15.3	15.3	15.3	15.3	16.0	16.2	16.5	17.3	17.8	17.8	18.0	18.0	18.1	18.2
1077	329	375	348	348	348	348	11096	9477	7068	659	1232	1038	1363	1042	1072	1072	1085	1026	1036	1088
σ	σ	œ	œ	8	œ	v	4	4	4	œ	9	σ	Q	σ	7	σ	σ	œ	σ	ຫ
ABJ26121	ABU34127	ADI37312	ADV80926	ADV83074	ADV89673	ABP26034	AAB10129	AAE10144	AAE10142	ADS29586	ABM95065	ABU25711	ABU08100	ABU19362	ADK62202	ABR52806	ABU20747	ADS08184	ABU27203	ABP73361
Abj26121	Abu34127	Adi37312	Adv80926	Adv83074	Adv89673	Abp26034		Aae10144 .	Aae10142	Ads29586	Abm95065	Abu25711	_	Abu19362	Adk62202	Abr52806	Abu20747	_	Abu27203	Abp73361
Aspergill	Protein e	M. tuberc	Streptoco	Streptoco	Streptoco	Streptoco	Streptomy	Streptomy	Streptomy	Bacterial	M. xanthu	Protein e	Human kin	Protein e	Disease t	Protein s	Protein e	Staphyloc	Protein e	Candida a

### ALIGNMENTS

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ABU34693
                                                                                                                                                                                                                                                                                                                                  RESULT 1
                                                                                                                      Wang L, Wall D,
                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                   03-OCT-2002.
                                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                               Mycobacterium bovis.
                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #20220.
                                                                                                                                                                                                                                                                                        19-JUN-2003
                                                                                                                                                                                                                                                                                                       ABU34693;
                                                                                                                                                                                                                                                                                                                     ABU34693 standard; protein; 1041 AA.
                                                                                                                                            (ELIT-)
                                                                                                                                            BLITRA PHARM
                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                      Malone
, Carr G
                                                                                                                                            INC.
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                                                                                                                      Haselbeck R, Yamamoto R,
                                                                                                                      Ohlsen
Forsyth
                                                                                                                      3,2
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Xu HH;
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RESULT 2
ABUJ 6647
ID ABUJ
XX
AC ABUJ
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DT 19-J
XX
Prot
XX
AC ARUJ
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AC Prot
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ANTI
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #22174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1041 AA;
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                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU36647 standard; protein; 1041 AA
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                        2003-029926/02
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                                                                                                                                                           ELITRA PHARM INC.
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                                                                         Zamudio C,
Trawick JD,
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99.1%;
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Carr (
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Pred. No. 1.
                                                                            Haselbeck R, Yamamoto R,
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L.7e-54;
                                                                            Ohlsen
Forsyth
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                                                                            Zyskind JW;
Xu HH;
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CC of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

(2) cencoding a polypeptide whose expression is inhibited by the antisense

(3) an isolated

(4) an antisense in isolated

(5) contisense nucleic acid; (4) an antibody capable of specifically binding

(6) contisense nucleic acid; (4) an antibody capable of specifically binding

(7) contisense nucleic acid; (4) an antibody capable of specifically binding

(8) conjupeptide; (5) producing the polypeptide; (6) inhibiting cellular

(9) contiseration or the activity of a gene in an operon required for

(1) dentifying a compound that influences the activity of

(2) identifying a gene required for cellular proliferation or the biological

(3) pathway in which a proliferation, or that inhibits cellular proliferation; (8)

(8) compound's activity; (11) a culture comprising strains in which the gene

(2) compound's activity; (1) manufacturing an antibodic; (10) profiling a

(3) compound's activity; (11) a culture comprising strains in which the gene

(4) compound's activity; (11) a culture comprising strains in which the gene

(5) compound's activity; (11) a culture comprising strains in which the gene

(6) compound's activity; (11) a culture comprising strains in which the gene

(6) compound that inhibits the extent

(7) identifying the target of a compound that inhibits the

(8) compound that inhibits the

(9) strains; or (13) identifying the target of a compound that inhibits the

(1) determining the extent

(2) identifying proteins or screening for homologous nucleic acids are useful for

(8) control is overexpressed or underexpressed; (12) determining the extent

(13) identifying the target of a compound that inhibits the

(14) control is overexpressed or underexpressed; (12) determining the extent

(15) control is overexpressed or underexpressed; (12) determining the extent

(15) control is overexpressed or underexpressed; (12) determining the extent

(15) control is ov
the 6213 antisense sequences given in the specification where of the nucleic acid inhibits proliferation of a cell. Also inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolate candidate molecules for rational drug discovery programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; SEQ ID NO 64571; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising any one of
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S S 밁 닭 Matches 107; Query Match Best Local Similarity 934 VAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM 61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT 1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM Conservative 99.3%; 99.1%; 1; Score 534; DB 6; Length 1041; Pred. No. 1.7e-54; Mismatches 0 Indels 0 Gaps 993 60

drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this

patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

Sequence 1041 AA;

ftp.wipo.int/pub/published\_pct\_sequences

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AAW72885;
                        AAW72885 standard; protein; 107
                          B
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Mycobacterium tuberculosis antigen CFP9

21-JAN-1999

(first entry)

Mycobacterium tuberculosis; infection. antigen; vaccine; immunological; immunogen;

Mycobacterium tuberculosis

WO9844119-A1

08-OCT-1998

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Best Local &
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                       10-NOV-1997;
05-JAN-1998;
01-APR-1998;
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18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                             Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CEP7A; CEP3OA; CFP7B; CFP19; CFP27; CFP3OA; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
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                                                                                                                                                                                                                                                                                                              AAY21902 standard;
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                                                                                                                                            Mycobacterium
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 (STAT-) STATENS
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ricanum or M. bovis
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DB; AAV63916.
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                                                                                                                                                                                                                                                                                                                                                                                                                       AADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMS
                                                                                                                                                                                                                                        sequence of antigen CFP9
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Florio |
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                                                                                                                                             tuberculosis.
                       97DK-00001277.
98US-0070488P.
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97US-0044624P.
97DK-00001277.
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  SERUM INST
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Pred. No. 1.1e-55;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC to the tuberculosis complex. The invention provides a (1) fusion
CC polypeptide comprising at least one polypeptide fragment (I) and at least
CC one fusion partner; (2) a fusion polypeptide fragment (I) and at least
CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
CC epitope from M. tuberculosis protein ESAT-6, or MPTS9 and a second
CC different amino acid sequence from M. tuberculosis, and/or including a
CC sequence which protects the first amino acid sequence from in vivo
CC degradation or post-translational processing; (3) a nucleic acid fragment
CC that encodes the above polypeptides. The polypeptides and nucleic acid
CC are useful as pharmaceuticals, for diagnosis of and as antigens for
CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
CC previous sensitization in an animal with bacteria belonging to the
CC tuberculosis complex. The invention also describes the use of CPP7A or
CC CP30A or a T-cell epitope of for the induction of a strong immune
CC response in a mammal; use of CPP30A, RD1-ORF3, RD1-ORF5, MPT59-ESAT6,
CC ESAT6-MPT59, CPP10A, CPP16, CPP19, CPP23, CPP23A, CPP25B, CPP28 or a T-cell
CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
CC est; use of CPP27, CPP30A, RD1-ORF3, RD1-ORF5, MPT59-ESAT6,
CC ESAT6-MPT59, CPP10A, CPP16, CPP19, CPP23, CPP23A, CPP25B, CPP2B or a T-
CC cell epitope of for the preparation of an immunological composition; and
CC for the preparation of a subunit vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 107
                                                                                                                                                                                                                                                                                                                          09-SEP-2004
12-AUG-1998
                                                                                                                                                                                                                        Isoleucyl-tRNA
antimicrobial;
                                                                                                                                                                                                                                                                                M. tuberculosis isoleucyl-tRNA synthetase (IleRSs) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57448 standard; protein; 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging
                                                                                                       Misc-difference
                                                                                                                                                                Unidentified.
                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic fragment of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Fig 4; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVPAERGDWARTHROLIAGEILATDFEFADLADGVAIGDGVRVSIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAADPESTAALPDGAGLVVLDGTVTAELEABGWAKDRIRELQELRKSTGLDVSDRIRVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAADPESTAALPDGAGLVVLDGTVTABLEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skjot R;
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                               synthetase; IleRSs; Mycobacterium tuberculosis;
                                                                                                                                                                                                                        tester strain;
                                                                                                     Location/Qualifiers
/note= "if the first GTG codon at position 640 is used for initiation of translation, the GTG codon at position 670 would be translated as Valine at this position to yield a 1045 amino acid protein; if the GTG codon at position 670 is used for initiation, it would be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.7%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 531; DB 2;
Pred. No. 1.9e-55;
0; Mismatches 1
                                                                                                                                                                                                                        leprosy; tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                             A
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
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60

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ABU34060
ID ABU3
XX
AC ABU3
XX
AC ABU3
XX
AC Prot
XX
AC Anti
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                                                                                                                                                 RESULT 6
                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                            This represents a Mycobacterium tuberculosis isoleucyl-tRNA synthetase (IlleRSs). Mycobacterial strains are responsible for leprosy (M. leprae) and tuberculosis (M. tuberculosis). RSs's are mycobacterial enzyme that are generally responsible for the reaction: aaRS+aa+ATP => aaRSaa-AMP+PPi -AMP+LENA => aa-RNA+aaRS+AMP, where aa is an amino acid. IleRSs is the enzyme specific for Isoleucine, with each amino acid having its own specific enzyme. These enzymes are essential for protein production. As more and more mycobacteria become resistant to drugs and antibiotics, tester strains comprising host cells containing a recombinant mycobacterial isoleucyl-tRNA synthetase gene, can be used to rapidly assess the antimicrobial effect and specificity of isoleucyl-tRNA synthetase inhibitors. The recombinant enzymes are also useful for biochemical studies of the enzyme in elucidation of further treatment strategies. The cloning and recombinant production of the enzyme has not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding mycobacterial isoleucyl-tRNA synthetase - and corresponding vectors, recombinant hosts and tester strains for recombinant production of the enzyme used in assays to identify inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                             Protein encoded by Prokaryotic essential gene #19587.
                                                                                                                     ABU34060 standard;
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schimmel PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995;
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                                                            19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                       Revised record issued on 09-SEP-2004 : Correction to feature table key
                                                                                                                                                                                              1004
                                                                                                                                                                                                                                                                                                                                                                                                                                 previously possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998-321533/28
                                                                                                                                                                                                                                                      944
                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                 1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVM
                                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV32142
                                                                                                                                                                                                                                                       SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGD 1042
                                                                                                                                                                                                                  SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGD
                                                                                                                                                                                                                                                                                                                                                                           1045
prokaryotic essential gene; cell
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5A-0; 62pp;
                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00452083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translated as Met at this position yielding a protein 1035 amino acids (residues 12 to 1045 of AAW57448)" 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "encoded by STG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Leu,
                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                             90.1%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                     1061
                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                             Score 485; DB 2;
Pred. No. 1.3e-48;
                                                                                                                                                                                                                                                                                                                  Mismatches
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proliferation;
                                                                                                                                                                                                                                                                                                                                            Length 1045;
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 gurb
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S 밁 Ś

1013

0

61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEK 107

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CC the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

((1) a vector comprising a promoter operably linked to the nucleic acid concoling a polypeptide whose expression is inhibited by the antisense comprising at promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated (3) polypeptide or its fragment whose expression is inhibited by the cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of a gene in an operon required for conjudent or that has an activity against a biological pathway capable of specifically binding conjudentifying a gene required for cellular proliferation; (8) compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene conjudent is overexpressed or underexpressed; (12) determining the extent convolute acids activity; (11) a culture comprising strains in which the extent convolute acids act useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for conjudent acids activity action and conjudent manufacturing the text candidate molecules for rational confusions of force acids are useful for force acids acids
  Matches
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang L, Wall D,
                                                                                                                                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                            Sequence 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 61984; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium avium.
                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolate candidate molecules for rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-)
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                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
  Conservative
                                                                                              A
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Carr GJ,
                     83.5%;
Score 449; DB 6;
Pred. No. 2.8e-44;
4; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen
Forsyth
                                           Length 1061;
    Indels
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Xu HH;
    0
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  Gaps
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밁
19-JUN-2003
                            ABU35902
                                                       ABU35902 standard; protein; 1059 AA
(first entry
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Protein encoded by Prokaryotic essential gene #21429

Antisense; prokaryotic essential gene; cell proliferation; drug design.

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Mycobacterium leprae.
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21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 06-SEP-2001; 25-OCT-2001; 08-FEB-2002; 2002US-00072851. 2002US-0362699P. 2001US-00815242. 2001US-00948993. 2001US-0342923P.

(BLIT-) BLITRA PHARM INC.

Zamudio Trawick Ą, Malone Carr G ရ်ပို မ Haselbeck R, Yamamoto R, Ohlsen Forsyth 줮 Zyskind Jw; Xu HH;

WPI; 2003-029926/02 ACA39772

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 63826; 1766pp; English.

ABUJIT 7
ABUJS 902
ID ABUJS 902
XX ABUJS 902
XX ABUJS 902
XX ABUJS 902
XX Prot
XX ARUJS 902
XX ARUJS 902
XX ARUJS 902
XX ARUJS 903
XX ARUS 903
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell concaining the vector; (3) an isolated collection or its fragment whose expression is inhibited by the activity of a gene in an operan required for proliferation or the activity of a gene in an operan required for concaining the vector; (3) an isolated continuous co the 6213 antisense sequences given in the specification where expres of the nucleic acid inhibits proliferation of a cell. Also included invention relates to an isolated nucleic acid comprising any one expression are:

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Best Local
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Wall D,
                                                                                                                                                                                   WPI; 2003-029926/02.
N-PSDB; ACA29957.
                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242

06-SEP-2001; 2001US-00948993

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-03072851

06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                  03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                 WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                Antisense;
                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #11614.
                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                 ABU26087;
                                                                                                                                                                                                                                                                                                                                                                                                                                ABU26087 standard; protein; 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1059 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                   (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 VAANPEFTAELPDGSGLVVLDDTVTPELEAEGWAKDRIRELQELRKLIGLDVSDRIRVLM 1011
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                                                                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                  BLITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPAERADWARVHRDFIAREILATSFEFGEPADSVAIGDGVRVSLLK 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                            Malone
Carr G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.6%;
80.4%;
                                                                                                                                                                                                           <sub>යි</sub> දී
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 423; DB 6;
Pred. No. 3.7e-41;
                                                                                                                                                                                                            Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                            Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                            Zyskind JW;
Xu HH;
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New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs or screening ដូ

Claim 25; SEQ ID NO 54011; 1766pp; English

The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense cC antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibited by the cc antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibited by the confideration or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) confidentifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an

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RESULT 9
AAG92098
ID AAG9
XX AAG9
XX AAG9
XX AAG9
XX COI,
XX II 6-
PR 03-
XX II 6-
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C glutamicum
   The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum are useful for identifying the mutation point of a gene derived fi
                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                       Claim 17; SEQ ID NO 5852; 246pp +
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DB; AAH67317.
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acid synthesis
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Senoh A, Ikeda M,
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Pred. No. 2.2e-22;
8; Mismatches 25;
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Ozaki A;
                                                                                                                          Sequence Listing; English
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      glutamicum.
derived from
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RESULT 10
ADD13268
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XX ADD13
XX ADD13
XX ADD13
XX O1-JA
XX O1-JA
XX Genet
KW Genet
KW Lysin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic scatting, with the production; gene expression; protein folding; fine chemical production; lysine production; nucleotide production; nucleotide production; nucleotide production; lipid production; diol production; carbohydrate production; aromatic compound production; vitamin production; co-factor production; food; animal feed; cosmetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                  WPI; 2003-505062/47.
N-PSDB; ADD13267.
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                                                                                                                                                                                                                                                                                                                                                                      Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                 Zelder
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Pred. No. 2.2e-22;
5; Mismatches 33;
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New nucleic acid encoding variant forms of proteins required genetic stability and proper protein folding, useful for procine chemicals, specifically lysine, in microorganisms.

ired for e.g

Claim 1; SEQ ID NO 76;

265pp; German.

This invention describes novel polynucleotides and polypeptides involved in genetic stability (DNA repair and recombination, transposition of genetic material), gene expression and folding of proteins in

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RESULT 11
ABP66334
ID ABP66
XX ABP6
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Matches 59
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                             The present invention describes a polynucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABQ81842 and ABQ81843, or a sequence given in least 90% identity or which hybridises with the sequences given in ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding fusion protein, comprising a sequence selected from 1097 sequences giver in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a heterologous polypeptide. (I) has antidiarrheic and antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrheea; pathogenic bactrotavirus; food composition; pharmaceutical composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                a biological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-668397/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide comprising Bifidobacterium genome sequence useful
be or primer for detecting and/or identifying Bifidobacterium lon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROD NESTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 NO 1078;
                                                                                                                                                                                                                                                                                                                                                                                                                                    sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SA.
                                                                                                                                                                                                                                                                                                                                                          80pp; English
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Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORF amino acid
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inhibitor of

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Claim

SEQ

ID NO

76512; 1766pp; English

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC a probe) is useful for the detection and/or identification of CC Bifidobacterium longum in a biological sample. A carrier containing the CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be CC used for preventing and/or treating diarrheae brought about by pathogenic CC bacteria and/or rotavirus. The carrier is a food composition selected CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented CC products, ice-creams, fermented cereal based products, milk based CC powders, infant formula, pet food or a pharmaceutical composition CC selected from tablets, liquid bacterial suspensions, dried oral CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. CC (I) is useful in DNA arrays or chips to carry out analysis of the CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent CC Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented CC in the printed specification but is based on sequence information CC supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                 Wang L,
Wall D,
                                                                                                                                                                                                                          21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-0094893.

25-OCT-2001; 2001US-0342923P.

08-PEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #34115
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                                                                                                                      2003-029926/02.
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                                                                                                        ACA52458
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Trawick JD,
                                                                                                                                                                                                ELITRA PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKVEQFRDLIAHETLATSFE---VKEGAELG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAERE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWARTHROLIAGEILATDFEFADLADGVAIG
                                                                                                                                                                                                                                                                                                                                                                                                              pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                          prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Carr G
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47.3%;
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Pred. No. 1.4e-12;
                                                                                                                                                 Haselbeck R,
Yamamoto R,
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                                                                                                                                                 Ohlsen
Forsyth
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                                                                                                                                                    ₹
                                                                                                                                                   Zyskind JW;
Xu HH;
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RESULT 13
ADN46385
ID ADN46
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archabacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immuno;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                              30-AUG-2002; 2002JP-00319011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermococcus kodakaraensis KOD1 protein sequence
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(NISC-) JAPAN
                                                                                                                                                                                        29-AUG-2003; 2003WO-IB003597
                                                                                                                                                                                                                                                                                           18-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                          WO2004022736-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermococcus kodakaraensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1039 DIVCARKAY-DLHRSYIVGETLAAHVQWARVRDGASAVYVKSDAVLWEVSIDK 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESLKAINEGTLTVALDTTLTEDLLLEGAIRDLVRGVQNLRKERGFSLVDRICLRVFSSDQ
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SCI & TECHNOLOGY CORP.
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Pred. No. 3.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biology; immunology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I arbitrary region in the sequence, providing a vector that contains a CC sequence homologous with the selected region and a marker gene, cc transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly cc Thermococcus kodakaraensis KODI. The method is for targeting the cc disruption of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the cdisruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein cencoded by the genome of Thermococcus kodakaraensis which was derived cusing the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1065 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
ABU24074;
                                      ABU24074 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                      959
                                                                                                                                                                                                                                                                 11 LPD------GAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; SEQ ID NO 263; 598pp; Japanese.
                                                                                                                                                                                        64 AEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGV--RVSIEK 107
                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                 DENRELLQENLDY IMRETRAVEVRFEEAKGYVVEWPEVQAKIGIEK
                                                                                                                                                                                                                                      LPDFFVAEEFDGGRVFVDKTLTRELLAEGLAREFVRRIQEMRKRLDLDVNDRIVVTIETT 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atomi H
                                                                                                                                                                                                                                                                                                                            Conservative
                                    protein; 1035
                                                                                                                                                                                                                                                                                                                                              24.4%;
                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                          Score 131.5; DB 8
Pred. No. 3.6e-06;
6; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                     Length 1065;
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ABU24074
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                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #9601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003
(ELIT-)
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     BLITRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC polypeptide or its fragment whose expression is inhibited by the continuence of the polypeptide; (5) producing the polypeptide; (6) inhibited by the continuence of the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for crown proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway cc required for proliferation, or that inhibits cellular proliferation; (8) compound that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an cc compound's activity; (11) a culture comprising strains in which the gene crownict is overexpressed or underexpressed; (12) determining the extent compound that inhibits proliferation of an compound that inhibits of compound's activity; (11) a culture comprising strains in which the gene compound that inhibits the gene crownich each of the strains is present in a culture or collection of compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the compound that inhibits are useful for cellular proliferation to isolate candidate molecules for rational compound discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, compound that inhibits the printed specification, but was obtained compound that of the printed specification, but was obtained con in electronic format directly form willog at
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                     Propionibacterium acnes immunogenic protein #3899
                                                                                                                                                                                                              27-PEB-2002
                                                                                                                                                                                                                                                                                                                                             AAU43003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any one 6213 antisense sequences given in the specification where express
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Trawick
                                                                                                                                                                                                                                                                                                                                         standard; protein; 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKETLATDIIYSENKEAAIYNINGEELNVFVKK 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1035 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGBILATDFEFADLADGVAI --- GDGVRVSIBK 107
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30.1%;
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Carr G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
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ရိပ္
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Pred. No. 7.9e-06;
6; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
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Xu HH;
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                           presence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                               Sequence 1185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides. The proteins and their associated DNA sequences the treatment, prevention and diagnosis of medical conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 4198; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e treatment, prevention and diagnosis of medical conditions acnes. The disorders include SAPHO syndrome (synovitis, acr
1158
                                                                   1098 EITPELARAGQAREVIRFVQDSRKKAGLDVSDRITLAWSASADLATAIEEHAEQISQEVL 115
                                                                                                                                       1038 AADPEWLASELAIKGSVEMDVPEVEGGKAVVTADDVIVSERPREGWSVVNEQGETVALDL 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-616774/71.
DB; AAS59519.
                                83
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                                                                                                                                                                                                                             Similarity
ÁVQMSREPRÁDDWÁVEPDLGLAVKVVK 1184
                                                                                                   -----AKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRDLIAGEIL 82
                                                                                                                                                                        AADPESTAA------LPD---GAGLVVLDGTVTAELEAEGW------
                                ATDFEFADLADGVAIGD--GVRVSIEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0199047P.
; 2000US-0208841P.
; 2000US-0216747P.
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                           23.7%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides and nucleic acids useful diagnosing infections, especially use
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, Jen S, Carter
                                                                                                                                                                                                           18;
                                                                                                                                                                                                         Score 127.5;
Pred. No. 1.3e
18; Mismatches
                                                                                                                                                                                                           . 1.3e-05;
cches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang SS,
                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                             Length 1185;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 14, 2006, 17:19:08; Search time 6.33288 Seconds (without alignments) 1640.866 Million cell updates/sec

Title: US-10-620-246-4
Perfect score: 538
Sequence: 1 MAADPESTAALPDGAGLVVL......ADLADGVAIGDGVRVSIEKT 108
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

#### SUMMARIES

2	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	σ	.4.	w	2	بر	No.	Degis 1+
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14.7	14.7	14.7		15.0						17.3	17.6	17.8	17.8	18.1	18.7	18.9		19.5	20.4				23.9			32.4	78.6	99.3	Match	*
1254	485	375	309	309	332	659	1039	1018	1086	1042	1106	1064	1072	1036	1070	1064	986	1036	1045	1044	1067	1066	1035	1091	1047	1078	1059	1041	Length	
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T04047	T01968	G70966	AC2971	G98311	AH1994	D84286	C64418	A69329	B71667	H70203	A97819	B72729	SYBYI4	F81719	H84369	T40751	B90220	P71565	SYEXI	H69049	H75139	F71100	G97273	B71322	T34946	B75407	E87058	B70760		
isoleucine-ckNA ii	isoleucine-tRNA li	hypothetical prote	hypothetical prote	probable rhizopine	hypothetical prote	3-hydroxyacyl-CoA	isoleucine-tRNA li	probable isoleucin	isoleucine-tRNA li	isoleucine-tRNA li	isoleucine-tRNA li	probable isoleucyl	isoleucine-tRNA li			isoleucyl-trna syn	isoleucine-tRNA sy	probable isoleucin	isoleucine-tRNA li	isoleucine-tRNA li	isoleucyl-tRNA syn	isoleucine-tRNA li	isoleucyl-tRNA syn	isoleucine-tRNA li	probable isoleucyl	isoleucyl-tRNA syn	isoleucyl-tRNA syn	probable iles prot		

A; Molecule type: DNA

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30
72.5	72.5	72.5	73.5	73.5	74	75	75.5	76	76	76.5	76.5	76.5	76.5	77	77.5
13.5	13.5	13.5	13.7	13.7	13.8	13.9	14.0	14.1	14.1	14.2	14.2	14.2	14.2	14.3	14.4
435	301	256	396	393	368	441	449	1266	432	1199	668	662	431	8563	569
N	N	N	N	N	N	N	N	N	N	-	N	N	N	N	N
C69194	A32498	H83002	A70581	S38875	T35150	T35788	B75451	I59314	T35263	S76549	A41234	I38400	A59474	T30226	T35476
L-asparaginase I -	Mx resistance prot	imidazoleglycerol-	hypothetical prote	methionine adenosy	probable glycosyl	probable transcrip	NADH oxidase - Dei	isoleucine-tRNA li	probable carboxype	transcription-repa	melanocyte-specifi	melanoma-associate	tRNA adenylyltrans	polyketide synthas	probable regulator

### ALIGNMENTS

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A; Gene: DR1335
A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-J
C;Daccession: E75407
R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1059 <STO>
A;Cross-references: UNIPROT:Q9X7E5; UNIPARC:UPI00001364F8; GB:AL450380; NID:g13093159; C;Genetics:
A;Gene: 11eS
C;Superfamily: isoleucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Statue, FINA
A; Molecule type: DNA
A; Residues: 1-1078 < WHI>
A; Cross-references: UNIPROT: Q9RUP8; UNIPARC: UPI00000D3E29;
A; Cross-references: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: E75407 A;Status: preliminary
                                                                                                                                                                                     C;Accession: T34946
R;Saunders, D.C.; Harris, D.; James, K.D.; submitted to the EMBL Data Library, August
                                                                                                                                                                                                                           probable isoleucyl-tRNA synthetase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change C;Accession: T34946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:QS
A;Experimental source: strain
C;Genetics:
O.≯
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                                                   ;Status: preliminary; translated fi; Molecule type: DNA; Residues: 1-1047 < CSAU>;Cross-references: UNIPROT:Q9S2X5;Experimental source: strain A3(2);
                                                                                                                                                  Reference number: Z21563;Accession: T34946
;Superfamily:
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Best Local (
                   Gene:
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Best Local
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                   SCOEDB:SC4A10.09
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isoleucine-tRNA ligase
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37.1%; Pred. No. 1.6;
tive 16; Mismatches
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                                                                                                                                  from
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Pred. No. 3.5e-32;
                                                                           UNIPARC: UPI00000DB2CC;
                                                                                                                                  GB/EMBL/DDBJ
                                                                                                                                                                                           Parkhill, J.; Barrell,
1999
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T.; Zalewski,
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C.; Ma
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                                                           ;Superfamily:
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   Query Match
Best Local :
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1055 <KUR>
A;Cross-references: UNIPROT:Q97ESO; UNIPARC:UPI00000CA6EC;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: TP0452
C;Superfamily: isoleucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1091 <COL>
A;Cross-references: UNIPROT:083466; UNIPARC:UPI0000136505; GB:AE001222; GB:AE000520;
A;Experimental source: strain Nichols
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                                                                                                                                                                   A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: G97273
                                                                                                                                                                                                                                                                                                                isoleucyl-tRNA synthetase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoleucine-tRNA ligase (EC 6.1.1.5) (ileS) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation
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Best Local :
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Local Similarity 37.2%; Pred. No. 0.00018;
heb 42; Conservative 16; Mismatches 43
CAC3038
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Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                     Markarova,
Smith, D.R.
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                                                                       GB:AE001437; PIDN:AAK80978.1
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                                                                                                                                                                                                                                                                                              Q.; Gibson,
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Similarity

23.9%;

Score Pred.

128. No.

.5; DB 2; 0.00036;

Length 1035;

Lee

isoleucine-tRNA ligase

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A;Description: Pyrococcus at A;Reference number: A75001 A;Accession: H75119 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1067 <KAW>
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A; Cross-references: UNIPROT:058792; UNIPARC:UPI00001364PE;
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a C; Genetics:
A; Gene: PH1065
C; Superfamily: isoleucine-tRNA ligase
C; Keywords: aminoacyl-tRNA symphomena.
                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-1067 <KAW>
A;Cross-references: UNIPROT:Q9V072; UNIPARC:UPI00000344D8; GB:AJ248285; GB:AL096836;
A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                      A;Gene:
C;Superf
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H75139
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A;Title: Complete sequence and gene organization of the genome of A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: F71100
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
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F71100
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R; anonymous, Genoscope
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                isoleucyl-tRNA synthetase (iles) PABO616 - Pyrococcus abyssi (strain Orsay)
                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                              Species: Pyrococcus abyssi
Date: 20-Aug-1999 #sequence_revision
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Best Local
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                                                   Matches
                                                                                                                       Superfamily:
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                                                  Similarity 39; Conserv
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LPD-----GAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABREDWARTHRDLIAGEILATDFEFADLADGVAIGDGV--RVSIEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPDFLVAEDFEGGRVYVDKTLTRELLAEGLAREFVRRIQEMRKRLDLDVNDRIVVTIETT 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPD-----GAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDNRELLQENLDYIMRETRAIEVRFEEAKGYVVEWPEVQAKIGIEK 1064
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                                                   Conservative
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                                          Score 123.5; Db 2,
Pred. No. 0.0011;
                                                   14;
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; Pred. No. 0.00057;
17; Mismatches 44
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                                                                                                                                                                                                                                                                                            genome sequence:
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                                                                                Length
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Kushida,
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                   934
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A;Description: EC 6.1.1.5 [validated, MUID:91244836] C;Superfamily: isoleucine-tRNA ligase C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein
                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1045 <JEN>
A;Cross-references: UNIPARC:UPI000016FBA0; GB:M59245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoleucine-tRNA ligase (EC 6.1.1.5) [validated] - Methanobacterium thermoautotrophicum N;Alternate names: isoleucyl-tRNA synthetase C;Species: Methanobacterium thermoautotrophicum C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A40398
R;Jenal, U.; Rechsteiner, T.; Tan,
J. Biol. Chem. 266, 10570-10577, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA
A;Residues: 1-1044 <MTH>
A;Cross-references: UNIPROT:027428; UNIPARC:UPI0000165BE
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan; ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7115-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H:
                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A40398;
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Isoleucyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: MTH1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: isoleucine-tRNA ligase; protein biosynthesis; Reywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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Best Local :
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                                                                                                              20.4%; Score 110; DB 1; Length 1045; 28.1%; Pred. No. 0.021;
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                                                                                      Pred. No. 0.0:
0; Mismatches
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Pred. No. 0.017;
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A; Molecule type: DNA
A; Residues: 1-986 <KUR>
A; Cross-references: UNIP)
C; Genetics:
A; Gene: ileS
C; Superfamily: isoleucine
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F71565
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell. Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia traceleference number: A71570; MUID:99000809; PMID:9784136
A;Accession: F71565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable isoleucine-tRNA ligase (BC 6.1.1.5) - Chlamydia trachomatis (serotype C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: F71565
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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A;Accession: E90220
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Best Local S
Matches 27
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                                              948 FIKSETRASNIILGEAKGDITMDWDIEGESYIIGIKKS 985
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                                                                                                                                                                                 GLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRD
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28.3%;
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Pred. No. 0.062;
.8; Mismatches 48
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                                                                      RESULT 15
F81719
isoleucyl-tRNA synthetase TC0288 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hon Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1064 <LYN>
A;Residues: 1-1064 <LYN>
A;Cross-references: UNIPROT:013651; UNIPARC:UPI00001364E3; EMBL:AL022072; PIDN:CAA17821
A;Experimental source: strain 972h-; cosmid c8D2
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C; Superfamily:
                                                                                                                                                                                                                                         A;Gene: ileS
C;Superfamily: isoleucine-tRNA ligase
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A; Residues: 1-1070 <STO>
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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thauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.
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                                   74 RDLIAGEILATDFEFADLADG
                                                                                                               15 AGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAER-EDWARTH
                                                                                                                                                           27;
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BPLITAETRAR - - ELGEVEDG
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33.3%; Pred. No. 0.17;
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30.4%; Pred. No. 0.14;
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C;Accession: F81719
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81719
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Result
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      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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Q9p919
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Q9p819
Q4nb83
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InterPro; IPR002300; tRNA-synt_1.

InterPro; IPR002301; tRNA-synt_1!e.

InterPro; IPR002301; tRNA-synt_1!e.

Pfam; PF00133; tRNA-synt_1; 1.

PRINTS; PR00984; TRNASYNTHILE.

TIGRPAMS; TIGR00392; iles; 1.

PROSTER; PS00178; AA TRNA_LIGASE I; 1.

PROSTITS; PS00178; AA TRNA_LIGASE I; 1.

Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Aminoacyl-tRNA synthetase; ATP-binding; Protein biosynthesis; Zimerro.

Metal-binding; Nucleotide-binding; region.
                                                                                                                                                                                                                                                                                                                                  STRAIN=AP2122/97;
MEDLINB=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
MEDLINB=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.
Harris B., Atkin R., Doggett J., Mayes R., Keating I., Wheeler P.I.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTVEZO MYCBO PRELIMINARY; PRT; 1041 AA QTVEZO; 10-0CT-2003 (TrEMBLrel. 25, Created) 10-0CT-2003 (TrEMBLrel. 25, Last sequence up 61-MAR-2004 (TrEMBLrel. 26, Last annotation 1 isoleucyl-trna synthetase iles (EC 6.1.1.5). Name=iles; OrderedLocusNames=Mb1563;
                        InterPro; IPR002300; tRNA-synt 1a.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002301; tRNA-synt 1le.
Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR00994; TRNASYNTHILE.
TIGRPAMS; TIGR00392; ileS; 1.
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EMBL; AE000516; AAK4
PIR; E70760; E70760.
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                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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MYCBO
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IP; P56690; IILB.
GO:0005524; F:ATP binding; IEA.
GO:0004822; F:ASOleucine-tRNA ligase activity; IEA.
GO:0016874; F:ligase activity; IEA.
GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
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        PS00178; AA
TIGR00392; ileS; 1.
PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
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AAK45854.1;
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22 ATP (By similar
117340 MW; B5023822848
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GO; GO:0005824; F:ATP binding; IEA.
GO; GO:0016874; F:Isigase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
R GO; GO:0006428; P:isoleucyl-trNA aminoacylation; IEA.
R GO; GO:0006412; P:protein biosynthesis; IEA.
R InterPro; IPR002300; trNA-synt La.
R InterPro; IPR002301; trNA-synt I.
R InterPro; IPR002301; trNA-synt I.
R Pfam; PR00133; trNA-synt I; 1.
R Pfam; PR00133; trNA-synt I; 1.
R PINTYS; PR00094; TRNA-SYNTHILE.
R TIGREAMS; TIGR00392; ileS; 1.
R PROSITE; PS00178; AA TRNA-LIGASE I; UNKNOWN 1.
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                               SYI MYCLE
Q9X7E5;
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13-SEP-2005
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05-JUL-2004
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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SEQUENCE 1041 AA; 117313 MW; 4513382E3248D3AB CRC64;
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(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 48, Last annotation updat
""" avnthetase (EC 6.1.1.5) (Isc
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; Pred. No. 2.3e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q., Amonsin A., Alt D., Kapur V.; EMBL/GenBank/DDBJ databases.
-; Genomic_DNA.
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Best Local S
Matches 86
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TIGRPAMG; TIGR00392; iles; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-trNA synthetase; ATP-binding; Complete proteome; Ligase; Metal-binding; Nucleotide-binding; Protein biosynthesis; Zinc.
Metal-binding; Nucleotide-binding; Protein biosynthesis; Zinc.
MOTIF 59 69 "KMSKS" region.
MOTIF 637 641 "KMSKS" region.
MOTIF 637 641 "KMSKS" region.
BINDING 640 640 ATP (By similarity).
BINDING 640 640 ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leproma; ML1195; ... IRNA-synt_la.
InterPro; IPR002300; tRNA-synt_l.
InterPro; IPR002301; tRNA-synt_l.
InterPro; IPR002301; tRNA-synt_le.
Pfam; PP00133; tRNA-synt_l; 1.
PRINTS; PR00984; TRNASYNTHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL049478; CAB39575.1; -;
EMBL; AL583921; CAC31576.1; -;
PIR; E87058; E87058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
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MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
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Bacteria; Actinobacteridae;
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Mycobacterium
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COPACTOR: Binds 1 zinc ion per subunit (By similarity SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                 1012
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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80.4%;
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Created)
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Pred. No. 1
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Genomic_DNA.
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1 Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).

1 Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).

1 C -! CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP

2 diphosphate + L-isoleucyl-tRNA(Ile).

2 -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

2 EMBL; AP006618; BAD56622.1; -; Genomic_DNA.

3 GO; GO:0005524; F:ATP binding; IEA.

4 GO; GO:0005524; F:ATP binding; IEA.

5 GO; GO:0006822; F:isoleucine-tRNA ligase activity; IEA.

5 GO; GO:0016874; F:ligase activity; IEA.

5 GO; GO:0016874; F:isoleucine-tRNA iminoacylation; IEA.

5 GO; GO:006428; P:isoleucyl-tRNA aminoacylation; IEA.

6 GO; GO:0006412; P:protein biosynthesis; IEA.

6 GO; GO:0006412; P:protein biosynthesis; IEA.

7 GO; GO:0013; tRNA-synt 1.

8 InterPro; IPR00230; tRNA-synt 1.

8 R InterPro; IPR00230; tRNA-synt 1.

8 R PRINTS; PR00984; TRNASYNTHILE.

8 PRINTS; PR00984; TRNASYNTHILE.
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TIGRPAMS; TIGRO0392; iles; 1.
PROSITE; PSO0178; AA TRNA LIGASE I; UNKNOWN 1.
PROSITE; PSO0178; AA TRNA SYNTHETABE; Complete proteome;
ATP-binding; Aminoacyl-trNa synthetase; Complete proteome;
Metal-binding; Nucleotide-binding; Protein biosynthesis; Z;
Genome
EMBL; E
                                                                                                                                                                                                                                                  STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINS=22723752; PubMed=12840036; DOI=10.1101/gr.1285603
Nishio Y., Nakamura Y., Kawarzabayasi Y., Usuda Y., Kimura
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Putative isoleucyl-ENNA synthetase.
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                                                                                                                                                                                                          Sugimoto S., Matsui
Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=CE2043
                                                                                   efficiens.";
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                                                                                                                                                              Comparative
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Ishikawa J., Yamashita A., Mikami Y., Hoshino
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Corynebacterineae; Nocardi
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BA000035; BAC18853.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                           complete genome sequence analysis of the amino responsible for the thermostability of Coryneba
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Pred. No. 3.5
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InterPro; IPR001412; tRNA-synt 1.
InterPro; IPR001412; tRNA-synt 1!e.
InterPro; IPR002301; tRNA-synt 1; 1.
Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR00984; TRNASYNTHILE.
TIGREAMs; TIGR00392; 11eS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; UN Aminoacyl-tRNA synthetase; Complete pr SEQUENCE 1103 AA; 123718 MW; B9129
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SEQUENCE
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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11-SEP-2005 (TREMBLR)
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR931997; CAI36922.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen Corynebacterium jeikeium K411, a Lipid-Requiring Bacterium of the Human Skin Flora.";
J. Bacteriol. 187:4671-4682 (2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005; Tauch A., Kaiser O., Hain T., Goesman A., Weisshaar B., Pauch A., Kaiser A., Bekel T., Bischoff N., Brune I., Chakraborty Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoever P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium jeikeium (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Q4JW85;
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GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
1040
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54.5%;
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Best Local 9
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Q6NGD7_CORDI
Q6NGD7;
Q6NGD7;
05-JUL-2004
                                                                                                                                                                                                QÜNNPO CORGL PRELIMINARY; PRT; 1054 AA.
QBUNPO; Q6M3S6;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
1soleucyl-tRNA synthetase (EC 6.1.1.5) (ISOLEUCINB-TRNA LIGASE-LIKE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G., Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D. De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T., Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch B., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J.; "The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129."; Nucleic Acids Res. 31:5516-6523(2003).

EMBL; BX248358; CAE50114.1; -; Genomic_DNA.
                                                                                                                 Name=ileS; OrderedLocusNames=Cgl2148, cg2359;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; EXUUJOS, AMERICA, 1.
TIGREAMS; TIGRO0392; ileS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; UNKNOWN 1.
AMINOACY1-tRNA SYNTHETASE; COMPLETE PROTEOME; Liga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002301; tRNA-synt ile.
Pfam; PF00133; tRNA-synt 1; 1.
PRINTS; PR00984; TRNASYNTHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P56690; IJZS.
GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006428; F:soleucyl-tRNA aminoacylation; IEA.
GO; GO:0006412; F:protein biosynthesis; IEA.
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05-UIL-2004 (TYEMBLrel. 27, Last sequence update)
05-UIL-2004 (TYEMBLrel. 27, Last annotation update)
Isoleucyl-tRNA synthetase (BC 6.1.1.5).
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                                             NCBI_TaxID=1718;
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MEDLINE=22965443; PubMed=14602910;
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                                                                                     Corynebacterineae;
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   SEQUENCE
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                                                                                        Corynebacteriaceae;
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Pred. No. 2.2
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                                                                                           Corynebacterium
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RESULT Q4H737 ID Q4H737 ID Q4H737 ID Q4H737 ID Q4H 
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GO; GO:0005524; F:ATP binding; TEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0004822; F:isoleucyl-tRNA aminoacylation; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016876; P:isoleucyl-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_1ie.
R InterPro; IPR001412; tRNA-synt_1ie.
R InterPro; IPR002301; tRNA-synt_1ie.
R Pfam; PF00133; tRNA-synt_1; 1.
R Pfam; PF00133; tRNA-synt_1ii.
R RRINTS; PR000944; TRNASYNTHILE.
R RINTS; PR000944; TRNASYNTHILE.
R RINTS; PR000178; AA TRNA_LIGASE I; UNKNOWN_1.
R PROSITE; PS00178; AA TRNA_LIGASE I; UNKNOWN_1.
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Matches 59
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Nakagawa S.;
"Complete genomic seq
Submitted (MAY-2002)
                                                                                                                                                                             Q4H737;
13-SEP-2005 (TrEMBLrel. 31, Creat
13-SEP-2005 (TrEMBLrel. 31, Last
13-SEP-2005 (TrEMBLR), Last
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PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Ralinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe
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       NUCLEOTIDE
STRAIN=DSM
                                                                                                                                                   "Sequencing
DSM 11300.";
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J. Biotechnol. 104:5-25(2003).
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"The complete Corynebacterium glutamicum ATCC 13032 genome sequence
                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=319795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deinococcus geothermalis DSM 11300.
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                                                                                                                 (MAY-2005)
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
                                         SEQUENCE
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CAF20488.1; -;
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)2) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                 the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 266.5;
Pred. No. 2.
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Genomic_DNA.
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C3333C86C8554B1F CRC64;
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ches 33;
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                                                                                                                                                                                     Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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RESULT 11
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Proc. Natl. Acad. Sci. U.S.A. 99:14427-14427(2002).

EMBL, AE8014295; AAN25560.1; -; Genomic_DNA.

RMBL, RE014295; AAN25560.1; -; Genomic_DNA.

RSSP; P56690; IILE.

GO; GO:0004822; F:isoleucine-tRNA ligase activity; IE.

GO; GO:0004822; F:isoleucyl-tRNA aminoacylation; IEA.

GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.

InterPro; IPR002300; tRNA-synt_1a.

InterPro; IPR001412; tRNA-synt_1i.

InterPro; IPR002301; tRNA-synt_1i.

Pfam; PF00133; tRNA-synt_1; 1.

PRINTS; PR00984; TRNASYNTHILE.
                                                                                                                  Matches
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QBG312_E
                                                                                                                                                                         Schell M.A., Karmirantzou M., Snel B., Vilanova D., F
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley
Pridmore R.D., Arigoni F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE STRAIN=NCC 2705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=ileS; OrderedLocusNames=BL1777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22294977; PubMed=12381787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria;
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EMBL; AAHE01000010; I
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Larimer F., Land M.;
"Annotation of the draft genome assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                             The genome sequence of Bifidobacterium longum reflects
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DWARTHRDLIAGBILATDFBFADLADGVAIG
                                                  SAALPTG-GFVILDTALDADLLAEGYARDVIRSVQDARKAADLDIADRISLVLTVPAVDV
                                                                     TAALPDGAGLVVLDGTVTABLEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAERE
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nilarity 41.0%;
Conservative 10
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                                                                                                                 Conservative
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                                                                                                                                  34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122774 MW;
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                                                                                                                      Score 185; "" | No. 5.7e-08;
                                                                                                                 Pred. No. 5.70
); Mismatches
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NUCLEOTIDE SEQUENCE.

STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Metchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
                                                                                                                                                                                   OBTN62;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
Isoleucyl-tRNA synthetase.
Name=ileS; OrderedLocusNames=MA2431;
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62 METAC
QBTN62_M
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:00004822; F:isoleucyl-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt 1a.
InterPro; IPR002300; tRNA-synt 1ie.
Pfam; PF00133; tRNA-synt 1; 1.
PFINTS; PR00984; TRNA-SYNTHILE.
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AMINOACY1-tRNA synthetase; Complete proteome.
SEQUENCE 1078 AA; 120272 MW; DF007ED70528F70F CRC64;
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01-MAY-2000
                                                                                                                  Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanomicrobia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001980; AAF10907.1; -; PIR; E75407; E75407.
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   NUCLEOTIDE SEQUENCE
                                                                                              Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 286:1571-1577(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMS
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RESULT 14
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SEQUENCE
                                                                                                      MEDLINE=20225863; PubMed=10762266;
DOI=10.1128/JB.182.9.2611-2618.2000;
Boccazzi P., Zhang J.K., Metcalf W.W.;
"Generation of dominant selectable markers for pseudomonic acid by cloning and mutagenesis of archaeon Methanosarcina barkeri fusaro.";
J. Bacteriol. 182:2611-2618(2000).
J. Bacteriol. 182:2611-2618(2000).
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PROSITE; F
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InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002301; tRNA-synt_1le.
Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00984; TRNASYNTHILE.
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HSSP; P56690; IIIE.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
                   HSSP; P56690; 1ILE.
GO; GO:0005524; F:A
GO; GO:0004822; F:i
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                                                                                                                                                                                                                                                                                                                                                           STRAIN=Fusaro;
                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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AE010935; AAM05817.1;
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PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
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                      F:ATP binding; IE
F:isoleucine-tRNA
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FRNA ligase
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GO; GO:0006428; P:isoleucyl-trnA aminoacylation; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR002300; tRNA-synt la.
InterPro; IPR002311; tRNA-synt lie.
InterPro; IPR002301; tRNA-synt l.
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Refam; PF0013; tRNA-Synt l.
Refam; PF0013; TRNA-SYNTHILE.
INTERPAMS; TIGR00392; ileS; l.
RPROSITE; PS00178; AA TRNA-LIGASE_I; UNKNOWN_1.
REFOSITE; PS00178; AA TRNA-LIGASE_I; UNKNOWN_1.
REFOSITE; PS00178; AA TRNA-LIGASE_I; UNKNOWN_1.
REFOSITE; PS00178; AA TRNA-LIGASE_I; UNKNOWN_1.
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GO; GO:0004822; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006428; P:lsoleucyl-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt la.
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STRAIN=GOe1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

STRAIN=GOe1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINEs-2120827; PubMed=12125824;

Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel

Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsall

Fritz H.-J., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fritz H.-J., Gottschalk G.;
"The genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
EMBL; AB013550; AAM32663.1; -; Genomic_DNA.
                                                                                                                      TIGRPAMS; TIGR00392; iles; 1.

PROSITS; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.

COMplete proteome.

SEQUENCE 1058 AA; 120410 MW; 8BASCODEOFDCE.
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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Methanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
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Q8PSV9;
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40.6%; Pred. No. 2.3e
tive 15; Mismatches
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2.3e-05;
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Search completed: April 14, 2006, 17:32:32 Job time : 41.8484 secs

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/cgm2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-98-3-110-3245
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Biocceleration
                               Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1,264, A
Sequence 121, Appl
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 6, Appli
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Sequence
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
68.5	68.5	69	69	70	70	70.5	70.5	71	71	71.5	71.5	72.5	73.5	73.5	74.5	74.5	76
12.7	12.7	12.8	12.8	13.0	13.0	13.1	13.1	13.2	13.2	13.3	13.3	13.5	13.7	13.7	13.8	13.8	14.1
5588	1044	530	406	966	462	1481	507	809	460	448	448	311	463	396	327	327	1266
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US-09-036-987A-6	US-09-252-991A-24495	US-09-949-016-10017	US-09-107-532A-5673	US-09-902-540-14084	US-09-252-991A-19002	US-09-231-899-70	US-09-605-703B-2522	US-09-252-991A-26210	US-09-949-016-8029	US-10-650-369-22	US-09-878-766A-22	US-09-252-991A-23527	US-09-902-540-16722	US-09-712-363-231	US-08-460-907B-9	US-08-463-092B-9	US-09-357-251-32
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
6, Appli	24495, A	10017, A	5673, Ap	14084, A	19002, A	70, Appl	2522, Ap	26210, A	8029, Ap	22, Appl	22, Appl	23527, A	16722, A	231, App	9, Appli	9, Appli	32, Appl

## ALIGNMENTS

RESULT 1 US-09-050-739-4

4, Application o. 6641814

US/09050739

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, FACET Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RELDINCH, Karin
APPLICANT: RELDINCH, Karin
APPLICANT: FLORIO, Walter
ITILE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/070,488
EARLIER APPLICATION NUMBER: 60/070,488
EARLIER APPLICATION DATE: 1998-01-05
NUMBER: OF SEQ ID NOS: 173
COPTWARE: DETERMINED DATE: 1998-01-05
NUMBER: OF SEQ ID NOS: 173
COPTWARE: DETERMINED DATE: 1998-01-05
RESULT 2
US-08-452-083-2
; Sequence 2, Application US/08452083
; Patent No. 5756327
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; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-4
                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 538; DB 2; Best Local Similarity 100.0%; Pred. No. 6.1e-59; Matches 108; Conservative 0; Mismatches 0;
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                                                                                                                                                                                         SVPABREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT 108
                                                                                                                                                             SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
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US-08-898-978-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                       Sequence 2,
Patent No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,765
FILING DATE: 13-SEP-1994
ATTORNEY/ACENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP194-08B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                       APPLICANT: Reichard, Raymond W.
APPLICANT: Brown, James R.
APPLICANT: Lawlor, Elizabeth J.
TITLE OF INVENTION: No. 6001602el ileS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1%-
STREET: Lexington
CITY: Lexington
TMATE: Massachusetts
                 COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1045 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sassanfar, Mandana
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISOLEUCYL-trna
TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASS
                                                                                                                 STREET: 997 Lenox Dr. CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1004 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGD 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGD 99
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IBM Compatible
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Pred. No. 5.7e-51;
1; Mismatches 1; Indels
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US-09-372-858-2
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                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Chlamydia trachomatis US-09-372-858-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRABTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1041
                                                                                                                                                               Matches
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09372858 Patent No. 6361970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.5%; Score 105; DB 2; Length 1041; Best Local Similarity 28.3%; Pred. No. 0.00074; Matches 26; Conservative 18; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reichard, Raymond
APPLICANT: Brown, James
APPLICANT: Lawlor, Blizabeth
TITLE OF INVENTION: NOVEL ileS
FILE REFERENCE: GM10051-D1
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/372,858
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 08/898,978
PRIOR FILING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                             Match 19.5%; Score 105; DB 2; Length 1041; Local Similarity 28.3%; Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 609-520-3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       991 PVIVQEAFALHKEYICEETLTTSVSVIDYKEG 1022
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991 PVIVQEAFALHKEYICEETLTTSVSVIDYKEG 1022
                                                                              931 ASAEGFVARSSASFVAVLDCQLTEPLIMEGIARELVNKINTMRRNRKLHVSDRIAIRLHA 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 PABREDWARTHRDLIAGEILATDFEFADLADG 94
                                                                                                                    3 ADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSV 62
                                                                                                                                                               26;
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                                 PAEREDWARTHRDLIAGBILATDFEFADLADG 94
                                                                                                                                                            Conservative
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                                                                                                                                                               Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Kaufmann, Chiio.
APPLICANT: Kaufmann, Chiio.
APPLICANT: Gallant, Paul L.
APPLICANT: Kranz, Janice B.
Frank, Fariba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 617-861-9540
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,026
FILING DATE:
                                                                                                                                                                                      APPLICANT: Houman, Fariba
TITLE OF INVENTION: Candida Isoleucyl-tRNA Synthetase
TITLE OF INVENTION: Comprising Same
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Houman, Fariba
TITLE OF INVENTION: Candit
TITLE OF INVENTION: Compri
                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
STREET: 1 -- STREET: Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         985 LIILDVNLHPELESEGLARELINRIQRLRKKAGLNTTDDVQVQYRVVKDTIDLPKVIKD 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 LVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDWARTHRD 75
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    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08742026
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Kaufmann, Christoph
Gallant, Paul L.
Kranz, Janice B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sassanfar, Mandana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.4%; Score 99; DB 1; 35.6%; Pred. No. 0.0044; ative 14; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida Isoleucyl-tRNA Synthetase
Proteins, Nucleic Acids and Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comprising Same
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                                                                                                                                                                                                                                                  ; ORGANISM: Saccharomyces cerevisiae US-09-357-251-31
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                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                             SEQ ID NO 31
LENGTH: 1072
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Best Local Similarity 35.6%;
Matches 21; Conservative 1
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-trnA Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/093,530
EARLIER FILING DATE: July 21, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,026
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                             TYPE: PRT
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NAME: BROOK, DAVId E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   Local
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1031 FDMLS-KTCRSDIAKYDGSKTDPIGD 1055
                                                                                971 LIIMDTNIYSELKSEGLARELVNRIQKLRKKCGLEATDDVLVEYELVKDTIDFEAIVKEH 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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                                                                                                                17 LVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRVVMSVPAEREDW---ARTH 73
                                      74 RDLIAGEILATDFEFADLADGVAIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LVVLDGTVTABLEAEGWAKDRIRBLQBLRKSTGLDVSDRIRVVMSVPAEREDWARTHRD 75
                                                                                                                                                                                   Similarity
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617-861-9540
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                                                                                                                                                              17.8%; Score 96; DB 2; Length 1072; 26.7%; Pred. No. 0.01; tive 25; Mismatches 34; Indels
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RESULT 8 US-09-902-540-14264

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FILE REFERENCE: PATHO0-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3245

LENGTH: 209
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; Sequence 43, Application US/08415593
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US-09-583-110-3245
                          RESULT 10
US-08-415-593-43
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APPLICANT: Lynn Dov
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Best Local Similarity 34.2%;
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LENGTH: 1232
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(11549)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae -09-583-110-3245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                             -- DGEKTGNYILAGEIFTTNEKGISQISYADYAIGL 190
                                                                                                                                                                                                                                GAGSLYIDETKTTRLLDTSDFPEEFKSLAKDQADELDLLRTKNNLNWTFVSPAVDFIP--
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                             14.5%; Score 78; DB 2
30.2%; Pred. No. 0.17;
tive 13; Mismatches
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Patent No. 5912140 5776726
                                                                                GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS A
TITLE OF INVENTION: THEIR USE IN DIAGNO
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Recombinant Pneumoycstis Aminoacyl trna
TITLE OF INVENTION: Synthetase Genes, Tester Strains and Ass
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                   STREET:
CITY: N
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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COUNTRY:
                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                874 IILDTKIYPELKTEYLVREVINRVQRLRKKVGLQVIDDIRMEYVIIDDSIGLEDAISQHQ 933
                                                                                                                                                                                                                                                                                                                                   934 ILLT-KILRRPLE 945
                                                                                                                                                                                                                                                                                                                                                                75 DLIAGEILATDFE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                  18 VVLDGTVTAELEAEGWAKDRIRELOELRKSTGLDVSDRIR----VVMSVPAEREDWARTHR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l: 978 amino acids
amino acid
XGY: linear
                                   NEW YORK
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                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
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   USA
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Politis-Virk, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 78; DB ilarity 32.9%; Pred. No. 1.5; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quinn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whoriskey, Susan K.
                                                                   MORGAN & FINNEGAN, L.L.P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435
                                                                                                    THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
126
                                                                                                                                                         MELANOMA ANTIGENS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/415,593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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Best Local
               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
PILING DATE: 22-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
PILLING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
PILLING DATE: 22-APR-1994
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
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NAME: CAROL M. GRUPPI
REGISTRATION UNMER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 14.2%; Score 76.5; Di
Local Similarity 25.2%; Pred. No. 1.3;
hes 30; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                   COUNTRY: U
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TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                              NEW YORK
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; MOLECULE TYPE:
US-08-231-565A-27
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US-08-231-565A-27
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Patent No. 5874560
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                                                                                                                       TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 751-684
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/
PILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 661
TYPB: amino acid
STRANDEDNESS: Unkr
TOPOLOGY: Unknown
MOLECULE TYPB: Prote
                                                                                                                                                           REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
US/08/231,565A
                                                                                                            SEQUENCE CHARACTERISTICS
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ADDRESSEE: MORGAN & FINNEGAN
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TITLE OF INVENTION:
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REGISTRACIO NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: N
COUNTRY:
                                             TYPE: amino of STRANDEDNESS:
                                 TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                                        LENGTH:
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US-09-007-961-27
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Best Local S
Matches 30
                                                                                                                                                                       Query Match
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LENGTH: 661
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Patent No. 5994523
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-41
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: KAWAKAMI,
APPLICANT: STEVEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                        TOPOLOGY: Unknown MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                          TOPOLOGY: Unl
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STATE: NEW YORK
                                                                                                                                                       Local
                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                    30;
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                                                                                                5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIREL------QELRKST 48
                                                                                                                                                   h 14.2%; Score 76.5; DB 1; Length 661; Similarity 25.2%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                           G--LDVSDRIRVV-MSVPAE----REDWARTHRDLIAGEILATDFEFADLADGVAIGDG 100
GPLLDGTATLRLVKRQVPLDCVLYRYGSFSVTLDIVQG-----IESABILQAVPSGEG
                                                                   PEATGMTPAEVSIVVLSGTTAÄQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSL 454
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                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                           Unknown
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THERR USE IN DIAGNOSTIC AND THERAPEUTIC
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25.2%; Pred. No. 1.
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US-09-267-439-27
Search completed: April 14, 2006, 17:38:00 Job time : 10.9865 secs
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Matches
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                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: Unkr
TOPOLOGY: Unknown
MOLECULE TYPE: Prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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REFERENCE/DOCKST NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION:
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ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
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                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 751-6849
                                                                                                                                                                                                                    Match 14.2%; Score 76.5; D. Local Similarity 25.2%; Pred. No. 1.3;
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STATE: NEW YORK
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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SUMMARIBS
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RESULT 2 US-09-804-980-4

Sequence 4, Application US/09804980 Publication No. US20030147897A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-620-246-4
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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
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Best Local Similarity
                                                         SOPTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PLORIO, Walter
TITLE OF INVENTION: DUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DUCLEIC ACIDS FRAGMENTS
TILE OF INVENTION: DUCLEIC ACIDS FRAGMENTS
FILE REFERENCE: 670001-2002.1A
CURRENT FAPPLICATION NUMBER: US/1620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR PELICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: OBTTINGER, Tho
                                                                                              PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                  PRIOR APPLICATION NUMBER: 1281/98 PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 0376/97 PRIOR FILING DATE: 1997-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 1277/97
                    LENGTH: 108
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                              APPLICATION NUMBER: 09/415,884 FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/044,624
                                                                                                                                                            FILING DATE: 1999-01-21
                                                                                                                                                                              APPLICATION NUMBER: 60/116,673
                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/791,171 FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 10/138,473
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/070,488
                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-04-18
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RASMUSSEN, Peter Birk
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WELDINGH, Karin
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                                                                                                                                                             ; ORGANISM: Mycobacterium bovis
US-10-282-122A-62617
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62617
                                                                              Matches
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                                                                                                  Query Match
Best Local Similarity
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                    TYPE: PRT
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
934 VAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKORIRELQELRKSTGLDVSDRIRVVM 993
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: Zamudio, Carlos
: Malone, Cheryl
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Zyskind, Judith
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Forsyth, R.
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Trawick, John
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RESULT 6

US-10-222-122A-61984

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; Publication No. US20040029129A1

; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-07
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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Best Local Similarity
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SEQ ID NO 64571
LENGTH: 1041
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
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Trawick, John
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APPLICANT: Wang, I
APPLICANT: Zamudd.
APPLICANT: Malon
APPLICANT: Hasell
APPLICANT: Ohlsel
APPLICANT: Zyskin
APPLICANT: Wall,

Haselbeck, Robert

Zamudio, Carlo Malone, Cheryl

Liangeu io, Carlos

Ohlsen, Kari Zyskind, Judith Wall, Daniel

APPLICANT:

APPLICANT:

Trawick, John Carr, Grant Yamamoto, Robert

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INFORMATION:

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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-23
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Sequence 63826, Application US/10282122A
Publication No. US20040029129A1
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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TYPE: PRT
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
                                                                                                                        1014 SVPAGRAEWAHTHRDLIAGEILATRFEFGEPADPVAIGDGVRVSISK 1060
                                                                                                                                                                                                       954 VAADPEFTAALPNGAGLVVLDGTVTPELEAEGWAKDRIRELQELRKSTGLDVSDRISVVM
                                                                                                                                               61 SVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEK 107
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Zamudio, Carlos
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Yamamoto, Robert
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Malone, Cheryl
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Pred. No. 1.5e-41;
4; Mismatches 11
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                                                                                                                                                                                                                                                                                                                    Sequence 54011, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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SEQ ID NO 63826
LENGTH: 1059
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Best Local Similarity
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
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PRIOR FILING DATE: 2000-03-21
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-02-16
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
                                                                                                                                              Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                       Carr,
                                                                                                                                                                                                        Trawick, John
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 5852
LENGTH: 1054
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                                                               ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5852
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SEQ ID NO 54011
LENGTH: 1052
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Publication No. US20020197605A1
                      Query Match
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APPLICANT: MIZOGUCHI, HIROSE
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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PRIOR APPLICATION NUMBER: 60/267,636
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                                                                                                       TYPE: PRT
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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49.5%;
53.6%;
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  Score 266.5; DB 3; Pred. No. 7.5e-21;
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                        Length 1054;
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Best Local Similarity

Matches

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19;

Gaps

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RESULT 10
US-10-494-541-76
                                                                             APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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SEQ ID NO 76
LENGTH: 1063
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Best Local Similarity
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13657
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13657, Application US/10156761 Publication No. US20030119018A1
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CURRENT FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/EP02/12138
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: DE 10154180
PRIOR FILING DATE: 2001-11-05
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APPLICANT: Pompejus, Mai
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Haberhauer, Gregor
                                                                                                                                                                                                                                                                              IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pompejus, Markus
Schroder, Hartwig
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Pred. No. 7.6e-21;
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US-10-282-122A-76512
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                                                                                                                               ; ORGANISM: Treponema pallidum
US-10-282-122A-76512
                                           Matches
                                                                                                                                                                                                                     SEQ ID NO 76512
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                                                                                 Query Match
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Best Local Similarity
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23
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APPLICANT:
APPLICANT:
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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TITLE OF INVENTION: Identification of Essential Genes
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                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-02-16
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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  6 ESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRI--RVVMS--
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Zyskind, Jud
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                                                               24.5%; Score 132; DB 4; 37.2%; Pred. No. 1.4e-05;
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t; Pred. No. 2.3e-07;
11; Mismatches 31;
                                           16; Mismatches
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                                           43; Indels
                                                                                 Length 1091;
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US-10-282-122A-51998
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RESULT 14
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 51998
LENGTH: 1035
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Best Local (
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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FILING DATE: 2000-11-27
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                                                               1001 KKETLATDIIYSENKEAAIYNINGEELNVFVKK 1033
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
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Trawick, John
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US-10-503-135-125

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GENERAL INFORMATION:

APPLICANT: Terry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Charles, Boone

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOPTWARE: PatentIn version 3.1

SEQ ID NO 7198

LENGTH: 1088

TYPE: PRT

ORGANISM: Candida albicans

US-10-032-585-7198
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Search completed: April 14, Job time: 38.999 secs
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LENGTH: 1036
TYPE: PRT
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                                                                                                                                                                                                                         Query Match 18.2%; Score 98; DB 4; Length 1088 Best Local Similarity 35.6%; Pred. No. 0.099; Matches 21; Conservative 14; Mismatches 24; Indels
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Publication No. US20050152926A1
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CURRENT APPLICATION NUMBER: US/10/503,135
CURRENT FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: PCT/IB03/01161
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: GB-0203403.1
PRIOR FILING DATE: 2002-03-13
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APPLICANT: GRANDI Guido
TITLE OF INVENTION: CYTOTOXIC T-CELL EPITOPES FROM CHLAMYDIA
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SOFTWARE: SegWin99, version 1.02
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seq length: 2000000000
Published Applications AA New:*

1: /SIDSS/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT NEW PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO3 NEW PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO3 NEW PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO1 NEW PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO1 NEW PUB.pep:*
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(without alignments)
991.565 Million cell updates/sec
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                                                                                                                                                                                                                                                                summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

0	י ר	24	23	22	21	20	19	18	17	16	15	14	13	12	Ľ	10	9	8	7	6	v	4	w	N	ч	No.
		64.5	64.5		64.5	65	65	66	66	66.5	66.5	67	70.5	70.5	70.5	71.5	71.5	72.5		76.5	76.5	76.5	76.5	112.5	134.5	Score
				12.0	12.0		12.1	12.3	12.3		12.4					13.3		13.5			14.2	14.2		20.9	25.0	Match
509	) i	258	239	239	239	587	552	963	859	506	239	328	2910	2910	2910	159	159	435	485	662	661	199	660	1080	1149	Length
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02-11-100-730-10140		US-11-055-822-390		US-11-165-211-37	US-10-518-019A-9	US-11-096-568A-10866	US-11-201-916-22	US-11-188-298-15124	US-10-467-657-6084	US-11-188-298-1725	-11-188	US-11-188-298-8241	US-11-087-085-2	US-11-087-084-2	US-11-087-100-2	US-11-055-822-566	US-11-055-822-564	US-11-188-298-8860	US-11-188-298-6318	US-11-090-439-9	US-11-119-502-1	US-11-155-288-13	US-11-033-039-385	US-10-506-454-899	US-11-079-463-5703	ID
sequence rorso, A		Sequence 390. App	Sequence 47, Appl	37,	Sequence 9, Appli	108	Sequence 22, Appl	15124,	Sequence 6084, Ap	1725,	Sequence 19411, A	82	'n	,2	'n	566	Sequence 564, App	Sequence 8860, Ap	631	9,	Sequence 1, Appli	Sequence 13, Appl	385	Sequence 899, App	Sequence 5703, Ap	Description

64.5 12.0 567 6 US-10-330-773-556 64.5 12.0 567 6 US-10-330-773-558 64.1 12.0 37.7 VS-11-188-298-121978 64.1 11.9 37.6 7 US-11-188-298-14205 64.1 11.9 37.6 7 US-11-188-298-14377 64.1 11.9 48.5 6 US-10-724-598-43 64.1 11.9 48.5 6 US-10-506-454-1412 63.5 11.8 23.9 7 US-11-165-226-48 63.5 11.8 23.9 7 US-11-165-226-48 63.5 11.8 23.9 7 US-11-165-226-48 63.5 11.8 23.9 7 US-11-188-298-15773 63.5 11.8 50.6 7 US-11-188-298-4288 63.5 11.8 50.6 7 US-11-188-298-4288 63.5 11.8 50.6 7 US-11-188-298-4288 63.5 11.8 50.6 7 US-11-188-298-15173 63.5 11.8 50.6 7 US-11-188-298-15111 63.5 11.8 50.6 7 US-11-188-298-1513 63.5 11.8 50.6 7 US-11-188-298-1516	45	44	43	42	41	40	39	38	37	36	35	34 4	ω u	32	31	30	29	28	27	6
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	29, Appl	166, App	6886, Ap	6, Appli	11111, A	8239, Ap	4385, Ap	4288, Ap	15773, A	48, Appl	38, Appl	2690, Ap	1412, Ap	43, Appl	14377, A	14205, A	21978, A	•	556, App	•

### ALIGNMENTS

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; Sequence 5703, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    RESULT 2
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US-11-079-463-5703
Sequence 899, Application US/10506454
Publication No. US20060068386A1
GENERAL INFORMATION:
APPLICANT: Slesarev, Alexi I
APPLICANT: Mezhevaya, Katja V
APPLICANT: Polushin, Nikolai N
APPLICANT: Shcherbinina, Olga V
APPLICANT: Shcherbinina, Olga V
APPLICANT: Shcherbinina, Olga V
APPLICANT: Shcherbinina, Sergei N
APPLICANT: Kozyavkin, Sergei A
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SEQ ID NO 5703
LENGTH: 1149
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CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOO-03DIV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 25.0%; Score 134.5; DB 7; I Similarity 28.7%; Pred. No. 7.6e-06; 27; Conservative 24; Mismatches 38;
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FILE REFERENCE: FID001

CURRENT APPLICATION NUMBER: US/10/506,454

CURRENT FILING DATE: 2004-08-31

PRIOR APPLICATION NUMBER: PCT/US03/06664

PRIOR APPLICATION NUMBER: B0/361,742

PRIOR APPLICATION NUMBER: 60/361,742

PRIOR FILING DATE: 2002-03-04

NUMBER OF SEQ ID NOS: 1722

SOFTWARE: Patentin version 3.2

SEQ ID NO 899

LENGTH: 1080
        RESULT 4
US-11-155-288-13
; Sequence 13, Application US/11155288
; Publication No. US20060008468A1
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US-11-033-039-385
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                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-033-039-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

ZILE REFERENCE: REH-2017US01

**CURRENT APPLICATION NUMBER: US/11/033,039

**CURRENT FILING DATE: 2005-01-11

**PRIOR APPLICATION NUMBER: 10/245,871

PRIOR RILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/197,000

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR APPLICATION NUMBER: 09/396,813

PRIOR TILING DATE: 1452

SOFTWARE: PATENTIN Version 3.3

SEQ ID NO 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 385, Application US/11033039 Publication No. US20060002947A1 GENERAL INFORMATION:
GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Methanopyrus kandleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 660
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                                                                                                                                                 454
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                                                                                                                                                                                       49 G--LDVSDRIRVV-MSVPAE----REDWARTHRDLIAGEILATDFEFADLADGVAIGDG 100
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RESULT 6
US-11-090-439-9
; Sequence 9, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
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APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REFERENCE: MANUK. 050A
CURRENT APPLICATION NUMBER: US/11/155,288
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR APPLICATION NUMBER: 60/580,969
ORDINATE: PASTEED HONG: 40
SOPTWARE: FASTEED FOR Windows Version 4.0
SOPTWARE: FASTEED FOR Windows Version 4.0
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APPLICANT: Genzyme Corporation
APPLICANT: Nicolette, Charles A.
TITLE OF INVENTION: Antigenic gp 100 Compounds
TITLE OF INVENTION: for Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/11119502 Publication No. US20060014668A1
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CURRENT FILING DATE: 2005-04-29
PRIOR APPLICATION NUMBER: 60/422,620
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 5247PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 661
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
LOCATION: (209)..(217)
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                                                                                              395 PEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSL
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                                              49 G--LDVSDRIRVV-MSVPAE----REDWARTHRDLIAGEILATDFEFADLADGVAIGDG 100
                                                                                                                                                                                               30;
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                                                                                                                                            5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIREL------OELRKST 48
                                                                                                                                                                                          h 14.2%; Score 76.5;
Similarity 25.2%; Pred. No. 4.
30; Conservative 16; Mismatche
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GPLLDGTATLKLVKRQVPLDCVLYKYGSFSVTLDIVQG-----IBSABILQAVPSGEG
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                                                                                                                                                                                               Indels
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                                                                                                                                                                                               Gaps
     507
                                                                                                   454
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Sequence 6318, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILLING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR PILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569
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                                                                                                                                                                                   RESULT 8
US-11-188-298-8860
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                                                        Sequence 8860, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
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Best Local (
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Best Local
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SEQ ID NO 9
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TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Ther
FILE REFERENCE: 24318-502
CURRENT APPLICATION NUMBER: US/11/090,439
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: 60/556,344
PRIOR PILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 62
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                               52 V-SDRIRVVMSVPAEREDWARTHRDLIAGEILATDFEFADLADGVAIGDGVRVSIEKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 G--LDVSDRIRVV-MSVPAB----REDWARTHRDLIAGEILATDFEFADLADGVAIGDG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                               3 ADPESTAALPDGAGLVVLD----GTVTAELBAEGWAKDRIRELQELR------KSTGLD 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 4.5;
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6; Mismatches
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Pred. No. 4.9;
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US-11-188-298-8860
                                                                                                                                                                                                                                                            Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1158 SEQ ID NO 564
                                                                                                              Matches
                                                                                                                                                Query Match
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NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 8860
LENGTH: 435
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Best Local :
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PRIOR
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/142,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/606,740
                                                                                                                                                                                                       ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE 19931418.7
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931419.5
FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/187,970
FILING DATE: 2000-03-09
APPLICATION NUMBER: DE 19930476.9
FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE 19931420.9 FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-07-02
APPLICATION NUMBER: 60/148,613
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: DE 19931415.2 FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-08-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 IRGRAVFNILSENMKPEYWVETAR-AVYGEI-----KDGADGVVVAHG 176
 59
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                                                                         1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRI-RELQELRKSTGLDVSD-RIRV 58
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                                                                                                                                Similarity
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VMSVPAEREDWARTHRDLIA-----GEILATDFBFADLADGVA-----
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                                     MAKEGLPAVELPDASGLKV--AVVTARWNAE--ICDRLHKHAVDAGRAAGATVSEYRVIG
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Zelder, Oskar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/11055822 o. US20050260707A1
                                                                                                            Conservative
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                                                                                                                              13.3%; Score 71.5;
27.1%; Pred. No. 2.
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Pred. No. 6.9;
                                                                                                              Mismatches
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 -IGDGV 101
                                                                                                              Gaps
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                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                   Sequence 2, Application US/11087100 Publication No. US20050266440A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                   APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding
TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1158
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PRIOR
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PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR APPLICATION NUMBER: 60/187,970
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
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CURRENT FILING DATE: 2005-02-11
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METHABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pompejus, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: DE 19930476.9 FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-07-08
APPLICATION NUMBER: US/11/087,100
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                                                                                                                                                                                                                                                                                                                                                57 ALELPVVVQELARTHDAVVALGCVVRGGTPHFDYVCDSVTEGLTRIALDTSTPIGNGV 114
                                                                                                                                                                                                                                                                                                                                                                                              59 VMSVPAEREDWARTHRDLIA-----GEILATDFEFADLADGVA------IGDGV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKEGLPAVELPDASGLKV--AVVTARWNAE--ICDRLHKHAVDAGRAAGATVSEYRVIG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAADPESTAALPDGAGLVVLDGTVTAELEAEGWAKDRI-RELQELRKSTGLDVSD-RIRV 58
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Zelder, Oskar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71.5; DB Pred. No. 2.4; 20; Mismatches
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                                                                       ORFA of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                       PUFA Polyketide
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                                                                       Synthas
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; TYPE: PRT
; ORGANISM: Schizochytrium sp.
US-11-087-084-2
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US-11-087-084-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 2910
                                                                                                                                                                           Matches
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PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthas
TITLE OF INVENTION: System and Uses Thereof
FILE REFERENCE: 2997-29
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PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
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CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                            Local
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Local Similarity 30.4%;
nes 31; Conservative 1:
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                                                                                   1877 AAAPAPAAAAPAVSSELLEKAETVVMEVLAAKTGYETDMIESDMELETELGIDSIKRVEI 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1937 LSEVQAMLNVBAKDVDALSRTRTVGEVV--DAMKABIAGGSA 1976
1937 LSEVQAMLNVBAKDVDALSRTRTVGBVV--DAMKABIAGGSA 1976
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                                     59 VMSVPA----EREDWARTHRDLIAGEILATDFEFADLADGVA 96
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                                                                                                                                                                         Similarity 30.4
31; Conservative
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                                                                                                                                                                       13.1%; Score 70.5; DB 7; 30.4%; Pred. No. 1.3e+02; tive 13; Mismatches 49
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Pred. No. 1.3e+02;
3; Mismatches 49
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Sequence 8241, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569

SEQ ID NO 8241

LENGTH: 328
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US-11-188-298-8241
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US-11-188-298-8241
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PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR PELICATION NUMBER: 60/284,066
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR PILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/288,796
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR APPLICATION NUMBER: 60/323,269
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Best Local Similarity
Matches 26; Conserv
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Best Local Similarity
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APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
TITLE OF INVENTION: System and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2997-29
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                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1877 AAAPAPAAAAPAVSSELLEKAETVVMEVLAAKTGYETDMIESDMELETELGIDSIKKVEI 1936
88 -LASIRSAAQQVNGWSDVHKIDVLVNNAGIMATDFKLTE--DG 127
                                       55 RIRVVMSVPAEREDWARTHR-DLIAGE--ILATDFEFADLADG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 VMSVPA----EREDWARTHRDLIAGEILATDFEFADLADGVA 96
                                                                                          28 TTGVSPGGLGALFVEATAVAEPELAILAGRNINKLQQTADHLASKHPNLKTKLLTLDLSS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                       7 STAALPDGAGLVVLDGTVTABLBABGWAKDRIRBLQBL------RKSTGLDVSD
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                     12.5%; Score 67; DB 7; Length 328; 25.2%; Pred. No. 18; ative 17; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 70.5; DB 7; Length 2910; 30.4%; Pred. No. 1.3e+02;
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Search completed: April 14, 2006, 18:42:18 Job time : 5.62788 secs
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; TYPE: PRT
; ORGANISM: Magnetospirillum magnetotacticum
US-11-188-298-19411
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US-11-188-298-19411
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TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 19411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19411, Application US/11188298 Publication No. US20060075522A1 GENERAL INFORMATION:
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                                                                                146 QDNGIAIDEKVAASEKRT
                                                                                                                      91 LADGVAIGDGVRVSIEKT 108
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                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                    5 PESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLD-----VSDRI-RV 58
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                VGREPSGSPFNSIVQLERENGIPRNPFINAGAIAVTDVILSGHQPREALGEILRFMQFLA 145
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26.8%; Pred. No. 14;
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Maximum
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## ALIGNMENTS

RESULT 1
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XX N 02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 01-APR-1998; 08-OCT-1998 WO9844119-A1 Mycobacterium Mycobacterium infection. Mycobacterium tuberculosis antigen CFP20. 21-JAN-1999 AAW72887; AAW72887 standard; protein; 165 (first entry) tuberculosis. tuberculosis; antigen; vaccine; 97DK-00000376. 97US-0044624P. 97DK-00001277. 98US-0070488P. 98WO-DK000132 ₽ . immunological; immunogen;

Andersen P, Oettinger T, Nielsen Florio € 70 Rosenkrands I, Weldingh K, Rasmussen

PB;

(STAT-)

STATENS SERUM INST.

N-PSDB; WPI; 1998-542705/46. AAV63918.

New isolated mycobacteria polypeptides and nucleic acids - developing products for the diagnosis of or vaccination aga mycobacterial infections, particularly tuberculosis. is - used 1 against

for

Claim 1; Page 129-130; 163pp; English.

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

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Best Local Simi
Matches 165;
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05-JAN-1998;
01-APR-1998;
           protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (1) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ereculos18; fusion polypeptide; T-cell elimine response; infection pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP97B; CFP7B; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23; CFP25A; CFP30B; CFP7B.
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 diagnosing
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Best Local S
Matches 165
The present sequence is that of the Mycobacterium current of 31 strain H37Rv gene Rv1932 product, designated Tpx. This is one of 31 immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see AAM50729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP3OA or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP3OA, RD1-ORP2, RD1-ORP3, RD1-ORP5, MPT59-ESAT6, ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP3OB, CFP7DB or a T-cell epitope of for the preparation of an immunological composition; and
                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine for boosting immunity to mycobacteria when administered in mid-
life in a subject who has been vaccinated in childhood with Bacillus
Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                   Claim
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Pred. No. 1.1e-83;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen polypeptides. The protesins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                   Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EIISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protective immunity has waned. The vaccine compositions comprise 1 or more of the 31 purified immunogenic proteins. When used as immunogens, the secreted Mtb proteins lack the secreted signal sequence. A preferred protein is Ag85A (see AAM50759), the secreted product of the Rv3084v generated is Ag85A (see AAM50759), the secreted product of the Rv3084v generated                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                SEQ ID NO 23164; 1069pp;
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                                                                                                                                                                                                                                                                                                           polypeptides and nucleic acids useful for diagnosing infections, especially useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang
, Jen S, Carter
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Pred. No. 1.1e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bhatia
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are used in
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RESULT 5
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Best Local S
Matches 103
                                                                                                                                                                 Mitcham Ji
Zhang Y,
Barth B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                          WPI; 2003-381789/36.
                                                                                                                                                                                                                                              15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                       11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                   24-APR-2003
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                                                                                                                                                                                                                                                                                                                            WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                     Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                           Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes predicted ORF-encoded polypeptide #23164
                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-2003
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                                                                                                                                                                                                                      (CORI-)
                                                                                                                                                                                                                                                                                                                                                                              immunostimulant;
                                                                                                                                         y, Wang S, Jen s, 1B, Vallieve-Douglass J;
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Lodes MJ,
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Pred. No. 1.5e-48;
1; Mismatches 38;
                                                                                                                                                                                Benson
                                                                                                                                                                                            Bhatia
                                                                                                                                                                               DR,
                                                                                                                                                                             Maisonneuve JL;
Jones R, Carter D;
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

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Example

1:

SEQ ID NO 23164; 1481pp; English.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

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RESULT 6
AROS249
AROS249
ARO 29-J
ARO
DT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC immunogenic fragments of P. acnes polypeptides. The invention CC additionally encompasses expression vectors and host cells comprising a CC polynucleotide of the invention; antibodies against polypeptides of the comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes CC polypeptide and an isolated T cell population comprising T cells prepared CC via this method; a vaccine composition (comprising P. acnes polypeptides, or composition) and compression of the inventions, or CC antigen-presenting cells that express the polypeptide), a method and kit CC for detecting or determining the presence or absence of P. acnes in a CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion CC protesins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes CC protesins, T cell populations or antigen-presenting cells that express the colypeptides are useful for diagnosing, preventing or treating acnes CC protesins, T cell population. The vaccine composition is useful for the cucleic acid hybridisation. The vaccine composition is useful for the companies against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present CC sequence represents a polypeptide predicted to be encoded by an ORF (open convention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 103; Conserv
      N-PSDB; ABD16064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #14668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB082493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO82493 standard; protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 170 AA;
                                    WPI; 2003-615309/58
                                                                                                   Rubenfield MJ,
                                                                                                                                                                                                                          18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                         18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2003.
                                                                                                                                                              (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATSVRTFDERAAASGAT-VLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADGPMQHLLARAIIVVNAEGKVTYTQLVDEITTEPDYDAALEA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATTALMGKPLNTVGDLPQVGSLLPSFALVKSDLSBLRSDBLKGKKLVLNIFPSVDTGVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                               Nolling
                                                                                                                                                                                                                             98US-0074788P
98US-0094190P
                                                                                                                                                                 THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                             9908-00252991
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                                                                                               Deloughery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                   Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                               Ö
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ID AAG98
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using blochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Pseudomonas aeruginosa polypeptides and the polynuclectides encoding them. The sentences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a
                           Nakagawa S,
Tateishi N,
                                                                                                                                                                          07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG90953 standard; protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ
                                                                                                                                                                                                                                    16-DEC-1999;
                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                       20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG90953;
                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATSYRTFD-ERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 MAQVTLKGNPVNVDGQLPQKGAQAPAFSLVGGDLADVTLENFAGKRKVLNIFPSVDTPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IASGPLAGLAARAVVVLDEQNKVLHSELVGEIADEPNYAAALAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IADGPMAGLLARAIVVIGADGNVAYTELVPBIAQBPNYEAALAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATSVRKFNVEAGKLANTVVLCISADLPFAQKRFCGAEGLENVVNLSTLRGREFLENYGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterium; amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                          99JP-00377484.
2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis.
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Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                           Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 31239; 455pp; English.
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                                                                                                                   줐
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 486; DB 7;
Pred. No. 2.7e-45;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 194
                                                            Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                                               Yokoi
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RESULT 8
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Best Local
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25-JUN-1999;
01-JUL-1999;
01-JUL-1999;
08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                   fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide, lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous
                                                                                                                                 23-JUN-2000;
                                                                                                                                                                  04-JAN-2001
                                                                                                                                                                                                                                    Corynebacterium
                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB78902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; SEQ ID NO 4707; 246pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                       glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides derived from Coryneform bacteria, for identifying ion point of a gene, measuring expression of a gene analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGSPLKGLLARSVIVVDENGKVAYTQLVDBISTEPDYDAALAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADGPMAGLIARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATSVRTEDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                  2000WO-IB000922
                                                                                                                                                                                                                                                                    study; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     SRT protein sequence SEQ ID
99US-0141031P.
99DE-01030429.
99US-0142692P.
99DE-01031413.
99DE-01031457.
99DE-01031541.
99DE-01032209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.0%;
57.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 473.5; DB 4
Pred. No. 5.3e-44;
4; Mismatches 45
                                                                                                                                                                                                                                                                    cofactor; polyketide; enzyme; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                         NO:64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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RESULT 9
AAB79108
ID AAB7
XX
AC AAB7
XX
AC AAB7
XX
AX
XX

standard;

protein;

165

119 60

30-APR-2001 AAB79108; AAB79108

(first entry)

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                                                                                                                                                                                                                                                                                                                                                          CC Paperson of the Corynebacterium glutamicum stress, CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. CC The C. glutamicum SRT genes (I) can be used in vectors (II) for Cexpression in host cells and production of fine chemicals, such as, an CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), CC a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a CC saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC compound, a voltamin, a cofactor, a polyketide, or an enzyme. The fine CC compound, a production can be modulated. The presence of (I) or the SRT CC containing them can be used to map the genomes of organisms related to C. CC clitity of Corynebacterium diphtheriae. (I), (II), (III) and host cells containing them can be used to map the genomes of organisms related to C. CC clitity of corynebacterium diphtheriae. (I), (II), (III) and host cells containing them can be used to map the genomes of organisms related to C. CC clitity of corynebacterium diphtheriae. (I), (II), (III) and host cells containing them can be used to map the genomes of organisms related to C. CC clitity of an SRT pathway. (II) are used to permit C. glutamicum to the sare used to permit C. glutamicum to chemical are used to permit C. glutamicum to conditions. But increase the curvival of C. glutamicum to chemical and environmentally or chemically hazards and convict of the conditions. By increasing the growth rate or continued growth rate or production of fine chemicals from a cculture may be increased.
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1999;
14-JUL-1999;
27-AUG-1999;
27-AUG-1999;
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Lee H, R
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 211-212; 526pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbohydrates, or enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Corynebacterium glutamicum nucleic acid encoding a tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-061972/07.
N-PSDB; AAF71015.
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121
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                                                                                                                                                                                                                                                                                                              165
                                    ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                ATSVRTFDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI
                                                                                                                                                     MAKTHFQGNETATSGELFQVGDNLAEFNLVNTELGEVSSKDFQGRKLVLNIFPSVDTGVC
                                                                                                                                                                         MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
EGSPLKGLLARSVIVVDENGKVAYTQLVDEIFTEPDYDAALAGL
                                                                            ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
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                                                                                                                                                                                                                               Conservative
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99DR-01032914.
99DR-01040764.
99US-0151214P.
99DB-01041382.
                                                                                                                                                                                                                                                                                                                                                increased
                                                                                                                                                                                                                                                   56.1%;
56.7%;
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                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                 Score 466.5; DB 4
Pred. No. 3.1e-43;
Pred. No. 3.1e-43;
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25-JUN-1999;
08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
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14-JUL-1999;
14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                 New isolated Corynebacterium glutamicum nucleic acid for production modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitami
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14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonproteinogenic amino acid; purine hase. .....
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                                                                                                                                                                                                                         AAF71138 to
                                                                                                                                                                                                                                                       Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (BADI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .JUL-1999;
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DB; AAF71223.
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                                                                                                                                                                                                                                                      Page 379-380;
                                                                                                                                                                                                          AAP71357 encode the Corynebacterium glutamicum homeostasis ion (HA) proteins given in AAB79023 to AAB79242. The C.
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                                                                                                                                                                                                                                                                                                                                                                                                          Kroeger
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99DB-01032928.
99DB-01032930.
99DB-01032933.
99DB-01032933.
99DB-01032973.
99DB-01033003.
99DB-01033003.
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99DB-01033003.
99DB-01041379.
99DB-01041379.
99DB-01041390.
99DB-01041390.
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99DE-01031636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamicum HA protein sequence SEQ ID NO:172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutamicum.
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-01032920.
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                                                                                                                                                                                                                                                      English
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                     The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, anethod of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for minimal diseases, as components of antibacterial vaccines. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins encoded by the (I) are used glutamicum or help the microorganism conditions
                                                                                                                                                                                                                                      New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 165
                                                                                                                                                                                                                                                                                                                                        Breton
                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000US-00543681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteus mirabilis infection; bacterial infection; antibacterial; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF04323 standard;
                                                                                                                                                                                               Disclosure; SEQ ID
                                                                                                                                                                                                                           biocontrol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteus mirabilis.
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                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME
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                                                                                                                                                                                                                                                                                               2003-895291/82.
DB; ADF00151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAKTHFQGNETATSGELPQVGDNLAEFNLVNTELGEVSSKDFQGRKLVLNIFPSVDTGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide #436.
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56.7%;
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                                                                                                                                                                                             870pp;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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No. 3.1e-43;
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                                                                                                                                                           The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                 New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful preparing a vaccine composition against Klebsiella pneumoniae.
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                                                                                                                                   Sequence 176 AA;
                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-2000; 2000US-00489039
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                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               GENOME THERAPEUTICS CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein; 176
 CATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGV 117
                                                    MAQ-ITLRGNAINTVGBLPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPLAGLTSRAVIVLDESNNVIYTQLVDBITTBPNYDAALAVL
                            MSQTVHFQGNFVSVQGTIFQAGAKAQFFTLVAKDLSDVALSQYAGKRKVLNIFFSIDTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVROPNKVANBLNNTVVLCISADLPFAQARFCGAEGLDNVVTLSTMRGAEFKENYGVAIT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVRTFDERA-AASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGVTIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVTLQGNAVTLAGNEPTVGQKAADESLVGKDLNDVSLAQEAGKRKVLNI FESVDTGVCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
                                                                                Conservative
                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression vector;
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                                                                                                                                                                                                                                                                      NO 7716; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%;
                                                                             50.4%; Score 418.5; DB 7; 53.0%; Pred. No. 7.3e-38; :ive 24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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Pred. No. 2.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulatory element; antibacterial; Vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 172;
                                                                                                        Length
                                                                                Indels
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                                                                                                                                                                 Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                               The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIME) polypeptide activity. The method comprises contacting an NIME polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIME nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIME expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAUJ9329-AAUJ29379 represent Escherichia coli NIME amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound.
                                                                                                                                                                                                                         Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 309-310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mar regulated polypeptide; NIMR; microbial infection; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TUFT )
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AIADGPLKGLAARAVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA
                       TIADGPMAGLLARAIVVIGADGNVAYTELVPBIAQBPNYBAALAALGA
                                                                                                                                     MAQ-ITLRGNAINTVGBLPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV
                                                    CAASVRKFNQLATBIDNTVVLCISADLPFAQSRFCGAEGLNNVITLSTFRNABFLQAYGV
                                                                             CATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGV 117
                                                                                                           MSQTVHFQGNPVTVANSIPQAGSKAQTFTLVAKDLSDVTLGQFAGKRKVLNIFPSIDTGV
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                                                                                                                                                                              50.2%; Score 417.5; DB 4; 52.4%; Pred. No. 8.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alekshun
                                                                                                                                                                                                                                                                                                                                                                                                                          526pp; English.
                                                                                                                                                                 23; Mismatches
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ABM69123
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the isolation of genes and their encoded CC proteins from Photorhabdus luminescens. The isolated sequences are gources of probes and primers for detecting the genome of P. luminescens CC and related species; to study polymorphisms; for gene analysis and for CC detection/amplification of the genes. Antibodies (Ab) raised against the CC polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that CC carry a gene-containing vector are used to select compounds that CC modulate, regulate, induce or inhibit expression of the genes in plants, CC animals or microcyganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for CC response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for CC antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the area as virulence CC factors and for identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This CC sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                Query Match
Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence of Photorhabdus luminescens a useful e.g. as therapeutic antimicrobials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM69123 standard; protein; 168 AA
                                                                                                                                                                                                                                                                                                                                          Sequence 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duchaud E,
Buchrieser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM69123
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CNRS CENT NAT RECH SCI.
                                VRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFR-DSFGEDYGVTIAD
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                                                                                         VKFQGNDISVSGQFPKSGEKAQDFTLTAKDLSDVSLSHYAGKRKVLNIFPSIDTGVCAAS
                                                                                                                                                   ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS
Taourit S,
                                                                                                                                                                                                                    Conservative
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50.6%;
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protein
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                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                Score 406; DB 6; I
Pred. No. 1.7e-36;
5; Mismatches 53;
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                                                                                                                                                                                                                                                                                 Length 168
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RESULT 14
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                                                                                                                                                                                                              14-JUL-1999;
14-JUL-1999;
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14-JUL-1999
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09-JUL-1999
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09-JUL-1999
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31-AUG-1999;
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                                                                                        2001-061974/07.
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                                                                                                                               AG.
                                                                                                           Kroeger
                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-IB000911.
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99DE-01032920.
99DE-01032922.
99DE-01032924.
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99DE-01032973.
99DE-01033003.
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99DE-01032125.
99DE-01032126.
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                                                                                                            Schroeder
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New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins

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Claim 20;

Page 381;

712pp; English

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RESULT 15
ABB48059
ID ABB48
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Best Local S
Matches 69
                                                                                     Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000FR-00004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001; 2001WO-FR001118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
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WPI; 2002-010914/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB48059 standard; protein; 165
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57.5%; Pred. No. 1.6e-29;
tive 14; Mismatches 36
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Cossart P;
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Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,

for treatment

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                                                                                                                                                                                                                                                                                                                                            The present invention relates to the genome sequence of Listeria CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of Ct it are useful for selecting probes and primers for detecting genes in L. CC monocytogenes and related organisms, and for studying genetic composytogenes and other genomes. The present sequence is a protein cencoded by the genome sequence of the present invention. Proteins compositely, identification of L. monocytogenes and related organisms, and cfor biosynthesis and biodegradation, especially biosynthesis of Vitamin cc antibodies, identification of L. monocytogenes and related organisms, and cfor biosynthesis and biodegradation, especially biosynthesis of Vitamin cc selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and concortogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained concortogenes and related organisms. Note: The sequence data for this patent into into the part sequence.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
121
                                       119
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                                                                                                                                                                                                                                                                              Similarity
MKB---LRLLARSVFVVNAVGEIVYTEVVPEGSDHPNYBAAIEA
                   IADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                                                                         ATSVRTEDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                                                                                             MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC 60
                                                                               STOTRKFNEEASNLDNTVVLTISVDLPFAOKKWCAAEGLPNAITLSDHRDLSFGEAYGVI
                                                                                                                                                                      MTQVTFKHNPVTLVGTERKVGDKAPNFTVVNRDLEEVTLHDYDGKVRLISVVPSIDTSVC
                                                                                                                                                                                                                                                        Conservative
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Pred. No. 3e-29;
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831
1 MAQITLRGNAINTV
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

pir1:\*
pir2:\*
pir3:\*
pir4:\*

Database

PIR\_80:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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116.5	120.5 118.5 118.5	122.5 122.5 122.5 122.5	135.5 133.5 133 128.5
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	C;Species: Mycobacterium tuberculosis	N; Alternate names: scavengase; thiol peroxidase p20	erc	
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			thioredoxin peroxidase (EC 1.11.1) - Mycobacterium tuberculosis (strain H37RV)	
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C;Date: 17-Jul 1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Accession: H70635
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natture 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70635
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-165 <COL>
A;Cross-references: UNIPROT:P95282; UNIPARC:UPI000004A4B5; GB:Z84498; GB:AL123456; NID:
C.Genericantal source: strain H37Rv

A;Gene: tpx C;Superfamily: thioredoxin peroxidase C;Keywords: oxidoreductase; redox-active disulfide F;60-93/Disulfide bonds: redox-active #status predicted

Query Match Best Local S Matches 165 tch 100.0%; Score 831; DB 2; al Similarity 100.0%; Pred. No. 3.5e-70; 165; Conservative 0; Mismatches 0; Length 165; Indels 0; Gaps

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S 밁 Ş 밁 121 13 61 DGPMAGILARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165 ATSVRTPDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAPRDSFGEDYGVTIA 120 MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC 60

121 DGPMAGLLARAIVVIGADGNVAYTELVPETAQEPNYEAALAALGA 165

thiol peroxidase PA2532 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C;Accession: E83328
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, i Lory, S.; Olson, M.V. M.J.; B: K.; Lim,

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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pst
A;Reference number: A82950; MUID:2043733
A;Accession: E83328
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <STO>
A;Cross-references: UNIPROT:P57668; UNIF
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: tpx; PA2532
C;Superfamily: thioredoxin peroxidase
RESULT 4
B85752
thiol perox
C;Species:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AGC285
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, Reparkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AG0265 A;Status: preliminary
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  peroxidase [imported]
cies: Escherichia coli
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| GPLAGLTARAVVVLDGQDNVIYSELVNEITTEPNYDAALAAL
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Pred. No. 4.8e-38;
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                        coli
                        (strain O157:H7,
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                          substrain
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                            EDL933)
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Barrell,
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A;Residues: 1-168 <ZHO>
A;Cross-references: UNIPROT:P37901; UNIPARC:UPI00000480C8; GB:U93212;
A;Experimental source: strain DH5alpha
R;Blattner, F:R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland,
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 02-Sep-1997 #sequence revision 19-Sep-1997 #text_change 09-Jul-2004 C;Accession: JC5504; G64881; PC4166 R;Zhou, Y.; Wan, X.Y.; Wang, H.L.; Yan, Z.Y.; Hou, Y.D.; Jin, D.Y. Biochem. Blophys. Res. Commun. 233, 848-852, 1997 A;Title: Bacterial scavengase p20 is structurally and functionally related to A;Reference number: JC5504; MUID:97312505; PMID:9168946
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A; Residues: 1-168 <STO>
A; Cross-references: UNIPROT: P37901; UNIPARC: UPI00000480C8;
A; Cross-references: Strain O157:H7, Substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thioredoxin peroxidase (EC 1.11.1.-) - Escherichia coli
N;Alternate names: scavengase p20; thiol peroxidase p20
C;Species: Escherichia coli
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R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasr iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
A;Cross-references: UNIPARC:UPI000017895B;
A;Experimental source: strain K-12
C;Comment: This enzyme belongs to a novel s
glutamine synthetase from inactivation by n
                                                                                                       A; Molecule type: DNA
A: Residues: 1-35 < KIM>
                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI00000480C8; GB:AE000230; GB:U00096; NID:gl787578; PIDN:A. A;Experimental source: strain K-12, substrain MG1655 R;Kim, H.K.; Kim, S.J.; Lee, J.W.; Lee, J.W.; Cha, M.K.; Kim, I.H. Biochem. Biophys. Res. Commun. 221, 641-646, 1966 A;Title: Identification of promoter in the 5'-flanking region of the E. coli thioredoxi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64881
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                                                                                                                                                                  A; Accession:
                                                                                                                                                                                            A; Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: nucleic acid sequence not shown; translation not shown;
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Pred. No. 1.2e-31;
                                                                                    GB:U33213
                                                                                                                                                                                              PMID:8630014
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imalanta, B.; Potamousis,
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K.; Apodaca
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RESULT 6
G90866
thiol peroxidase [imported] - Escherichia coli (strain 0157:H7, C;Species: Bscherichia coli
C;Date: 18-Uul-2001 #sequence_revision 18-Jul-2001 #text_change
C;Accession: G90866
C;Accession: G90866
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.
R;Bayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Battori, M.;
                                                                                                                          RESULT 7
G64090
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A;Gene: tpx
C;Function:
A;Description: oxidoreductase; antioxidant enzyme;
C;Superfamily: thioredoxin peroxidase
C;Keywords: oxidoreductase; redox-active disulfide
F;61-95/Disulfide bonds: redox-active #status predi
thioredoxin peroxidase (EC 1.11.1.-) - Haemophilus influenzae (strain Rd KW ,Alternate names: scavengase; thiol peroxidase p20 C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: G64090 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: G90866

A;Status: preliminary
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A; Residues: 1-168 < HAY>
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                                                                                                                                                                                                                                                                                                    CATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGV 117
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 417.5; DB 2;
Pred. No. 1.2e-31;
3; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 417.5; DB 2
Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.; Kurokawa, K.; Ishii, K.; Yokoyama, S.; Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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   B.F.; Kerlavage,
y, J.M.; Weidman,
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                                                                                                           KW20)
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A; Residues: 1-168 < PAR>
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A; Residues: 1-165 < TIGR>
                                                                                                                                                                                                                                                                                                                                                                             Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                              ;Cross-references:
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                                                                          BIVDGPLKGLAARAVIVLDENDNVIFSQLVDBITHBPDYDAALNVLKA
                                                                                                                                                                                                                                                                                                                                                           thioredoxin
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th, T.; commons, P.

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A.Fittle: Complete genome sequence of a multiple drug resistant

A;Title: Complete AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: ....-C;Keywords: oxidoreductase; redox-active F;59-93/Disulfide bonds: redox-active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thiol peroxidase [imported] - Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, Science 269, 496-512, 1995
A;Authors: Grehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae A;Reference number: A64000, MUID:95350630; PMID:7542800
A;Accession: G64090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Parkhill, J.; Dougan, G.; James,
th, T.; Connerton, P.; Cronin, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q57549; UNIPARC: UPI0000137296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: thioredoxin peroxidase;
Keywords: oxidoreductase; redox-active disulfide;
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                                                                                                                                                                                              MAQ-ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL
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TIADGPMAGLLARAIVVIGADGNVAYTELVPBIAQEPNYEAALAALGA
                                                CAASVRKFNQLATEVENTVVLCVSADLPFAQSRFCGAEGLSNVITLSTLRNNEFLKNYGV
                                                                                             CATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS-FGEDYGV
                                                                                                                                             MSQTVHFQDNPVTVANVIPQAGSKAQAFTLVAKDLSDVSLSQYAGKRKVLNIFPSIDTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPLAGLTSRAVIVLDEQNNVLHSQLVEEIKEEPNYEAALAVL
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                                                                                                                                                                                                                                                                  47.68;
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51.9%; Pred. No. 1.7e-30;
tive 21; Mismatches 55
                                                                                                                                                                                                                                                                                                                                           peroxidase
                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                         Score 395.5; DB 2;
Pred. No. 1.3e-29;
26; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.D.; Davis,
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                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AL513382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAD01648.1; PID:g16502500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dowd,
     165
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                                                                                                                                                                                                                                                Gaps
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I.; Farrar
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168

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A;Cross-references: UNIPACT:Q93TT8; UNIPARC:UPI00000AFC07; EMBJ R;Cross-references: UNIPACT:Q93TT8; UNIPARC:UPI00000AFC07; EMBJ R;Cross-references: U.S.A. 95, 3134-3139, 1998
A;Title: A Vibrio cholerae pathogenicity island associated with A;Reference number: Z16672; MUID:98169509; PMID:9501228
A;Accession: T09445
A;Recession: T09445
A;Recidues: DINA
A;Residues: 1-4 <KAR>
A;Residues: 1-4 <KAR>
A;Cross-references: UNIPARC:UPI000011E848; EMBL:AF034434; NID:9;Genetics:
A;Gene: tegD
C;Genetics:
A;Gene: tegD
C;Genetics: A;Gene: tegD
C;Superfamily: thioredoxin peroxidase
C;Keywords: oxidoreductase; redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable thioredoxin peroxidase (EC 1.11.1.) - Vibrio cholerae
N;Alternate names: scavengase; thiol peroxidase p20; toxR-activated tagD protein
C;Species: Vibrio cholerae
C;Date: 13-Jun-1995 #sequence revision 14-Jul-1995 #text_change 09-Jul-2004
C;Accession: JC2570; T09445
R;Hughes, K.J.; Everiss, K.D.; Harkey, C.W.; Peterson, K.M.
Gene 148, 97-100, 1994
A;Title: Identification of a Vibrio cholerae ToxR-activated gene (tagD) that is p
A;Reference number: JC2570; MUID:95011667; PMID:7523254
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JC2570
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera patho A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82274
A;Molecule type: DNA
A;Residues: 1-164 CHEI>
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C;Superfamily: thioredoxin peroxidase
C;Keywords: oxidoreductase; redox-active disulfide
F;59-93/Disulfide bonds: redox-active #status pred:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thioredoxin peroxidase (BC 1.11.1.-) [similarity] - Vibrio cholerae (strain N16961 serog C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: C82274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P39167; UNIPARC:UPIO000000A88; GB:AE004168; A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor C;Genetics: A;Gene: VC0824
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A; Residues: 1-164 < HUG>
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Best Local S
Matches 70
Query Match
Best Local S
Matches 69
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  69; Conserv
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                       42.0%;
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Pred. No. 1.4e-25;
                          Score 349; DB 2;
Pred. No. 2.7e-25;
    Mismatches
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                                             Length 164;
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    Indels
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E.C.; Kaper,
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H.; Dragoi,
                                                                                                                                                                                                                                                                                                                                                   epidemic and
    <u>ب</u>
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agoi, I.; Sellers,
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 NID:g407281;
J.B.; Reeves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE003852;
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                                                                                                                                                                                          D.; Jones, L., ....., 2001
Science 294, 849-852, 2001
A; Althors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, lok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J., A;Title: Comparative genomics of Listeria species.
A;Title: Comparative AB1077; MUID:21537279; PMID:11679669
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A; Molecule type: A;Status: preliminary

DNA

AG1272

Listeria monocytogenes

(strain

EGD-e)

A.; Baquero, F

F . ;

Entian,

Berche, P.; tian, K.D.; |

; Bloecke. Fsihi, H

ÞΒ

Maitournam, A.; M Voss, H.; Wehland

09-Jul-2004

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RESULT
AH1635
                                                                                                                                                                                                                                                                                                                                                                                                                          D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 C;Accession: AH1635 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, F.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; D
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C;Date: 27-
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吊
                                                                                                                                                                                                                                                                      C; Superfamily: thioredoxin peroxidase
                                                                                                                                                                                                                                                                                        A;Gene: lin1625
                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q92BC5; UNI
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: AH1635
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121 MKB---LRLLARSVFVVNAKGBIVYTEVVPEGSDHPNYBAAIBA 161
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                                                                                                                                                                                                                   h 41.2%;
Similarity 44.5%;
                     IADGPMAGLLARAIVVIGADGNVAYTELVPBIAQEPNYBAALAA 162
                                                               STOTRKFNEEASNLDNTVVLTISVDLPFAOKKWCAAEGLPNAITLSDHRDLSFGEAYGVI
                                                                                               ATSVRTFDERAA-ASGATVICVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT
                                                                                                                                 GALRGLAARAVIVADEFGVITHSELVNEITNEPDYDRILMSL
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                     27;
                                                                                                                                                                                                     Score 342.5;
Pred. No. 1.1e
27; Mismatches
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.1e-24;
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                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                      165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (strain Clip11262)
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Lian, K.D.;
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Fsihi, H
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3

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RESULT 14
A95192
c;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Cpate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: A95192
R;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peters on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; nson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pnd;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: UNIPROT: Q9K813;
A, Experimental source: strain C-125
C, Genetics:
A, Gene: BH3194
C; Superfamily: thioredoxin peroxidas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thioredoxin peroxidase BH3194 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (c;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: B84049 C;Accession: B84049 R;Takaki, Y;; Maeno, G;; Sasaki, R; Masui, N; Fuj
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A;Molecule type: DNA
A;Residues: 1-166 <STO>
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Nucletc Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium
A;Reference number: A83650; MUID:20512582; PMID:11058132
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Best Local S
Matches 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKB---LRLLARSVFVVNAVGBIVYTEVVPEGSDHPNYEAAIEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATSVRTFDBRAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
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                                                                                                                                                                                                                                                                                                                      IEE---LRLLARAVEVINANDEVTYVEYVSEATNHPDYEKAIEAAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 324.5; DB 2;
; Pred. No. 5.3e-23;
19; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Mismatches
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Pred. No. 1.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                       J.C.; Dougherty, B.A.; Morri of Streptococcus pneumoniae.
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J. Bacteriol. 18, 5709-5717, 2001
J. Bacteriol. 18, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, F. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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A; Residues: 1-172 < KUR>
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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren,
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C;Superfamily: thioredoxin
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <KUR>
A;Cross-references: UNIPARC:UPI0000165A91; GB:AE005672;
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Similarity 44.5%; Pred. No. 1.3e-22;
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                                    GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA
                                                                           TRRFNEELAGLDNTVVLTVSMDLPFAQXRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE
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Q4M097_DESEM
Q4ZTK2_PSESM
Q5A71_YSESP
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Length 165; Indels

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DARD; PRT; 1  Created) Last sequence up Last annotation Large SCALE GENOM DOGGETT J., Mayes B.G., Cole S.T., Grondin S., Lacro Doggett J., Mayes B.G., Cole S.T., Lacro Last annotation Local S.T., B.G., Cole S.T., Lacro L	
	TPX SHIFL Q6NGY6 CORDI TPX PASMU Q4QME7 HABIN Q4QME7 HABIN Q4QME7 HABIN Q505Q1_ERMCT Q7N3Y3 PHOLL TPX HABIN Q6H8J0 BURML TPX SALTY Q57NY0_SALCH Q5PHF7_SALPA Q4LLZ9_SHURK TPX SALTI Q5P4J4_AZOSE ALIGNMENTS
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STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed-12218036;

MEDLINE-22206494; PubMed-12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Pleischmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.B., Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jayels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R. "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P66952; P95282;
01-NOV-1997 (Rel. 35, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable thiol peroxidase (EC 1.11.1.-).
Name=tpx; OrderedLocusNames=Rv1932, MT1982; O
                                                                                                                                                                                                                                          laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
J. Bacteriol. 188:5479-5490(2002).
J. Bacteriol. Has antioxidant activity. Could remove peroxides
H(2)O(2) (By similarity).
H(2)O(2) (By similarity).
J. SIMILARITY: Belongs to the ahpC/TSA family. Tox subfamily.
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HAMAP; MF_00269; -; 1.
InterPro; IPR000866; AhpC-TSA.
                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Bioinformatics Institute
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AAK46254.1;
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Best Local S
Matches 165
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R InterPro; IPR012336; Thioredoxin-like.

R InterPro; IPR012336; Thioredoxin-like.

R Pfam; PF00578; AhpC-TSA; 1.

PROSITE; P801265; TPX; 1.

SEQUENCE 165 An.
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SMR; Q7AUIO; 2-165.
GO; GO: DONOCO.
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PANTHER; PTHR10681:SF4; TPX;
Pfam; PF00578; AhpC-TSA; 1.
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3D-structure; Antioxidant; Complete
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IPR012335; Thioredoxin_fold
IPR002065; TPX.
                                         ATSVRTFDERAAASGATV
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MEDLINE=22511501; PubMed=12623276; DOI=10.1016/S0882-4010(02)00209-7;
Mullerad J., Hovav A.H., Nahary R., Fishman Y., Bercovier H.;
"Immunogenicity of a 16.7 kDa Mycobacterium paratuberculosis
     Mullerad
                           NUCLEOTIDE SEQUENCE
                                                                      NCBI_TaxID=1764;
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NCBI_TaxID=1770;
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Bacteria; Actinobacteria; Actinobacteridae; Actinom
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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     J.,
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ilarity 84.1%;
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     Bercovier
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Pred. No. 5.1e.
12; Mismatches
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se activity; IEA.
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annotation updat
                                                                                                                     eridae; Actinomycetales; Mycobacterium;
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                                                                                             Query Match
Best Local Sim
Matches 104;
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Best Local Similarity
Matches 137; Conser
                                                                                                                                                                                          of human skin.";
Science 305:671-673(2004).
Science 305:671-673(2004).
EMBL; ARS017283; AAT82345.1; -; Genomic DN GO; GO:0016491; F:oxidoreductase activity GO; GO:0009031; F:thiol peroxidase activit InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012336; TPX.
Pfam; PF00578; AhpC-TSA; 1.
PROSITE; PS01265; TPX; 1.
Complete proteome; Oxidoreductase; Peroxi SEQUENCE 167 AA; 17691 MW; BB3F6B60BB
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EMBL; AX176763; AAO21122.1; -; Genomic_DNA.
HSSP; Q57549; 1Q98.
SMR; Q84672; 2-160.
GO; GO:0009031; F:thiol peroxidase activity; IE
InterPro; IPR000866; Ahpc-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR012335; Thioredoxin_fold.
InterPro; IPR002065; TPX.
Pfam; PF00578; Ahpc-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=KPA171202 / DSM 16379;
PubMed=15286373; DOI=10.1126/science.1100330;
Brueggemann H., Henne A., Hoster F., Liesegang H.,
Strittmatter A., Hujer S., Duerre P., Gottschalk G.
"The complete genome sequence of Propionibacterium of human skin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAA71 PROAC PRELIMINARY; PRT; 167 AA. Q6AA71; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation updat Thiol peroxidase (EC 1.11.1.-). OrderedLocusNames=PPA0590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.
STRAIN=KPA171202 / D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Propionibacterineae; Propionibacteriaceae; Propionibacterium.
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                                                                                                                          Similarity
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MATTAFMGKPLNTVGDLPQVGSLLPSFTLVKSDLSELRSDELKGKKLVLNIFPSVDTGVC
                             MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                  Conservative
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                                                                                                                                                                                                  Oxidoreductase; Peroxidase.
17691 MW; BB3F6B60B83CF0F2
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                                                                                                                       62.5%;
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-; Genomic_DNA.
                                                                                          Score 519.5; DB 2;
Pred. No. 5.8e-37;
0; Mismatches 38;
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Pred. No. 1.1e-52;
.1; Mismatches 12
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e activity;
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·: IBA.
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RX MEDLINEA-22882880; Pubmedc14500782; DOI=10.1073/pnas.1832124100;

RA Antonio R.V., Almedda P.C., de Almedda L.G.P., de Almedda R.,

RA Altonio R.V., Almedda P.C., de Almedda L.G.P., de Almedda R.,

RA Altonio R.V., Almedda P.C., de Almedda L.G.P., de Almedda R.,

RA Altonio R.V., Almedda P.C., de Almedda L.G.P., de Almedda R.,

RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.P.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Astolfi-Filho S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,

RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,

RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,

RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Pantinatti P., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,

RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Jardim S.N., Laurino J.,

RA Partinapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Marthia W.S.,

A Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Laurino J.,

RA Grattapaglia D., Grisard B.C., Hanna B.S., Jardim S.N., Noreira M.A.M.,

RA Grattapaglia D., Grisard B.C., Potto J.C., Woreira M.A.M.,

RA Grattapaglia D., Grisard B.C.
                                                                                                                                                              HSSP; Q57549; 1Q98.

GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:009931; F:thiol peroxidase activity; IE.
InterPro; IPR000866; AbpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
InterPro; IPR012335; Thioredoxin_fold.
R InterPro; IPR012335; Thioredoxin_fold.
R InterPro; IPR01235; TPX.
R PROSITE; PS01265; TPX.
R PROSITE; PS01265; TPX; 1.
R PROSITE; PS01265; TPX; 1.
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Best Local (
                                                               Matches
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=tpx; OrderedLocusNames=CV0870; Chromobacterium violaceum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thiol peroxidase (EC 1.11.1.-)
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CHRVO
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                                                                                                                                                                                                                                                                                                                                                     AE016912; AAQ58545.1; -; Q57549; 1Q98.
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                                                                                  Similarity
MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATSVRTFNEKAAGLDDTTVLCVSRDLPFAQARFCGAEGIKNVVVASAFRSHFGKDLGVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATSVRTFDERAAA-SGATVLCVSKDLFFAQKRFCGAEGTENVMFASAFRDSFGEDYGVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                               Conservative
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                                                                                                                                               Oxidoreductase; Peroxidase.
17002 MW; F01AB34A5A637206 CRC64;
                                                                                  60.6%;
                                                               19;
                                                            Score 504; DB 2;
Pred. No. 1.3e-35;
9; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                               Genomic
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                                                                                                                                                                                                                                                                                                                  IBA
                                                                 40;
                                                                                                      Length 165;
                                                                 Indels
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                                                               Gaps
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RESULT 8
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(C STRAIN=TLS / ATCC 49652 / DSM 12025;

(C STRAIN=TLS / ATCC 49652 / D
                                                                                                                                                                           Matches
                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
28-FEB-2003
13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FBB-2003 (Rel. 41, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Probable thiol peroxidase (EC 1.11.1.-).
                                                                                                                                                                                                                                                                                                                                                                         TIGR; CT0754; -.

HAMAP; MF 00269; -; 1.

InterPro; IPR0103066; AhpC-TSA.

InterPro; IPR012335; Thioredoxin-like.

InterPro; IPR012335; Thioredoxin_fold.

InterPro; IPR002065; TPX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=tpx; OrderedLocusNames=CT0754; Chlorobium tepidum.
                                                                                                                                                                                                                                                              PROSITE; PS01265; TPX; 1.

Antioxidant; Complete proteome; Oxidoreductase; Peroxidase.
SEQUENCE 168 AA; 17714 MW; 4FB46D04B5028073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlorobaculum
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                                                                                                                                                                                                                                                                                                                               Pfam; PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                      PANTHER; PTHR10681:SF4; TPX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; AE006470; AAM7
; P72500; 1PSQ.
; CT0754; -.
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AASVRRFNKEAGERGDAVVLCISADLPFAQGRFCTTEGLDNVVPLSVYRSPEFGLDYGLT
                                       ATSVRTFDERAAASG-ATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT
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                                                                                   MATITLKGNS IHTAGELPAVGSQLPAPTLVKSDLSEVSPADPAGKKLVLNIPPSLDTAVC
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                                                                                                                                                                           Conservative
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                                                                                                                                                                                                60.0%; Score 499; 60.6%; Pred. No.
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                                                                                                                                                                                             499; DB 1;
No. 3.4e-35;
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TPX_PSEAE
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HAMAP; MF_00269; -; 1.

InterPro; IPR010366; AhpC-TSA.

InterPro; IPR012336; Thioredoxin_fold.

R InterPro; IPR012335; Thioredoxin_fold.

R InterPro; IPR012365; TPX.

R InterPro; PTHR10881:SP4; TPX; 1.

PRANTHER; PTHR10881:SP4; TPX; 1.

PR Pfam; PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                 Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-ANCC 15692 / PAO1;

MEDLINE=20437337; pubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; pubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
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P57668;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
Probable thiol peroxidase (EC 1.11.1.-).
Name=tpx; OrderedLocusNames=PA2532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Has antioxidant activity. Could remove H(2)O(2) (By similarity).
-!- SIMILARITY: Belongs to the ahpC/TSA family. Tpx :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=287;
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121
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                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  PS01265; TPX; 1.
lant; Complete proteome; Oxidoreductase;
165 AA; 17234 MW; 6CBC3A350B57A47E
                                                                                                                                                                                                                                          MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
                                                                                                                                 ATSVRTED-ERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVT 118
                                                                                                                                                                                                         IADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL
                                                                                                   ATSVRKPNVEAGKLANTVVLCISADLPPAQKRPCGAEGLENVVNLSTLRGREFLENYGVA
                                                                                                                                                                                                                                                                                                               58.5%;
nilarity 60.0%;
Conservative 2
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                                                                                                                                                                                                                                                                                                               Score 486; DB
Pred. No. 4.5e
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                       486; DB 1;
No. 4.5e-34;
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estrictions on its
is statement is not
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RESULT 10
Q7MU37 PORGI PRELIMINARY;
AC Q7MU37;
AC Q7MU31837;
AC Q7MU318=22829867;
AC Q7MU37;
AC Q7MU
RESULT 11
Q4KCR9 PSEP5
ID Q4KCR9 P
AC Q4KCR9 T
AC Q4KCR9 T
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT Thiol pe
GN ORFNames
OS Pseudomo
OC Bacteria
OC Pseudomo
OX NCBI_Tax
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RC STRAIN-P
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Best Local S
Matches 96
                                                                                                                                                                                            QAKCR9_PSEF5 PRELIMINARY; PRT; 166 AN QAKCR9; QAKCR9; 13-SEP-2005 (TrEMBLrel. 31, Created) 13-SEP-2005 (TrEMBLrel. 31, Last sequence up 13-SEP-2005 (TrEMBLrel. 31, Last annotation Thiol percotidase (EC 1.11.1.-). ORFNames=PFL_2858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016491; F:oxidoreductase activity; GO; GO:0009031; F:thiol peroxidase activity InterPro; IDR000966; Ahpo-TSA.

InterPro; IPR012336; Thioredoxin-like. InterPro; IPR012335; Thioredoxin_fold. InterPro; IPR01235; Thioredoxin_fold. Pfam; PF00578; AhpC-TSA; 1.

PROSITE; PS01265; TPX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the oral path
Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
EMBL; AE017178; AAQ66736.1; -; Genomic_DNA.
HSSP; B37901; 1QXH.
                            NUCLEOTIDE SEQUENCE
                                                                             NCBI_TaxID=220664;
                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                  ORFNames=PFL 2858;
Pseudomonas fluorescens (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M. Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., G Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thiol peroxidase.
OrderedLocusNames=PG1729;
Porphyromonas gingivalis (Bacteroides g
Bacteria; Bacteroidetes; Bacteroidetes
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179 AA; 19188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAASVRRFNQEASSIDNTVVLCLSKDLPFAQARFCGAEGLDKVITVSAFRCDCFEKGYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATSVRTFDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFR-DSFGEDYGV
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llarity 57.8%;
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Last sequence update)
Last annotation update)
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Pred. No. 2.7
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                                                                                                                                            Pseudomonadales;
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RESULT 12
TPX COLD
ID TPX COLD
ID TPX COLD
ID TPX COLD
ID TPX COLD
ID 28-FE
DT 28-FE
DT 10-MA
DE Proba
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Best Local S
Matches 98
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J. Biotechnol.
-!- FUNCTION: H
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28-FEB-2003
28-FEB-2003
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=ARCC 13032 / DSM 20300 / NCIB 10025,

PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;

Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,

Kalinowski J., Busch N., Eggeling L., Elkmanns B.J., Gaigalat I

Burkovski A., Dusch N., Buggeling L., Elkmanns B.J., Gaigalat I

Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,

MCHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,

MCHardy A.C., Meyer F., Rupp O., Sahm H., Wendisch V.F., Wiegra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable thiol peroxidase (EC 1.11.1.-).
Name=tpx; OrderedLocusNames=cg11086, cg1336;
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                            Tauch A.; "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Biotechnol. 23:873-878 (2005).
EMBL; CP0000076; AA392130.1; -; Genomic_DNA.
Oxidoreductase; Paroxidase.
SEQUENCE 166 AA; 17418 MW; 198E61313AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of Corynebacterium Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakagawa S.;
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                                                                         88
                                                                                                                                                                                                                                                  SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                             FUNCTION: Has antioxidant activity. H(2)O(2) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [LARGE SCALE GENOMIC DNA]
DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.4%;
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Pred. No. 3.3e-33;
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R., Ren Q., Madupu R., Dodes
Y S.C., Sullivan S.A., Rosov
Weidman J., Watkins K., Tra
L. III, Thomashow L., Loper
                                                                         way
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MATTNEKGQPVKLIGEETQVGKVAPDEELVKSDLSSFALKDLKGKNIVLNIEPSLDTGVC

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RESULT 13
OSLBP6 BACEN PRELIMINARY;
ID OSLBP6_BACEN PRELIMINARY;
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Best Local
Matches
                                                    gene expression.";
Science 307:1463(2005).
Science 307:1463(2005).
Science 307:1463(2005).

REMBL; CRE626927; CAH08472.1; -; Genomic_DNA.
InterPro; IPR010866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin_1ike.
InterPro; IPR012336; Thioredoxin_fold.
InterPro; IPR012335; TPX.
InterPro; IPR01235; TPX.
REMBL; PS01265; TPX.
Pfam; PF00578; AhpC-TSA; 1.
RPGOSITE; PS01265; TPX; 1.
Complete proteome; Oxidoreductase; Peroxidase.
SEQUENCE 166 AA; 17938 MW; DE898C54074EAB68 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BA000036; BAB98479.1; -; Genomic_D

EMBL; BX927151; CRF19791.1; ALT_INIT; Ge

HSSP; P72500; 1PSQ.

HAMAP; MF 00269; -; 1.

InterPro; IPR000866; AhpC-TSA.

InterPro; IPR012336; Thioredoxin_fold.

InterPro; IPR012335; Thioredoxin_fold.

InterPro; IPR012335; TPX.

PANTHER; PTHR110681:SF4; TPX; 1.

PFAM; PFOSTTB; PS01265; TPX;

PROSITE; PS01265; TPX; 1.

Antioxidant; Complete proteome; Oxidored

SEQUENCE 165 AA; 17532 MW; 8A13B9710
                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15746427; DOI=10.1126/science.1107008;

Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely (
Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Q.
Barron A., Clark L., Corton C., Doggett J., Holden M.T.G.,

Line A., Lord A., Norbertczak H., Ormond D., Price C.,

Rabbinowitsch E., Woodward J., Barrell B.G., Parkhill J.;

"Extensive DNA inversions in the B. fragilis genome control
                                                                                                                                                                                                                                                                                                                                                          Bacteria; Bacteroidetes; Bacteroidetes (Bacteroideae; Bacteroides, NCBI TaxID=2775 Kra.)
                                                                                                                                                                                                                                                                                                                                                                                                Putative thiol peroxidase (EC 1.11.1.-)
Name=tpx; OrderedLocusNames=BF2777;
Bacteroides fragilis (strain ATCC 25285
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=272559;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2005
01-FEB-2005
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(TrEMBLrel. 29, Last sequence update)
(TrEMBLrel. 29, Last annotation updat
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             59.4%;
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ALT_INIT; Genomic_DNA.
Score 467; DB 2
Pred. No. 2e-32;
8; Mismatches
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8A13B971070B2CDE
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RESULT
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ID Q6AM98
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A Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Ok
A Kuhahara S., Hattori M., Hayashi T., Ohnishi Y.;

A Kuhahara S., Hattori M., Hayashi T., Ohnishi Y.;

"Genomic analysis of Bacteroides fragilis reveals extensive DNA
T inversions regulating cell surface adaptation.";

Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).

EMBL; AP006841; BAL49513.1; -; Genomic DNA.

R GO; GO:0016491; F:cxidoreductase activity; IEA.

R GO; GO:009031; F:thiol peroxidase activity; IEA.

R GO; GO:009031; F:thiol peroxidase activity; IEA.

R GO; GO:009031; F:thiol peroxidase activity; IEA.

R GO; GO:001236; Thioredoxin-like.

R InterPro; IPR01236; Thioredoxin-like.

R InterPro; IPR01236; TPX.

R InterPro; IPR01236; TPX.

R FORSITS; PS01256; TPX.

R POSITS; PS01256; TPX; 1.

R PGS1TS; PS01256; TPX; 1.

R PGS1TS; PS01256; TPX; 1.

R PGS1TS; PS01256; TPX; 1.
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Q64SL6;
25-CCT-2004 (TrEMBLrel. 28, C
25-CCT-2004 (TrEMBLrel. 28, L
25-CCT-2004 (TrEMBLrel. 28, L
Putative thiol peroxidase.
OrderedLocusNames=BF2763;
                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence updat
25-OCT-2004 (TrEMBLrel. 28, Last sequence updat
25-OCT-2004 (TrEMBLrel. 28, Last annotation upd
Probable thiol peroxidase.
OrderedLocusNames=DP1798;
Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria;
Desulfobulbaceae; Desulfotalea.
NCBI_TaxID=84980;
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98_DESPS
OGAM98_DESPS PRELIMINARY;
OGAM98;
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Bacteroidaceae; Bacteroides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IADGEMAGLLARAIVVIGADGNVAYTELVEEIAQEENYEAALAAL 163
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18; Mismatches 4
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STRAIN=LSv54 / DSM 12343;

K PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;

R Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B.,

Bauer M., Zibat A., Lombardot T., Becker I., Amann J.,

A Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N.

XI Teeling H.-P.;

The genome of Desulfotlas systhrophila, a sulfate-re
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                                                                                                                                                                                                               EMBL; CR522870; CAG36527.1; ; Genomic DNA.
GO; GO:00016491; F:oxidoxeductase activity; IR.
GO; GO:0009031; F:thiol peroxidase activity; IR.
InterPro; IPR000866; AhpC-TSA.
InterPro; IPR012336; Thioredoxin-like.
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                                                                                                                                                      Conservative
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tive 20; Mismatches
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Lupas A.N.,
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US-09-765-271-44
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Sequence 8, Appli
Sequence 31239, A
Sequence 64, Appl
Sequence 4608, Ap
Sequence 172, App
Sequence 7716, App
Sequence 5126, Ap
Sequence 5126, Ap
Sequence 5128, Ap
Sequence 5218, Ap
Sequence 5218, Ap
Sequence 5218, Ap
Sequence 3764, App
Sequence 444, Appl
Sequence 44, Appl
Sequence 16, Appl
Sequence 11, Appl
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DGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165

; LENGTH: 165 ; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-050-739-8

Query Match Best Local Sim Matches 165;

Similarity

100.0%;

Conservative

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Score 831; DB 2; Pred. No. 1.2e-85; ; Mismatches 0;

Length 165; Indels

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Gaps

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ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIA 120

RESULT 1  US-09-050-739-8  ; Sequence 8, Application US/09 ; Patent No. 6641814 ; GENERAL INFORMATION: APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: ROSENKRANDS, Ida APPLICANT: ROSENKRANDS, Ida APPLICANT: FLORIO, Walter [ITLE OF INVENTION: DERIVED FILE REFERENCE: 670001-2002. CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: EARLIER FILING DATE: 1997-01 EARLIER FILING DATE: 1997-11 EARLIER FILING DATE: 1997-11 EARLIER FILING DATE: 1997-03 EARLIER FILING DATE: 1997-01 EARLIER FILING DATE: 1997-01 EARLIER FILING DATE: 1997-01 EARLIER FILING DATE: 1997-01 EARLIER FILING DATE: 1998-01	28 117.5 14.1 29 117.5 14.1 30 117.5 14.1 31 117.5 14.1 32 117.5 14.1 33 114.5 13.8 34 114.5 13.8 35 114.5 13.7 36 113.5 13.7 37 113.5 13.7 39 111.5 13.4 40 111.5 13.4 41 111.5 13.4 42 111.5 13.4 43 111 13.4 44 111.1 13.4 45 111 13.4
9050739  Birk  ACIDS FRAGMENTS AND FROM M. TUBERCULOSIS 1 US/09/050,739 3-30 0376/97 4-02 1277/97 1-10 60/044,624 4-18 60/070,488 1-05	199 2 US-09-004-716-2 199 2 US-09-477-510-2 256 2 US-09-538-092-1039 256 2 US-09-949-016-6760 258 2 US-09-949-016-10249 198 2 US-09-538-092-1055 208-09-538-092-593 196 2 US-09-538-092-593 196 2 US-09-586-677-294 196 2 US-09-586-677-294 198 1 US-09-620-412C-294 198 1 US-09-620-412C-294 198 1 US-09-620-412C-294 198 1 US-09-620-412C-294 198 1 US-09-581-19-294 199 1 US-08-467-265-15 199 2 US-09-1672-65-15 199 1 US-08-467-265-15 199 1 US-08-467-265-14
POLYPEPTIDE FRAGMENTS	Sequence 2, Appli Sequence 2, Appli Sequence 1039, Ap Sequence 6760, Ap Sequence 1055, Ap Sequence 1055, Ap Sequence 537, App Sequence 594, App Sequence 294, App Sequence 294, App Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 5696, App Sequence 5696, App Sequence 57, Appl Sequence 17, Appl

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US-09-252-991A-31239
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Sequence 31239, Application US/09252991A

Patent No. 6551795

PATENCANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
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LENGTH: 194
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CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
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FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931541.8
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19932209.0
FILING DATE: 1999-07-09
                                                                                                              APPLICATION NUMBER: DE 19930429.7
FILING DATE: 1999-07-01
APPLICATION NUMBER: DE 19931413.6
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931457.8
                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 1999-0
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Lee, Heung-Shick
Kim, Hyung-Joon
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1999-08-27
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RESULT 4
US-09-602-777A-172
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PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
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SEQ ID NO 64
LENGTH: 165
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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CURRENT APPLICATION NUMBER: US/09/602,777A
CURRENT FILING DATE: 2000-06-23
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APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932914.1
PRIOR APPLICATION NUMBER: DE 19932914.1
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941382.7
PRIOR FILING DATE: 1999-08-31
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APPLICANT: Kroger, Burkhard
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                                                    APPLICATION NUMBER: DE 19932922.2 FILING DATE: 1999-07-14 APPLICATION NUMBER: DE 19932924.9 FILING DATE: 1999-07-14 APPLICATION NUMBER: DB 19932928.1 FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932920.6
FILING DATE: 1999-07-14
   APPLICATION NUMBER: DE 19932930.3 FILING DATE: 1999-07-14
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DATE:
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US-09-543-681A-4608
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LENGTH: 172
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SEQ ID NO 172
LENGTH: 165
                                                                                              Query Match
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Best Local Similarity
                                                           Matches
                                                                                                                                                                                                                        APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILICATION NUMBER: US 60/128,706
RIGOR DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                    -09-543-681A-4608
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ORGANISM: Corynebacterium glutamicum
-09-602-777A-172
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PRIOR FILING DATE: 1999-09-03
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                                                                          Local
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APPLICATION NUMBER: DE 19941390.8
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APPLICATION NUMBER: DE 19941378.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93,
                                                                            Similarity
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QITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQERGKSVLLNIFPSVDTFVCAT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGSPLKGLLARSVIVVDENGKVAYTQLVDEIFTEPDYDAALAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATSVRTFDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI 119
                                                           Conservative
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                                                       53.1%; Score 441; DB 2; Length 172; 55.2%; Pred. No. 1.1e-41; tive 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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Pred. No. 1.4
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                                                         2
                                                         Gaps
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CURRENT APPLICATION NUMBER: US/09/602,777A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION UNMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR APPLICATION NUMBER: DE 19932127.2
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US-09-489-039A-7716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 174, Application US/09602777A Patent No. 6831165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 7716
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                    APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OP INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OP INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CP
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                             Schroder, Hartwig
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1999-07-09
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Pred. No. 3.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 176;
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APPLICATION NUMBER: DE 19932128.0 FILING DATE: 1999-07-09

NUMBER: DE

19932129.9

1999-07-19

FILING DATE:

APPLICATION NUMBER: DE 19932920.6 APPLICATION NUMBER: DE 19932226.0

1999-07-14 1999-07-09

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                                                                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Corynebacterium glutamicum US-09-602-777A-174
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SEQ ID NO 174
LENGTH: 123
                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                    Sequence 3217, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
             APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT FILLING DATE: 2000-05-26
CURRENT FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE:
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APPLICATION NUMBER: DE 19933003.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                       ATSVRTFDERAAA-SGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTI
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1998-06-30
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57.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 123;
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Sequence 5126, Applic...
Sequence 5126, Applic...
Sequence 5126, Applic...
Patent NO. 6800744
Patent NO. 6800744
PAPPLICANT: Lynn A Doucette-Stamm and David Busn
APPLICANT: Lynn A Doucette-Stamm and David Busn
APPLICANT: Lynn A Doucette-Stamm and David Busn
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
TUTLE OF INVENTION: TO STREPTOCOCCUS PNEUMONIAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                 APPLICATION NUMBER: US/09/107,433
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40, 489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPAX: (781)893-5277
INFORMATION FOR SEQ ID NO: 5126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
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SEQ ID NO 3217
LENGTH: 172
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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MEDIUM TYPE: CD/ROM ISO9660
                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 W---HLLARAVFVLDTDNTIHYVEYVDNINSEPNFEAAIAAKA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 TRRFNESLAGIDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VRTFDER-AAASGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VTFLGNPVSFTGKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: <Unknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                      LENGTH: 201 amino acids
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1998-05-12
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US-08-956-171E-5218
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Best Local
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GENERAL INFORMATION:
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                                                                                                               TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5218:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/009,861
PILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
PILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
MOLECULE TYPE: protein SEQ ID NO: 5218:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 W---HILARAVFVLDTDNTIHYVBYVDNINSBPNFBAAIAAKA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GPMAGLIARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
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LOCATION:
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                                                                                                                                                                                                                NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                          LENGTH: 173 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus
                  TOPOLOGY: linear
ULB TYPE: protein
                                                       STRANDEDNESS: single
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Patrick S. Dillon
Craig A. Rosen
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Pred. No. 6.7e-28;
3; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae
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10: 5126:
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US-08-781-986A-5218
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                                                                                                                                        Matches
                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 941.
STREET: 941.
CITY: Rockville
CTATE: Maryland
TISA
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve-
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                         LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                      Match 37.8%; Score 314; DB 2; Local Similarity 42.3%; Pred. No. 2.3e-27; es 69; Conservative 28; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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 70
                   61 ATSVRTEDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
                                                                    10 MTBITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVPSIDTGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 WTBITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVPSIDTGVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 37.8%;
Similarity 42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Benson,
DQQTRKFNSDASKEEGIVLTISADLPFAQKRWCASAGLDNVITLSDHRDLSFGENYGVVM
                                                                                                    MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charles Kunsch
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                                                                                                                                                                                                                                             linear
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Pred. No. 2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 173;
                                                                                                                                                                       Length 173
                                                                                                                                          Indels
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3764
ENOTH: 168
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US-09-710-279-252
                                                                                                                        ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3764
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Matches
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3764, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 252
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                                           Matches
                                                            Query Match
Best Local Similarity
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS.
FILE REPERENCE: BU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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                                           66;
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MAQITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                        Conservative
                                                            36.9%;
                                           29;
                                                            Score 307;
Pred. No. 1
                                           Mismatches
                                                            DB 2;
1.3e-26;
                                           64;
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15283
LENGTH: 00/01-07-10
                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 171
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                        COMPUTER: HP Vectra 486, OPERATING SYSTEM: MSDOS SOFTWARE: ASCII Text
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                        STATE:
                                                                                                                                                                                                          STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VRTFDERAAASG--ATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTIA 120
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                                                                                                       Diskette,
                                                                MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.3%; Score 302; DB 2
40.6%; Pred. No. 5e-26;
tive 30; Mismatches
  US/08/961,083
                                                                                                       3.50 inch, 1.4Mb
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PILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION UNDER:

PRIOR APPLICATION UNDER:

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PRIOR APPLICATION UNDER:

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PRIOR SEQ ID NO: 44:

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Result
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Listing first 45 s
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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Sequence 45, Appli
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Sequence 44, Appli
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			Query Ma Best Loc Matches	SOULT 1 Sequence 8, 1 Patent No. UI GENERAL INFO APPLICANT: APPLICANT APPLICANT: APPLICANT		00000000000000000000000000000000000000
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PRIOR PILING DATE: 1998-03-30
PRIOR PELICNG DATE: 1997-04-02
PRIOR PELICNG DATE: 1997-04-02
PRIOR PELICATION NUMBER: 1277/97
PRIOR PELICATION NUMBER: 1277/97
PRIOR PELICATION NUMBER: 60/044,624
PRIOR PELICATION NUMBER: 60/070,488
PRIOR PELICATION NUMBER: 60/070,488
PRIOR PELICATION NUMBER: 10/138,473
PRIOR PELICATION NUMBER: 10/138,473
PRIOR PELICATION NUMBER: 09/791,171
PRIOR PELICATION NUMBER: 09/791,171
PRIOR PELICATION NUMBER: 09/115,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR PELICATION NUMBER: 09/116,673
PRIOR PELICATION NUMBER: 60/116,673
PRIOR PELICATION NUMBER: 60/116,673
PRIOR APPLICATION NUMBER: 1099-01-21
PRIOR APPLICATION NUMBER: 1099-01-21
PRIOR APPLICATION NUMBER: 1091-01-21
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Sequence 9, Application US/10332512A
publication No. US20040180056A1
GENERAL INFORMATION:
APPLICANT: ORME, Ian M.
APPLICANT: BELISLE, John T.
APPLICANT: INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMMU
FILE REFERENCE: 38861-186292
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Publication No. US20040115211A1
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
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Best Local Similarity 100
Matches 165; Conservative
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SEQ ID NO 8
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NUMBER OF SEQ ID NOS: 173
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CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
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APPLICANT: FIORIO, WALTER
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
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RASMUSSEN, Peter Birk
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RESULT 5 US-09-738-626-4707

Sequence 4707, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI

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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
ITILE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOPTWARE: PATENTIN Version 3.0
SEQ ID NO 8
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CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: PCT/US01/21717
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/217,646
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
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LENGTH: 165
TYPE: PRT
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                 121 DGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
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DGPMAGLLARAI VVI GADGNVAYTEL VPE I AQEPNYEAALAALGA
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                                                                                                                                                                                                                                            98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 831; DB 4;
100.0%; Pred. No. 2.4e-79;
tive 0; Mismatches 0;
                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                            Score 821; DB 3; Length 165; Pred. No. 2.7e-78;
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 165;
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APPLICANT: APPLICANT: APPLICANT: APPLICANT:

> HAYASHI, MIZOGUCHI,

RIKO MIKIRO SEIKO

HIROSHI

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US-10-893-671-45
(S-10-893-671-45); Sequence 45, Application US/10893671; Publication No. US20050064527A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4707
                                                                                                                 ; OTHER INFORMATION: complement of position 6467-6937 US-10-893-671-45
                                                                                                                                                                                                                            SOPTWARE: PatentIn Ver. 2.0 SEQ ID NO 45
                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                     Matches
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/893,671
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US/99/801,563
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/188,362
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Levy, Stuart, et. al.
TITLE OF INVENTION: NIMR COMPOSITIONS AND THEIR METHODS OF USE
FILE REFERENCE: PKZ-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR PILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059 SOPTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                      PEATURE:
                                                                                                                                                                ORGANISM: Becherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 165
                                                                                                                                                                                                            LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                     88;
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 1 MAQ-ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPLKGLLARSVIVVDENGKVAYTQLVDEISTEPDYDAALAAL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAKTHFQGNETATSGELPQVGDNLAEFNLVNTELGEVSSKDFQGRKLVLN1FPSVDTGVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATEISHI, NAOKO
SENOH, AKIHIRO
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                                       Conservative
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                                                     50.28;
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%; Pred. No. 1.2e-41;
24; Mismatches 45
                                     23;
                                   Score 417.5; DB 5;
Pred. No. 1e-35;
3; Mismatches 54;
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                                     Indels
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                                                                       Length 168;
                                                                                                                                of seq id
                                   3;
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RESULT 8
US-10-617-320-5126
US-10-617-320-5126
; Sequence 5126, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
   APPLICANT: Lynn A Doucette-Stamm and David Bush
   APPLICANT: Lynn A Doucette-Stamm and David Bush
   SEQUENCES RELATING TO STREPTOCCCCUS PNEUMONIAE

"""TTALE OF INVENTION: NUCLEIC ACID AND ANIMO ACID

SEQUENCES RELATING TO STREPTOCCCCUS PNEUMONIAE
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CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SegWin99, version 1.03
SEQ ID NO 3396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3396, Application US/10472928 Publication No. US20050020813A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Streptococcus pneumoniae
FEATURE:
OTHER INFORMATION: thiol peroxidase (psaD)
OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15903538 (1.E-96)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROI
                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 W----HLLARAVFVLDTDNTIRYVBYVDNINSBPNFEAAIAAAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TRRFNEELAGLDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
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                                                                                                       CITY: Waltham
                                                                                                                           STREET:
                                                                                                                                            ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAASVRKPNQLATEIDNTVVLCISADLPFAQSRFCGAEGLNNVITLSTFRNAEFLQAYGV
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                                                                                                                           100 Beaver Street
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  CD/ROM ISO9660
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Pred. No. 1.8e-25;
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                                                                                                                                              CORPORATION
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;
LOCATION: (B) LOCATION 1...2
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-617-320-5126
                                                                                                                                                                                                                                                                                                                                                                                US-08-781-986A-5218
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                    Sequence 5218, Application US/08781986A Publication No. US20030054436A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5126:
SEQUENCE CHARACTERISTICS:
                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                      APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: 10-Jul-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

PILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/ 085131

PILING DATE: May 12, 1998

APPLICATION NUMBER: 60/55153

PILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                  COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOPTWARE: ASCII Text
                                                                                                                                                                             STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REPERENCE/DOCKET NUMBER: GTC-011 TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: <Unknown>
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 GPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAALGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 TRRFNEELAGLDNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 W---HLLARAVFVLDTDNTIHYVEYVDNINSEPNFEAAIAAAKA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VRTFDER-AAASGATVLCVSKDLPPAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ITLRGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATS 63
APPLICATION DATA:
                                                                                                                     20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTFLGNPVSFTGKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/617,320
                                                                                                                                                             Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRGANISM: Streptococcus pneumoniae
                                                                                                                                      USA
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                                                                                                                                                                                                                     Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.4%; Score 319.5; DB 5
44.5%; Pred. No. 2.9e-25;
tive 23; Mismatches 63
                                                                           3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                  and Sequences
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; MOLECULE TYPE: protein US-08-781-986A-5218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BeHSON, BOD
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 173 amino TYPE: amino acid STRANDEDNESS: sing TOPOLOGY: linear
          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
RILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diske
                                                                                                                                                                                                                                                                                                                                                                                                                                    Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ADGPMAGLIARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 EE---LRLLARAVFVLDADNKVVYKEIVSEGTDFPDFDAALAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 MTEITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVPSIDTGVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
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                                                                                                                                                                                 COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                   STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                  STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human
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. US20040043037A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patrick S. Dillon
Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charles Kunsch
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  NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi
January 5, 1996
NUMBER: 08/781,986
                                                                                                                                                                                                                                              Diskette, 3.50 inch, 1.4Mb storage
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Pred. No. 8.9e-25;
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US-10-724-972A-5919
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US-10-724-972A-5919
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                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 5919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: PATH03-16 CURRENT APPLICATION NUMBER: US/10/724,972A CURRENT FILING DATE: 2003-12-01
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: 09/450,969
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR PILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                      LENGTH: 168
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SEQUENCE CHARACTERISTICS:
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Local Similarity 42.3%;
tes 69; Conservative 28
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 BE---LRILARAVFVLDADNKVVYKEIVSEGTDFPDFDAALAA 169
    65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 MTBITFKGGPIHLKGQQINEGDFAPDFTVLDNDLNQVTLADYAGKKKLISVVPSIDTGVC
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  DSQTRKFNEEASAEDGVVLTISVDLPFAQKRWCASSGLDNVITLSDHKDLSFGRNYGLVM 124
                                       ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
                                                                                                                    MAQITLRGNAINTVGBLPAVGSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQQTRKFNSDASKEEGIVLTISADLPFAQKRWCASAGLDNVITLSDHRDLSFGENYGVVM 129
                                                                              MTQTTFKNNPIKLSGSEVNEGDIAPNPTVLDNSLNQITLDDYKNKKKKLISVIPSIDTGVC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                             36.9%;
ilarity 40.5%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                               29; Mismatches
                                                                                                                                                                                Score 307; DB 4; Length 168; Pred. No. 4.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 314; DB 4;
Pred. No. 8.9e-25;
8; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PB248P1D1
                                                                                                                                                               64;
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                                                                              RESULT 13
US-11-106-649-44
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Sequence 44, Application US/11106649
Publication No. US20050181439A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
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RESULT 12
US-09-765-272-44
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 65; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application U
Patent No. US20020061545A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
APPLICANT: Cho:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PERENCE/DOCKET NUMBER: PERENCE/DOKET NUMBER: PERENCOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
PILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
120
                                          133 VVIGADGNVAYTELVPEIAQEPNYE 157
                                                                                                                                          74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                                          63 DNTVVLTVSMDLPFAQKRWCGAEGLDNAIMLSDYFDHSFGRDYALLINEW---HLLARAV 119
                                                                                                                                                                                                                                         15
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FVLDTDNTIRYVEYVDNINSEPNFE 144
                                                                                                                                       SGATVLCVSKDLPFAQKRFCGAEGTEN-VMPASAFRDSFGEDYGVTIADGPMAGLLARAI 132
                                                                                                                                                                                                                                       GELPAVGSPAPAFTLTGGDLGVISSDOFRGKSVLLNIFPSVDTPVCATSVRTFDER-AAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB---LRLLARSVFVLNENNKVVYKEIVSEGTNYPDFEAALKA 164
                                                                                                                                                                                         GKOLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQTRRFNEELAGL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEB: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 144 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20850
                                                                                                                                                                                                                                                                                 34.0%; Score 282.5; DB 3;
44.8%; Pred. No. 1.5e-21;
tive 19; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     te, 3.50 inch, 1.4Mb storage 486/33
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                                                                                                                                                                                                                                                                                                                                    Length 144;
                                                                                                                                                                                                                                                                                         Indels
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US-10-335-977-7878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-106-649-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7878, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

APPLICANT: DOUGLAS SMITH et al

APPLICANT: FOR RELATING TO HELICOBACTER PYLORI FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/029,960 PRIOR FILING DATE: 1996-10-31 NUMBER OF SEQ ID NOS: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 09/765,271
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/536,784
PRIOR PILING DATE: 2000-03-28
PRIOR PILING DATE: 1007-03-08
PRIOR PILING DATE: 1997-10-30
PRIOR FILING DATE: 1997-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/106,649
CURRENT FILING DATE: 2005-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
     INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
PRIOR NUMBER: 08/993,002
PRIOR NUMBER: 08/993,002
PRIOR NUMBER: 08/993,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE: PB340P2C3D1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)27-7400
TELEPAX: (617)742-4214
RMATION FOR SEQ ID NO: 7878:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 FVLDTDNTIRYVBYVDNINSEPNFE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 VVIGADGNVAYTELVPEIAQEPNYE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
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STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GELPAVGSPAPAFTLIGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDER-AAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKQLQVGDKALDFSLTTTDLSKKSLADFDGKKKVLSVVPSIDTGICSTQTRRFNEELAGL 62
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44.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 282.5; DB 6
Pred. No. 1.5e-21;
                                                                                                   GTN-018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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; Sequence 7877, Application US/10335977
; Publication No. US20040052799A1
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LOCATION: (B) LOCATION 1...166
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7878:
US-10-335-977-7878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dileation AND THEORMATION:
GENERAL INFORMATION:
GENERAL THEORMATION: SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
                                                                                                                       INFORMATION FOR SEQ ID NO: 7877: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: UNIX
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
     MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 IADGPMAGLIARAIVVIGADGNVAYTELVPBIAQEPNYBAALAAL 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATSVRTFDERAA-ASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFR-DSFGEDYGVT 118
                                                  TOPOLOGY: linear
                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                       TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TY: Boston
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11361, p.
2013, p.
1040, p.
105, p.
105, p.
107, p.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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s derived by a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA New:*

1: /SIDSS/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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    GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration
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               VUS-11-079-463-6489
VUS-10-454-437-172
VUS-10-454-437-174
VUS-10-793-626-522
VUS-11-098-686-81
VUS-11-098-686-81
VUS-11-074-176-70
VUS-10-642-272A-5
VUS-10-642-272A-6
VUS-10-642-272A-4
VUS-10-642-272A-4
VUS-10-642-272A-1038
VUS-10-642-272A-1038
VUS-10-642-272A-1038
VUS-10-642-272A-1038
VUS-10-642-272A-1038
VUS-10-921-234-1039
VUS-11-096-568A-1037
VUS-11-096-568A-21440
VUS-11-096-568A-21440
VUS-11-108-172-1121
VUS-11-052-554A-213
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991.565 Million cell update
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Sequence 6489, Ap
Sequence 172, App
Sequence 174, App
Sequence 10841, A
Sequence 10841, A
Sequence 81, Appl
Sequence 70, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 1038, Appl
Sequence 1038, Appl
Sequence 1037, Ap
Sequence 1137, Ap
Sequence 11410, A
Sequence 11410, Ap
Sequence 1156, Appl
Sequence 1151, Ap
Sequence 1171, Ap
Sequence 1181, Ap
Sequence 1181, Ap
Sequence 556, App
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US-11-079-463-6489
; Sequence 6489, Application US/11079463
; Publication No. US20060073161A1
 ; Sequence 172, Application US/104; Publication No. US20050277115A1; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus APPLICANT: Kroger, Burkhard; APPLICANT: Schroder, Hartwig; APPLICANT: Zelder, Oskar
                                                                                                       RESULT 2
US-10-454-437-172
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                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: B.fragilis US-11-079-463-6489
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLERIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOO-03DIV2
FILE REFERENCE: PATHOO-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR PELICATION NUMBER: US 60/128,705
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR PILING DATE: 2000-04-04
PRIOR PILING DATE: 1000-04-04
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 6489
LENGTH: 172
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                                                                                                                                                                                                                           ATSVRKPNKMAAGMKDTVVLAISKDLPPAQGRFCTTEGIENVIPLSDFRFSDFDESYGVR
                                                                                                                                                                                                                                          ATSVRTEDERAAASGAT-VLCVSKDLPFAQKRECGAEGTENVMDASAFRDS-FGEDYGVT
                                                                                                                                                                                                                                                                                    MATTNEKGQPVKLIGBEIQVGKVAPDEELVKSDLSSFALKDLKGKNIVLNIEPSLDTGVC
                                                                          Application US/10454437

o. US20050277115A1
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US-11-075-554A-283
US-11-075-185-5
US-11-188-298-13811
US-11-188-298-17714
US-10-506-454-206
US-11-188-298-15480
US-11-188-298-15480
US-11-188-298-15480
US-11-188-298-15066
US-11-188-298-15065
US-11-188-298-15207
US-11-096-568A-10657
US-11-096-568A-27148
US-11-096-568A-30526
US-11-096-568A-30526
US-11-096-568A-30526
                                                                                                                                                                                                                                                                                                                                             Score 467; DB 7;
Pred. No. 9.4e-40;
8; Mismatches 47
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466.5 341.5 307 2280 225 121.5 117.5 1117.5 1114.5

Minimum DB Maximum DB

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Title: Perfect score:

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Scoring table: Sequence:

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                                                                                                                                                                                                                                                                                                                                                     Sequence 174, Application US/10454437 Publication No. US20050277115A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 442 SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                    CURRENT APPLICATION NUMBER: US/10/454,437
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                             APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
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PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
PRIOR APPLICATION NUMBER: DE 19932125.6 PRIOR FILING DATE: 1999-07-09
                                                                                                                                                                             FILE REFERENCE: BGI-128CPCN
                                                                                                                                                                                                                                                                                                            APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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FILING DATE: 1999-07-14
APPLICATION NUMBER: DE 19932922.2
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FILING DATE: 1999-07-19
APPLICATION NUMBER: DE 19932226.0
FILING DATE: 1999-07-09
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FILING DATE: 1999-07-09
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Pred. No. 1e-39;
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US-10-793-626-252
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US-10-793-626-252
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                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 252
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 252, A Publication No.
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CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
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NUMBER OF SEQ ID NOS: 4472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 442
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT
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OR APPLICATION NUMBER: DE 19932127.2
OR FILING DATE: 1999-07-09
OR APPLICATION NUMBER: DE 19932128.0
OR FILING DATE: 1999-07-09
OR APPLICATION NUMBER: DE 19932129.9
OR APPLICATION NUMBER: DE 19932129.9
OR FILING DATE: 1999-07-19
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                                  120 ADGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAA 162
                                                                          61 DSQTRKFNERASAEDGVVLTISVDLPFAQKRWCASSGLDNVITLSDHKDLSFGRNYGLVM
                                                                                                              61 ATSVRTFDERAAASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTI 119
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                                                                                                                                                                                                                                                  Similarity
DE---LRLLARSVFVLNENNKVVYKEIVSEGTNYPDFEAALKA
                                                                                                                                                    MTQTTFKNNPIKLSGSEVNEGDIAPNPTVLDNSLNQTTLDDYKNKKKLISVIPSIDTGVC
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o. US20050255478A1
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Pred. No. 1.1e-23;
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TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAMSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 81, Application US/11098686 Publication No. US20060024696A1 GENERAL INFORMATION:
                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 81
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METH
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR PILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: WS 60/416,395
PRIOR FILING DATE: 2002-10-04
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                 LENGTH: 126
TYPE: PRT
ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 33.7%; Score 280; DB 7; Length 172; Local Similarity 38.7%; Pred. No. 6.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 E---LRILARAVFVVDTNGMITYQBIVPEMTHEPNYTAIFEAV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DGPMAGLLARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 VRTPDBRAAASG--ATVLCVSKDLPPAQKRFCGAEGTENVMPASAFRD-SFGEDYGVTIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Conservative
                                                                                                                                                            h 27.1%; Score 225; DB 7; Length 126; Similarity 42.9%; Pred. No. 1.5e-15; Similarity 42.9%; Mismatches 44; Indels
  SAFRD-SFGEDYGVTIADGPMAGLLARAIVVIGADGNVAYTELVPBIAQEPNYBAALAA 162
                                                        LILSAVPSLDTGVCDIETQRFNSEAAKLGEKVRILTISCDLFFAQARWCGATGVSAVETL 70
                                                                                                           VLLNIFPSVDTPVCATSVRTFDERAAASG--ATVLCVSKDLPFAQKRFCGAEGTENVMPA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TORPNSEAAKLGEKVRILTISCOLPPAQARWCGATGVSAVETLSDHRELSFGYAYGIAIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITFLGNPLTLMGNPVSIGEKAPDFTVLANDLSPRTLSDYANNILILSAVPSLDTGVCDIE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
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                                                                     US-10-642-272A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-642-272A-5
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US-11-074-176-70
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                                                                                                                                    SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10642272A Publication No. US20050277606A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 381
SOFTWARE: PastSEQ for Wind
SEQ ID NO 70
                        Query Match
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Best Local Similarity
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                                                                                                                                                                                                   APPLICANT: Hattori, Pumiyuki
APPLICANT: Sugimura, Keijiro
APPLICANT: Puruya, Mayumi
TITLE OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777.000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: PCT/JP02/01358
PRIOR FILING DATE: 2001-02-18
PRIOR APPLICATION NUMBER: JP 41003/2001
PRIOR FILING DATE: 2001-02-16
RIOR SEQ ID NOS: 30
RUMBER OF SEQ ID NOS: 30
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Klaenhammer, Todd R.
                                                                                           ORGANISM: Rattus norvegicus
                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GPWAGILARAIVVIGADGNVAYTELVPEIAQEPNYEAALAAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 QTKTFNKAMDKFPEINFLTISTNTIEDQQTWCAAEDVKNMKLMSDKNLSFGKATGLLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 SVRTFDERA-AASGATVLCVSKDLPFAQKRFCGAEGTENVMPASAFRDSFGEDYGVTIAD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QITLEGNAINTYGELPAYGSPAPAFTLTGGDLGVISSDQFEGKSVLLNIFPSVDTPYCAT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altermann, Bric
McAuliffe, Olivia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Russell, William M.
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14.6%;
26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.9%; Score 215; DB 7; Length 164; 32.7%; Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches
Score 121.5; DB 6
Pred. No. 9.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                     9
                        Length 257;
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Matches

18

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126

RESULT 9

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RESULT 10
US-10-642-272A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-642-272A-6
                                                                                                                                                                                                             Sequence 28, Application US/10642272A
Publication No. US20050277606A1
GENERAL INFORMATION:
APPLICANT: Hattori, Fumiyuki
APPLICANT: Sugimura, Keijiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hattori, Fumiyuki
APPLICANT: Sugimura, Keijir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10642272A Publication No. US20050277606A1
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Best Local Similarity
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APPLICANT: Furuya, Mayumi
TITLE OP INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OP INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777.000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT PILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: PCT/JF02/01358
PRIOR PILING DATE: 2001-02-18
PRIOR PILING DATE: 2001-02-18
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
APPLICANT: Sugimura, Keijiro
APPLICANT: Furuya, Mayumi
TITLE OP INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OP INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777,000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT FILING DATE: 2003-08-18
FRIOR APPLICATION NUMBER: DCT/DP02/01358
PRIOR APPLICATION NUMBER: JP 41003/2001
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NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GIALRGLFIIDPNGVVKH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 HDVNCEVVAVSVDSHFSHLAWINTPRKNGGLGHMNITLLSDITKQISRDYGVLLES---A 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PAVGSPAPAF---TLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDERAAA- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 --SGATVLCVSKDLPFAQKRFC-----GAEGTENVMPASAFRDSFGEDYGVTIADGEMA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 -- SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAVTQHAPYFKGTAVVNGEFKELSLDDFKGKYLVLFFYFLDFTFVCPTEIVAFSDKANEF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAVGSPAPAF---TLTGGDLGVISSDQFRGKSVLLNIFFSVDTFVCATSVRTFDERAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.6%; Score 121.5; DB 6; Length ilarity 29.0%; Pred. No. 9.6e-05; Conservative 19; Mismatches 64; Indels
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                                                                           RESULT 12
US-10-821-234-1038
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US-10-642-272A-4
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     Sequence 1038, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10642272A Publication No. US20050277606A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 28
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APPLICANT: Sugimura, Keijiro
APPLICANT: Sugimura, Keijiro
APPLICANT: Puruya, Mayumi
TITLB OF INVENTION: Therapeutic Methods and Agents for Diseases Associated with
TITLE OF INVENTION: Decreased Expression of AOP-1 Gene or AOP-1
FILE REFERENCE: 58777.000012
CURRENT APPLICATION NUMBER: US/10/642,272A
CURRENT PILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: PCT/JP02/01358
PRIOR APPLICATION NUMBER: JP 41003/2001
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 14.1%; Score 117.5; DB 6; Local Similarity 29.0%; Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 AYRGLFIIDAKG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 LARAIVVIGADG 139
                                                                                                                                                                                                                       126 GLLARAIVVIGADGNVAY 143
                                                                                                                                                                                                                                                                      123 HDVNCEVVAVSVDSHFSHLAWINTPRKNGGLGHMNIALLSDLTKQISRDYGV-LLEG--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                   18 PAVGSPAPAF---TLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVCATSVRTFDERAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMAGL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 VGSPAPAFTLTG---GDLGVISSDQFRGKSVLLNIFPSVDTFVCATSVRTFDERA---AA 73
                                                                                                                                                                                                                                                                                                                      74 -- SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
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                                                                                                                                                                          GLALRGLFIIDPNGVIKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTKSLSQNYGVLKND---EGI 124
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US-10-527-771-6
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US-10-821-234-1038
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
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SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1038
LENGTH: 206
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Best Local :
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TITLE OF INVENTION: Ostertagia vaccine
FILE REFERENCE: 2002-015
CURRENT EPPLICATION NUMBER: US/10/527,771
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US 10/243,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Ostertagia ostertagi
PEATURE:
NAME/KEY: misc_feature
LOCATION: (72)...(72)
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  128 LARAIVVIGADG 139
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                                                                                                                                                                                                36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNAINTVGELPAVGSPAPAFTLTG----GDLGVISSDQFRGKSVLLNIFPSVDTPVCATSV 64
                                      IDAAVLACSXDSVFSHLAWINTPRKMGGLGDMNIPVLADTNHQIAKDYGVLKED---EGI 119
                                                                           SGATVLCVSKDLPFAQ-----KRFCGAEGTENVMPASAFRDSFGEDYGVTIADGPMAGL 127
                                                                                                                  IĞKPAPDFATKAVYNĞDFIDVKLSDYKĞKYTVLFFYPLDFTFVCPTBIIAFSDRVBBFKK 62
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                                                                                                                                                                                                                 12.8%;
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                                                                                                                                                                                                                 Score 106.5; DB Pred. No. 0.0021;
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, NAME/KEY: misc feature
; LOCATION: (1). (216)
; OTHER INFORMATION: Ceres Seq. ID no. 13599403
US-11-096-568A-1038
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US-11-096-568A-1038
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; LENGTH: 216
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1037
                                                                                                                                Matches
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                                                                                                                                                  Query Match
Best Local Similarity
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TITLE OF INVENTION: Sequence-Determined DNA
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1592FUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(226)
OTHER INFORMATION: Ceres Seq. ID no. 13599402
                                                                                                                                                                                                                                                                                                           LENGTH: 226
TYPE: PRT
ORGANISM: Zea mays subsp.
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                                            82
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                                                                               21 GSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC---ATSVRTFDERAAASGAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GSPAPAFTLTGGDLGVISSDQFRGKSVLLNIFPSVDTPVC---ATSVRTFDERAAASGAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 11.9%; Score 99; DB 7; Similarity 28.1%; Pred. No. 0.014; 36; Conservative 25; Mismatches
VLCVSKDLPFAQKRFCGAEGTENVMPASAFRDS----FGEDYGVTIADGPMAGLL-ARAIV 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOSAPDETLKOQNGKPVSLKKYKGKPVVVYFYPADETPGCTKQACAFRDSYSKFKKAGAS 131
                                            GOSAPDFTLKDQNGKPVSLKKYKGKPVVVYFYPADETPGCTKQACAFRDSYEKFKKAGAE
                                                                                                                                Conservative
                                                                                                                            11.9%; Score 99; DB 7; Length 226;
28.1%; Pred. No. 0.015;
tive 25; Mismatches 53; Indels
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Maximum Match
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Abm41697 Prop
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21-JAN-1999 AAW72889;

(first entry)

tuberculosis antigen CFP22.

tuberculosis; antigen; vaccine; immunological; immunogen;

AAW72889 standard; protein;

182 AA

Mycobacterium Mycobacterium

infection.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25
352	352	358.5	358.5	358.5	359	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	359.5	370	373	374
36.6	36.6	37.3	37.3	37.3	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	38.5	38.8	38.9
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## ALIGNMENTS

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RESULT 1
AAW772889
ID AAW7
XX AAW7
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XX MYCC

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18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                                                                                                                                                                 New isolated mycobacteria polypeptides and nucleic acids developing products for the diagnosis of or vaccination a mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-542705/46.
N-PSDB; AAV63920.
                                                                                                                                                                                                                                           Claim
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Oettinger T,
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97US-0044624P.
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against
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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

or M. bovis

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RESULT 2
AAY21906
ID AAY2
XX AAY2
AC AAY2
XX CAAY2
XX DT 06-S
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XX Immu
XX Immu
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Matches 182;
The invention describes a substantially pure immunogenic polypeptide fragment (1) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (1) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic; Mycobacterium tuberculosis; immune response; intuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; Mt pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP7B; CFP19; CFP27; CFP3OA; RD1-ORF; CFP1OA; CFP16; CFP19;
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01-APR-1998;
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98US-0070488P.
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Pred. No. 3.2e-93;
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Best Local :
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                                                                                                        WPI; 2001-376931/40.
N-PSDB; AAH65004.
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Senoh A,
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Ikeda M,
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Pred. No. 3.2e-93;
                                                                                                                                                                                 S, Hayashi
Ozaki A;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                        21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, oardicularly 1-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                           20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                              01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                              WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes immunogenic protein #6074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU45178 standard; protein; 182
                                                                                     WPI; 2001-616774/71.
                                                                                                                        L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17;
                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIQGEMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPHLNNAHTIFGEVTDAESOKVVDAIATTATDRYDRPADAVVIESVEIT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIDGFMIQGGDPTGTGRGGPGYTFADBFHPELRFDRAYLLAMANAGPGTNGSQFFITVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAILHTURGDITIDLFGNHAPETVANFVGLAQGTKDYQSANAQGDSEGPFYNGSVFHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                      Persing DH, |
e J, Zhang Y,
                                                                                                                                                                                                        2000US-0199047P.
2000US-0208841P.
2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.5%;
                                                                                                                      Mitcham ,
Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 716; DB 4;
Pred. No. 2.9e-67;
1; Mismatches 23
                                                                                                          n JL,
c Carter
                                                                                                                                      Wang
                                                                                                                      g ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 187
                                                                                                                                        Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 5
ABM41697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. cones is also involved in infections of bone, joints and the central conervous system, however it is particularly involved in the inflammatory lesions associated with acnes vulgaris. A method for detecting the corresponding the amount of bone proteins of the invention and determining the amount of bound protein in the sample. The condition of antibodies specific for P. acnes proteins. These antibodies can be used to convergulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins. The satisface of the invention converged in the diagnostic agents for determining P. acnes presence, for example, by central did not form part of the printed specification, but was considered in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                            Mitcham JL, Skeiky YAW, Pe
Zhang Y, Wang S, Jen S, I
Barth B, Vallieve-Douglass
WPI; 2003-381789/36
                                                                                                                              15-OCT-2001; 2001US-00978825
                                                                                                                                                            11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                               WO2003033515-A1
                                                                                                                                                                                                                                                              Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                              ABM41697;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM41697 standard; protein; 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                            Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                            immunostimulant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 ATATLHTURGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV 74
                                                                                                 CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATERTNHGDIVENEPADQAPKTVDNFVGLAGGTKEYVDPHTGQPTTGKFYDGETFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHLNRRHTIFGEVADEESRKVVDEIAQVRTGRMDRPVEPVVIESVELA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHLNRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDGFMIQGGCPLGTGGGGGGRFADEFHPELTFSKPYLLAMANAGPGTNGSQFFITVAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQGFMIQGGDFTGTGRGGFGYKFADBFHFBLQFDKFYLLAMANAGFGTNGSQFFITVGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6373; 1069pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                            immune response; vaccine;
                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%;
                                               Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 607; DB 4;
Pred. No. 9.9e-56;
6; Mismatches 37
                                               Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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                                                                                                                                                                                                                                                                                                                                               #6373
                                                                Maisonneuve JL;
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ABM94799
ID ABM9
XX ABM9
AC ABM9
XX O2-J
XX Trai
XX Trai
XX Myx
XX Mx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC encoding a Propionibacterium acnes protein. The invention also relates to CC polypeptides encoded by the polypucleotides (ABM3524-ABM64536) and to CC immunogenic fragments of P. acnes polypeptides. The invention CC additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; a comprising a polypeptide of the invention; a comprising a polypeptide of the invention; a cc invention; an isolated T cell population comprising T cells prepared CC via this method; a vaccine composition (comprising P. acnes polypeptides, or complete the composition proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a cc patient; and a method for inhibiting the development of P. acnes in a cc patient; and a method for inhibiting the development of P. acnes in a cc patient; and a method for inhibiting the development of P. acnes in a cc patient; and a method for inhibiting the development of P. acnes in a cc patient; and a method for inhibiting presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes crocked proteins, T cell populations or antigen-presenting cells that express the polypeptides can also be used as probes or primers for collect acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes polypeptide which is equence represents a specifically claimed P. acnes polypeptide which is thought to contain an immunogenic region. Note: The sequence data for the role of the present contains an immunogenic region. Note: The sequence data for the contain an immunogenic region.
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Best Local &
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                                                                                                                                                                                                                                                                                                                         M. xanthus
                                                                                                            US6833447-B1
                                                                                                                                                                               Myxococcus xanthus
                                                                                                                                                                                                                                                  Transgenic
                                                                                                                                                                                                                                                                                                                                                                                                   02-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this patent did not form part of the printed specification, obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATTHTURGDIKIALFGNHAPKTVANFYGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHLNRRHTIFGEVADEESRKVVDBIAQVRTGRMDRPVBPVVIESVELA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDGFMIQGGCPLGTGTGGPGYRFADEFHPELTFSKPYLLAMANAGPGTNGSQFFITVAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 AA;
                                                                                                                                                                                                                                                  plant; DNA
                                                                                                                                                                                                                                                                                                                         protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.2%;
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                                                                                                                                                                                                                                                     replication; gene regulation;
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Pred. No. 9.9e-56;
6; Mismatches 37;
                                                                                                                                                                                                                                                                                                                     seq id 13998.
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                                                                                                                                                                                                                                                     gene
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89 75 N

RRSULT 7
ABB66190
ID ABB66
XX ABB6
XX ABB6
XX B1f1
XX Iden
XX

rotavirus;

food

composition; pharmaceutical

Bifidobacterium

longum

30-JAN-2001; 2001EP-00102050 30-JAN-2001; 2001EP-00102050

208

PROD NESTLE SA

31-JUL-2002.

antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;

Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;

Bifidobacterium longum NCC2705 ORF amino

acid sequence SEQ

ä

NO:884.

ABP66140;

19-NOV-2002

(first entry)

ABP66140 standard; protein;

182

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                                                                                                                                                                                                                    Query Match
Best Local &
                                                                                                                                                                                                                                                                                                  The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDS 9692-16825 represent a group of 7134 Mayococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldman
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 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BS,
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                       182
 YLNNRHTIFGEVVSGYD--VVEKISNVQRDPRDKPLEPVVIQKIAMS
                              HLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIBSITIS 182
                                                                                             QGFMIQGGDPTGTGRGGPGYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP
                                                                                                                                   ATLETNOGAIVVRLFSKDAPKTVANFVGLATGEKAWTDPKTGQRVEGKPLYDGVIFHRVI
                                                                                                                                                                  ATLHTNRGDIKIAL FGNHAPKTVAN FYGLAQGTKDYSTQNASGGPSG-PFYDGAVFHRVI
                                                                   PGFMIQGGDPTGTGRGDPGYRFEDEFQSGRTFDKKGLLAMANAGPGTNGSQFFITTSTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                       AA,
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                                                                                                                                                                                                                      51.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13998;
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                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25pp; English.
                                                                                                                                                                                                                      Score 494.5; DB 9
Pred. No. 8.2e-44;
                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                       9,
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                      Length 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC sequences given in ABQ81842 and ABQ81843, or a sequence given in aC (1) east 90% identity or which hybridises with the sequence given in CC ABQ81842 and ABQ81843. Also described is a polymucleotide (II) encoding a CC fusion protein, comprising a sequence selected from 1997 sequence given in ABP65258 to ABP66354 ligated in frame to a polymucleotide encoding a CC heterologous polymeptide. (I) has antidiarrheic and antibacterial CC activities, and can be used as an inhibitor of Salmonella. (I) (which is CC a probe) is useful for the detection and/or identification of CC lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM 1-2618) can be CC used for preventing and/or treating diarrhoea brought about by pathogenic CC bacteria and/or rotavirus. The carrier is a food composition selected CC products, ice-creams, fermented cereal based products, milk based from milk, yogurt, curd, cheese, fermented milks, milk based fermented CC products, infant formula, pet food or a pharmaceutical composition selected CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent CC nifthobacterium related milesting diven in the Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                              detection;
                                                                                                                                                                                                                                08-SEP-2005 (first entry
                                                                                                                                                                                                                                                                                                                  AEB41604 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bifidobacterium related nucleotide sequences given in the Sequence Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of a Bifidobacterium genome selected sequences given in ABQ81842 and ABQ81843, or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a polynucleotide (I) comprising sequence of a Bifidobacterium genome selected from the nucleotion
                                                                WO2005049642-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 884; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                       pneumophila protein SEQ ID NO 5936
                                                                                                                                                                                                                                                                                                                                                                                                                       125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                     QFFITTVPTPWLDGHHTIFGEVADDDSKKVVDKLEALDTDPMDRPLEPAVILSVDVA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQGFMIQGGDFTGTGRGGFGYKFADEFHPELQFDKFYLLAMANAG-------PGTNGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIIMNTSEGSITINLEDDKAPNTVANFLGLATGEKEWA-DPYTGQPSHGKFYNGLTFHRI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS-GPFYDGAVFHRV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I KQFMI QGGCPLGTGTGGPGYEFDDE I DPSLKFDKPYLLAMANAGLRRGMDGKVHGTNGS
                                                                                                     pneumophila
                                                                                                                                              infection; Antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                               protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 465.5; DB 5
Pred. No. 9.6e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
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RESULT 9
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Best Local (
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Rusniok C, Bo
Jarraud S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as veccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents the amino acid sequence of a processive contains the present squence represents the amino acid sequence of a prevention of the present squence of a prevention of the present squence represents the amino acid sequence of a prevention of the present squence of a prevention of the preventi
                                                                                          WO2005049642-A2
                                                                                                                                    Legionella pneumophila.
                                                                                                                                                                                  detection; infection; Antibacterial; Vaccine
                                                                                                                                                                                                                                L. pneumophila protein SEQ ID NO 2657
                                                                                                                                                                                                                                                                                 08-SEP-2005
                                                                                                                                                                                                                                                                                                                             AEB38325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 5936; 660pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides, useful for detection or ident for treatment and prevention of infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-2004; 2004WO-IB003578
                                                                                                                                                                                                                                                                                                                                                                         ABB38325 standard; protein; 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-388305/40
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INST NAT SANTE & RECHUNIV LYON 1 BERNARD CLAUDE.
CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGFMIQGGDFTGTGRGGFGYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
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                                                                                                                                                                                                                                                                               (first entry)
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56.6%;
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Zidane N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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Pred. No. 3.4e-40;
L7; Mismatches 52
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Vandenesch F;
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23-SEP-2004; 2004WO-IB003578

02-JUN-2005

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RESULT 10
AAW44191
ID AAW44
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Best Local Similarity
Matches 94; Conserv
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Rusniok C,
Jarraud S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 205 AA;
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(INRM)
(UYLY-)
(CNRS)
                                                                                                                                                                      Cyclophilin cyclosporin
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08-JUN-1998
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                                                                           JP09313184-A
                                                                                                                          Halobacterium
                                                                                                                                                                                                                                                    Cyclophilin
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INSERM INST NAT SANTE & RECH MEDICALE.
UNIV LYON 1 BERNARD CLAUDE.
CNRS CENT NAT RECH SCI.
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Bouchier C,
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ilarity 56.6%;
Conservative 1:
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                                                                                                                                                                                                                                                 type PPIase.
                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                          salinarum
                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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Zidane N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 460.5; DB y;
Pred. No. 3.8e-40;
""" matches 52;
                                                                                                                                                                                                  archaebacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                               Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cazalet C, A, Kunst F,
                                                                                                                                                                                                  ımmunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glaser P;
Vandenesch F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  片
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     片
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RESULT 11
ABU0198
ID ABU01
XX ABU01
XX ABU01
XX ABU01
XX ABU01
XX Bacte
XX Bacte
XX Bacte
XX Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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                                       WPI; 2003-040579/03.
N-PSDB; ABX07287.
                                                                                                                                                                                                                                                                                                          Bacterial meningitis; pneumonia;
antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2003
11-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a cyclophilin type PFIase gene from a halophilic archaebacterium, Halobacterium cutrubrum. The cyclophilin type PFIase may be combined with an immunosuppressant cyclosporin A. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                 27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; type 4 strain
                                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae type 4 strain protein from coding
                                                                                                                                                                                                                                                                                                                                                                                                                         ABU01998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               archaebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                 Masignani V,
                                                                                                                                                      27-MAR-2001; 2001GB-00007658
                                                                                                                                                                                                                                        WO200277021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU01998 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cyclophilin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-080075/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1996;
                                                                                                            (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5;
                                                                                                                            (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 OFFITVGKTPHLNRRHTIFGEVIDAESORVVEAISKTATDGNDRPTDPVVIESITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 YAGVSFHRIIEGFMIQGGDPTGTGRGGPGYEFADEFHDDLTHDGPGVLSMANSGPDTNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 YDGAVFHRVIQGFMIQGGDFTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNA------SGGPSG-PF
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                                                                                                            CHIRON SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFFITLDAQPHLDGRHAVFGAVTD--GMDVVETIGDVETDANDAPASEITIDRVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATVHTSEGEFDIELYDERAPRTVENFLNLARHEPAADADPAPDTVTWEDPESGEIRGDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.9%; Score 431.5; llarity 50.0%; Pred. No. 3.: Conservative 20; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
                                                                                                             GENOMIC
                                                                                 Tettelin
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                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                             RES.
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                                                                                 Ξ
                                                                                   Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                            sepsis; otitis media; ear infection;
immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purified from halophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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124 125 64

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New proteins and nucleic acid molecules useful as medicaments for treating or pr

preventing

Streptococcus ting a disease

pneumoniae, or infection

from

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RESULT 12
ABP81616
ID ABP81
XX ABP81
XX ABP81
XX ABP81
XX ABP81
XX Strep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC identity to any of the 2469 amino acid sequences, identity to any of the 2469 amino acid sequences, identitied in the CC specification (available on a computer readable format), or its fragment, CC expressed from 2469 of 2489 identified DNA coding regions from the CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC treating a patient by administering the protein, DNA or antibody (in a CC composition), a kit comprising first and second primers, which are the CC sequence contained within a Streptococcus nucleic acid sequence where the second primer is substantially complementary to the target sequence to the target sequence, and where the parts of the primers having CC substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound with the carding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus successed by the identified coding regions from the genomia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, contactives and antiblotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins of the putner sequence.

CC expressed by the identified coding regions from the genomic sequence.

CC expressed by the identified coding regions from the genomic sequence.

CC expressed by the identified of the printed of the printed specification, but was obtained in electronic format directly from WIPO at the printed on 27.0CT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
  Streptococcus pneumoniae
                                                                                                              Streptococcus
                                                                                                                                                         04-MAR-2003
                                                                  Streptococcus pneumoniae;
                                                                                                                                                                                                                                            ABP81616 standard; protein; 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences. (Updated
undardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to streptococcus bacteria, such as pneumonia, sepsis, otitis media or infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                               376
                                                                                                                                                                                                                                                                                                                                                          436
                                                                                                                                                                                                                                                                                                                                                                                                   153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GPFYDGAVFHRVIQGFMIQGGDPTGTGRGGP---GYKFADBFHPBIQFDKPYLLAMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                          YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                                                                                                                                                                                                                                                                                                                                                   QRVVEAISKTATDGNDRPTDPVVIESITI
                                                                                                                                                                                                                                                                                                                                                                                                                                          PNTNGSQFFIVQNQHLFYSKKEITRGGWPEFIAEIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGTNGSQFFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3150; 56pp; English
                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                         (first entry)
                                                                                                           pneumoniae polypeptide SEQ ID NO 694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%;
                                                                  infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein comprising or having at least 50 gamino acid sequences, identified in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 407.5; DB 6
Pred. No. 4.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TVGKTPHLNRRHTIFGEVIDAES
                                                                  otitis media; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on 23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152
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                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                         variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABBR1299-ABR91674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus pneumoniae polynucleotides, useful preventing S. pneumoniae infections, or non-systemic otitis media, which are induced or exacerbated by S.
                                                                                                                                                                                                                                                                                                                 Sequence 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 42; Page 987-989; 1091pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-2001; 2001US-0283948P
18-APR-2001; 2001US-0284443P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zagursky RJ,
Wooters JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2002; 2002WO-US011524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200283855-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-093010/08
                                                                                                                         318 -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                         277
                             153 QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                        63
                                                                                                                                                                                                                     3 DCDSVTNSPLATATATHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the polynucleotide or a nucleic
YAVLDAIAAVETGAMDKPVEDVVIETIEI
                                                                                          PGTNGSQFFI----------TVGKTPHLNRRHTIFGEVIDAES
                                                                                                                                              GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP----GYKFADEFHPELQFDKPYLLAMANAG
                                                                                                                                                                                         DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD-------
                                                            PNTNGSQFFIVQNQHLPYSKKBITRGGWPEPIAEIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masi AW,
                                                                                                                                                                                                                                                                   42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green BA,
                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                    Score 407.5; DB 6
Pred. No. 4.8e-34;
3; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                           Chakravarti DN,
 464
                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                 Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l for treating c diseases, e.g. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Russell DP;
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ADM92196
ID ADM92
XX
AC ADM92
DT 03-JU
XX
OR
DB S pne
XX
AR
AR
XX
AR
DB S pne
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AR
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119

317

375

62

7

152

ADM92196

03-JUN-2004 (first entry)

S pneumoniae antigenic protein ведиепсе SeqID393

antibacterial; gene therapy; Streptococcus pneumoniae infection;

Streptococcus pneumoniae

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RESULT 14
ADK46830
ID ADK46
XX ADK46
XX ADK46
XX ADK46
XX ATEL
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus pneumoniae infection. The present sequence is that of an S pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 466 AA;
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      02-JUL-1997;
                                                               26-MAY-2000;
                                                                                                                               02-MAR-2004.
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                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                  Antibacterial;
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                                                                   2000US-00583110
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                         pneumoniae protein, Seq ID No 3345.
                                                                                                                                                                                                                                                     pneumoniae
                                                                                                                                                                                                                                                                                                            Gene therapy;
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Pred. No. 4.8e-34;
3; Mismatches 41
                                                                                                                                                                                                                                                                                                               Vaccine; Streptococcus
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ADR95835
ADR95835
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Best Local 9
      02-JUL-1997;
12-MAY-1998;
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                                                                                                   30-JUN-1998;
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The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypeptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
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30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                               ADR95835 standard; protein; 472
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                                                                                                                                                                                                         Meningitis; bacteraemia; pneumonia; otitis media; vaccine;
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DB; ADK44169.
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98US-00107433
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                                                                                                                                                                                                                                           sequence,
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Pred. No. 1.3e-33;
23; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC encoding a Streptococcus pneumoniae ADR91365polypeptide, or its CADR94489, ADR94800, ADR94837, ADR94969, ADR95253, ADR95682, ADR94689, ADR94800, ADR94837, ADR94969, ADR95253, ADR95682, ADR96079) or any of the fully defined sequences (appearing as ADR94308, CC ADR96079) or any of the fully defined sequences appearing as ADR91705, CC ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or CC ADR93476 or at least 40, 60 or 300 consecutive nucleotides, which is CC hybridisable under high stringency conditions to the nucleotide sequence. CC The nucleic acids and proteins are chosen from 5206 disclosed sequences. CC Also included are a recombinant expression vector comprising the isolated CC element, a cell comprising the recombinant expression vector and a probe CC comprising at least 20 consecutive nucleotides of the nucleotide comprising at least 20 consecutive nucleotides of the present comprising at least 20 consecutive nucleotides of the present CC invention are useful for the diagnosis, prevention and/or treatment of CC pathological conditions resulting from bacterial infection by CC Streptococcus pneumoniae e.g. pneumonia, bacteraemia, meningitis and CC otits media. The present sequence is one of the 2603 disclosed S. CC pneumoniae porcein sequences. Note: The sequence data for this patent did CC electronic format directly from USPTO at the 2003 disclosed S. CC gneumoniae porcein sequences. Note: The Sequence data for this patent did CC electronic format directly from USPTO at twas obtained in
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.0%; Score 403.5; DB 8; Length 472; Best Local Similarity 44.5%; Pred. No. 1.3e-33; Matches 93; Conservative 23; Mismatches 42; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html?DocID=6800744B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 4470; 151pp; English.
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                                                                                                                                                                                                                                                                                           324 -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG 381
                                                                                                                                                                                                                         63 GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHFELQFDKFYLLAMANAG 119
|:: |: | |:| : ||||:| | 470
                           QRVVBAISKTATDGNDRPTDPVVIESITI 181
                                                                                                PNTNGSQFFIVQNQHLPYSKKEITRGGWPEPIABIYANQGGTPHLDRRHTVFGQLADEAS 441
                                                                                                                                   PGTNGSQFFI------------TVGKTPHLNRRHTIFGEVIDAES 152
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Search completed: April 14, 2006, 17:18:40 Job time: 73.5178 secs

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Title: Perfect score: Scoring table: Sequence: US-10-620-246-12
961
1 MADCDSVTNSPLATATATLH.....ATDGNDRPTDPVVIESITIS BLOSUM62

Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Length DB ID Descrip  182 2 G70698 peptidy  182 2 G70691 probabl  175 2 T36725 peptidy  177 2 T36725 peptidy  189 2 D84342 peptidy  189 2 D84342 peptidy  180 2 A95179 hypothe  466 2 A95179 hypothe  466 2 R98045 peptidy  466 2 R98045 peptidy  466 2 R98045 peptidy  466 2 R98045 peptidy  466 2 A95179 hypothe  466 2 R98045 peptidy  466 2 R98045 peptidy  466 2 R98046 peptidy	.0 466 2 H98045 .1 215 2 A71261	34.8 201 2 T40819	34.8 201 2 T408171 34.8 201 2 T408171 34.7 164 2 H82708	3 3 4 5 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1	5527.55 560			ID G70698 C86910 T51359 T36725 D84342 T43805 A95179	Description  peptidylprolyl isc probable peptidyl- peptidylprolyl isc probable cyclophil peptidylprolyl isc
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CSNCM	CSHUB	A40516	T18577	T18573	T18575	P75261	2 351497	T05314	T26500	A54204	JT0686	CSYC42	S71849	T27467	
peptidylprolyl iso	peptidylprolyl iso	peptidylprolyl iso	peptidylprolyl iso	peptidylprolyl iso	cyclophilin isofor	peptidylprolyl iso	peptidylprolyl iso	hypothetical prote	peptidylprolyl iso	hypothetical prote					

## ALIGNMENTS

ppiA [similarity] - Mycobacterium tuberculosis 8

peptidylprolyl isomerase (EC 5.2.1.8) ppiA [similarity] - Mycobacterium tuberculo N;Contains: cyclophilin
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: G70698
C;Accession: G70698
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70698 Holroyd, Gordon,

Ø

genome

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-182 <COL>

A;Cross-references: UNIPROT:P71578; UNIPARC:UPI000013206D; GB:Z80233; GB:AL123456; NID: A;Experimental source: strain H37Rv Genetics:

A;Gene:

Superfamily: peptidylprolyl isomerase; cyclophilin homology;Keywords: cis-trans-isomerase;9-182/Domain: cyclophilin homology <CYP>

Query Match 100.0%; Score 961; DB 2; Best Local Similarity 100.0%; Pred. No. 4.5e-80; Matches 182; Conservative 0; Mismatches 0; Length 182; Indels 0 Gaps

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S 맑 ঠ 밁 S 밁 S 181 IS 182 121 GTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESIT 180 121 GTNGSOFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIBSIT 61 PSGPFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGP 61 PSGPFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGP 120 1 MADCDSVTNSPLATATIHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGG 1 MADCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGG 60 120 180 60

181

SI 182

RESULT 2 C86910 probable peptidyl-prolyl cis-trans isomerase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

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137

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LTGKHTIFGEVSGEAGRKVVDAIAATPTNPRTDRPLEDVVIESVVV LNRRHTIFGEVIDAESQRVVEAISKTATD-GNDRPTDPVVIESITI 181

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R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltweil, T.; Fraser, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Ske A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C86910
A;Status: preliminary
A;Molecule type: DNA
A;Crose-references: UNIPROT:Q9CDE9; UNIPARC:UPI000013206C; GB:ACGenetics:
A;Gene: ppiA
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidylprolyl isomerase (EC 5.2.1.8) B [validated] - Streptomyces chrysomallus N;Alternate names: cyclophilin; peptidyl-prolyl cis-trans isomerase C;Species: Streptomyces chrysomallus C;Date: 18-Aug-2000 #sequence_revision #sequence_r
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C; Superfamily: peptidylprolyl is
C; Keywords: cis-trans-isomerase
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R;Cole, S.T.; Eiglmeier, K.; Parkhill,
R.; Davies, R.M.; Devili, K.; Duthoy,
                                                                                                                                                                                S
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A;Title: ScCypB is a novel second cytosolic cyclophilin
A;Reference number: Z25383
A;Accession: T51359
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A; Residues: 1-175 < PAH>
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;Accession: T5:159
;Pahl, A.; Gewies, A.; Keller, U.
icrobiology 143, 117-126, 1997
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 104; Conserv
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                                       GFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPH 136
                                                                                                                                                                   ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQ 76
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GFMIQGGDPLGNGTGGPGYKFADEFHPELGFTQPYLLAMANAGPGTNGSQFFLTVSPTAW 126
                                                                                                                            ATLKTNRGDIEIRLLPNHAPKTVRNFVELATGQREWVNPETGEKSTDRLYDGTVFHRVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSGPFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAHCDEVTNSLIQNATATLHTNRGDIKVALEGNHVPKTVANEVGLAQGTKEYSTQNASGG
                                                                                                                                                                                                                                                                                                                                                                                                    (EC 5.2.1.8) [validated, Neptidylprolyl isomerase;
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIPROT: P77949; UNIPARC: UPI0000132073; EMBL: U64692; PIDN: AAB51775.1
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90.1%;
                                                                                                                                                                                                                                                                                  54.9%;
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                                                                                                                                                                                                                                              Score 527.5; DB
Pred. No. 1e-40;
6; Mismatches 4
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Pred. No. 8.4e-73;
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; cyclophilin h
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Fraser, P
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Holroyd,
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R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G. Jung, K.H.; Alam, M.; Freitas T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Contains: cyclophilin
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: D84342
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C;Superfamily: peptidylprolyl isomerase;
C;Keywords: cis-trans-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T36725
R;Murphy, L.; Harris, D.; Bentley, S.D.;
submitted to the EMBL Data Library, June
A;Reference number: Z21612
                                                                                                                                                                       A; Gene: ppiA
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptidyl-prolyl isomerase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
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A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9HNW6; UNIPARC:UPI00000639D6; GB:AE004437; NID:g10581353;
                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-189 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                       Status: preliminary
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Best Local (
                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 WLNRKHTIFGEVTDAASQKVVDTIAAARTNPRTERPLTDIVIESVVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 HLNRRHTIFGEVIDAESQRVVEAISKTATD-GNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS-GPFYDGAVFHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
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                                      2 ADCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNA----
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                                                                                                                                                                     peptidylprolyl isomerase; cyclophilin homology
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-MPVDATVHTSEGEFDIELYDERAPRTVENFLNLARHEPAADADPAPDTV
                                                                                                       45.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                  21;
                                                                                                       Score 434; DB 2;
Pred. No. 3.6e-32;
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Pred. No. 1.3e-40;
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                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [similarity] - Streptomyces coelicolor
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                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                       18;
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                                                                                  Gaps
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RESULT 7
A95179
A95179
hypothetical protein SP1538 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95179
R;Tettelin, H; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, B.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95179
A,Science 1900.
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-180 <IID>
A;Cross-references: UNIPROT:O50586; UNIPARC:UPI0000062A42; EMBL:AB002414; NID:g2760611;
A;Cross-references: UNIPROT:O50586; UNIPARC:UPI0000062A42; EMBL:AB002414; NID:g2760611;
A;Onte: the source is designated as Halobacterium cutirubrum
C;Genetics:
A;Gene: Cyp
C;Function: A;Gene: Cyp
C;Function: cyclophilin-type peptidyl-prolyl cis-trans isomerase [validated, MUID:980
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
C;Keywords: cis-trans-isomerase
F;1-179/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptidylprolyl isomerase (BC 5.2.1.8) cyp [similarity] - N;Contains: cyclophilin C;Species: Halobacterium salinarum C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_C;Accession: T43805 R;Iida, T.; Furutani, M.; Iwabuchi, T.; Maruyama, T. Gene 204, 139-144, 1997
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A;Title: Gene for a cyclophilin-type peptidyl-prolyl cis-trans
A;Reference number: Z22692; MUID:98094265; PMID:9434176
A;Accession: T43805
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Best Local S
Matches 88
                                     Molecule type: DNA
Residues: 1-466 <KUR>
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           Cross-references: UNIPROT:Q97PR4; UNIPARC:UPI00000518B5; GB:AE005672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDGAVFHRVIQGFMIQGGDFTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGPGTNGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWEDPESGEIRGDSLYAGVSFHRIIEGFMIQGGDPTGTGRGGPGYEFADEFHPELQFDKP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNA-----SGGPSG-PF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASEITIDRVEI 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVLSMANSGPDTNGSQPPITLDAQPHLDGRHAVFGAVTD--GMDVVETIGDVETDANDAP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLLAMANAGPGTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFFITLDAQPHLDGRHAVFGAVTD-
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Pred. No. 5.7e-32;
O; Mismatches 55;
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        PIDN: AAK75626.1;
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RESULT 9
A71261
peptidylprolyl isomerase (EC 5.2.1.8) TP0947 [similarity] - syphili N;Contains: cyclophilin
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-
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hypothetical protein spr1393 [imported] - Streptococcus pneumoniae (strain i C/Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H98045
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dei
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; Mt
y, P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Ja:
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H98045
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C;Genetics:
A;Gene: SP1538
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                                                                                                                                                                              63
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YAVLDVIAAVETGAMDKPVEDVVIETIEI 464
                                   QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                    PNTNGSQFFIVQNQHLPYSKKBITRGGWPEPIABIYANQGGTPHLDRRHTVFGQLADBAS
                                                                                                           PGTNGSQFFI-----
                                                                                                                                             -GYYDGVIFHRIIKOFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                              GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADSFHPSLQFDKPYLLAMANAG 119
                                                                                                                                                                                                                    DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD----
                                                                                                                                                                                                                                      DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GYYDGVIFHRIIKDFMIQGGDFTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
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                                                                                                                                                                                                                                                                                                         Score 403.5; DB 2;
Pred. No. 6.4e-29;
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Pred. No. 2.8e-29;
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                                                                                                           TVGKTPHLNRRHTIFGEVIDAES 152
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(BC 5.2.1.8) TP0947 [similarity] - syphilis spirochete

#text\_change 09-Jul-2004

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179 QDKPVDDVVIESVEI

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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: A71261
A;Accession: A71261
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <COL>
A;Cross-references: UNIPROT:066105; UNIPARC:UPI0000132074; GB:AE001263; GB:AE000520; A;Experimental source: strain Nichols
C;Genetics:
A;Experimental source: strain Nichols
C;Genetics: TP0947
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;34-206/Domain: cyclophilin homology <CYP>
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R;Fraser; C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, Nthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-196 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain
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167
                                             119 KNLPYPKDSLIQGGWPEEVAETYTGGGTPHLDGRHTVFGQLVDEESYKVLDEIAAVRVGA 178
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NDRPTDPVVIESITI
                                                                                                                                     KDFMVQGGDPTGTGMGGSSIYGEKFEDEFSMDL-FNLRGALSMANAGPNTNGSQFFIVQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFYQGLTFHRVIKDFMIQGGDPQGNGTGGPGYQFPDECDPALRHDSPGVLSMANAGPGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VREEGLAVADGIYAVMETNRGTIVLSLFFEKAPLTVCNFVGLAEGT------LAVCKGR
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.1%;
                                                                                                                                                                                                                                                                                                                                              41.1%; Score 394.5; DB 2
43.1%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 395; DI
; Pred. No. 1.50
15; Mismatches
                                                                                                                                                                                                                                                                                                                        26; Mismatches
                                                                                     TVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
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                                                                                                                                                                                                                                                                                                                                                                   Length 196;
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                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                        45;
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M.; Utterback,
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                   129
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RESULT 11
T48940
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A;Residues: 1-629 <UGR>
A;Residues: 1-629 <UGR)
A;Cross-references: UNIPROT:Q9LXM7; UNIPARC:UPI00000A046D; EMBL:AL353818; GSPDB:GN00061;
A;Experimental source: cultivar Columbia; BAC clone F14L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F14L2.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 62/2; 91/1; 120/3; 200/3; 241/2; 266/3; 302/3; 361/3; 434/2; 476/3; 551/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T48940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z25008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T48940
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
Gene: ATSP:F14L2.150
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
583 WLDNKHTVFGRVV--KGMDVVQGIBKVKTDKNDRPYQDVKILNVTV
                                                  136 HLWRRHTIFGEVIDAESQRVVEAISKTATDGWDRFTDFVVIESITI 181
                                                                                                     523 MIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDRPFTLSMANAGPNTNGSQFFITTVATP
                                                                                                                                                                                                          478 MHTTLGDIHMKLYPEECPKTVENF
                                                                                                                                                                                                                                                                                                             79;
                                                                                                                                                79 MIQGGDPTGTGRGGP----GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
                                                                                                                                                                                                                                             19 LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGF 78
                                                                                                                                                                                                                                                                                                                                  h 39.5%; Score 380; DB 2; Length 629; Similarity 47.6%; Pred. No. 1.3e-26;
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                             21; Mismatches 46;
                                                                                                                                                                                                             -TTHCRNG----YYDNHLFHRVIRGF
                                                                                                                                                                                                                                                                                                             Indels
     626
                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                        582
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Ryfheologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li., J.H.; Li., Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
C86151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F22M8.7 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                          A; Map position: 1
C; Superfamily: pel
                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-160 <STO>
                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9LPC7; UNIPARC:UPI000000BE15;
                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: C86151
                                                                                                                                                                                                                   Genetics:
h 38.9%; Score 374; DB 2; Similarity 47.3%; Pred. No. 8.2e-27;
                                                                                                                              peptidylprolyl isomerase; cyclophilin homology
                                          Length 160;
                                                                                                                                                                                                                                                         GB:AE005172; NID:g8570445;
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Matches

Conservative

22;

Mismatches

Indels

20;

Gaps

פ

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probable cyclophilin-related peptidyl prolyl cis-trans isomerase - fission yeast (Schizd C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T41399
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D. submitted to the EMBL Data Library, May 1998
A;Reference number: Z21991
A;Accession: T41399
A;Accession: T41399
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-610 <WOO>
A;Residues: 1-610 <WOO>
A;Residues: 1-610 <WOO>
A;Cross-references: UNIFROT:074942; UNIPARC:UDI0000069EF1; EMBL:AL023704; PIDN:CAA19257.
A;Experimental source: strain 972h-; cosmid c553
C;Genetics: SPDB:SPCC553.04
A;Map position: 3
A;Introns: 24/1
F;449-608/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z21818
A;Accession: T38930
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-155 <BAD>
A;Cross-references: UNIPROT:P87051; UNIPARC:UPI0000128C69;
A;Experimental source: strain 972h-; cosmid c57A10
C;Genetics:
A;Gene: SPDB:SPAC57A10.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptidylprolyl isomerase (EC 5.2.1.8) SPAC57A10.03 [similarity] - fission y. N;Contains: cyclophilin (;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T38930 R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.: Rajandream M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1
A;Introns: 10/3; 24/3; 69/2; 101/3
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;1-155/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
T38930
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APTPWLDGKHTIFGRVVSGLS--VCKRMGLIRTDSSDRPIBPLKIIKAVAL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKTPHLMRRHTIFGEVIDAESQRVVBAISKTATDGNDRPTDPV-VIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQGFMIQGGDFTGTGRGGF---GYKFADBFHFBLQFDKPYLLAMANAGFGTNGSQFFITV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTPHLNRRHTIFGEVIDAESQRVVBAISKTATDGNDRFTDPVVIESITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGFMIQGGDPKGTGKGGTSIWGKKFNDEIRDSLKHNARGMLSMANSGPNTNGSQFFITYA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPDFVIQGGDPTGTGRGGTSIYGDKFDDEIHSDLHHTGAGILSMANAGPNTNSSQFFITL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQPHLNGLYTIPGKVI--HGFEVLDIMEKTQTGPGDRPLAEIRLNRVTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTLHTNLGDIKCEIFCDEVPKSAENFLALC-----ASG----YYDGTIFHRNI 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 358.5; DE Pred. No. 2e-25; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155;
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Search completed: April 14, Job time: 12.6721 secs

2006, 17:34:32

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A;Introns: 69/1; 102/1
C;Superfamily: peptidy!prolyl isomerase;
C;Keywords: cis-trans-isomerase
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T29283
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R;Du, Z; Le, T.T.
submitted to the EMBL Data Library, May 1996
submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T29283
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                                                                                                                                                                                                                                                                                                         A;Gene: CESP:C34D4.12
                                                                                                                                                                                                                                                                                                                                      A; Experimental source:
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q18445; UNIPARC:UPI000007D84B; EMBL:U58755; PIDN:AAB00697.1
A;Experimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-169 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T29283
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                         ;Genetics:
                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544
                            136 HLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VTNSP-----LATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNAS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                            MIQGGDPTGTGRGGASIYGDKFSDEIDERLKHTGAGILSMANAGPNTNGSQFFITLAPTQ 118
                                                                                       MIQGGDPTGTGRGGP---GYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
                                                                                                                       LDTTMGKIALELYWNHAPRTCQNFSQLAKRN--
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HLDGKHTIFGRV--AAGMKVIANMGRVDTDNHDRP
                                                                                                                                                  LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANSGPNTNGSOFFITTDLTPWLDGKHTIFARAYAGLD---
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Pred. No. 1.3e-24;
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Pred. No. 5.3e-24;
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Total number of hits satisfying chosen parameters:
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Q9XAÑB STRCO
Q4NK3 9MICC
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Q5UXKB HALMA
Q5XJTB LEGPL
Q5XJTB LEGPL
Q5XJTB LEGPL
Q5XJ46 LEGPL
Q5XJ46 LEGPH
Q5XJ46 HALSA
Q5X586 HALSA
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Q7XL19 9BACT
Q7XL19 9BACT
Q7XJTRN
Q73JM6 TREDE
Q8K6FZ STRP3
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Q8CYJI STRR6
Q7UPO1_RHOBA
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Q6A9UI PROAC
Q82PGC STRAW
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08nua5
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08a9a08
07x308
09xx88
05wx88
05wx81
05wv81
05wv81
05x3t8
05x3t8
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-i- PUNCTION: PPIAses accelerate the folding of proteins. It catalyze

the cis-trans isomerization of proline imidic peptide bonds in

oligopeptides (By similarity).

-i- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Q5XQ1 DESPS
Q6AMQ1 DESPS
Q9CH46 LACLA
Q8DUT7 STRNU
Q8EIN1_STRA5
Q8P09 STRPA
Q8P09 STRP1
Q8MON3_STRT1
Q5M569_STRT2
Q8MC42_PARUW
Q7XXQ2 ORYSA
Q6ZJ09_ORYSA
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      961; DB 1;
No. 3.7e-84;
                           Length 182;
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O66105
Q6amq1
Q9ch46
Q9ch46
Q9ch97
Q8dvj7
Q8e1n1
Q8p009
Q5m0n3
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Q8m247
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WEDLINE=88295997; PubMed=9634230; DOI=10.1038/31159;

WA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,

A Harris D.B., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

WA Harris D.B., Badcock K., Basham D., Brown D., Chillingworth T.,

Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

A Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,

HOlroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

A Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

A Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence.";

RL Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.194.19.5479-5490.2002;

Ple18chmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393:
[2]
NUCLEOTIDE :
STRAIN=CDC:
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                                                                                                                                                                 J. Bacteriol. 184:5479-5490(2002).
-I- FUNCTION: PPIABES accelerate the folding of proteins.
the cis-trans isomerization of proline imidic peptide oligopeptides (By similarity).
-I- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
MCBI_TaxID=1773;
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25-OCT-2004 (Rel. 45, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase
(Rotamase A).
Name=ppiA; OrderedLocusNames=Rv0009, MT0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P65762; P71578;
01-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                            laboratory strains.
                                                                                                                                                                                                                                                                                                                                      "Whole-genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE
                                                 (omega=0).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the cyclophilin-type PPIase family.
SIMILARITY: Contains 1 PPIase cyclophilin-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYCTU
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  through a collaboration
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Best Local Sim
Matches 182;
                                                                         Holroyd S., Hornsby T., o
Murphy L.D., Oliver K., (
Rutter S., Seeger K., Si
Squares S., Stevens K., 1
Barrell B.G.;
                                                                          STRAIN=IN;

MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B.,

Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Davies R.M., Jevin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; G70698; G70
PDB; 1W74; X-ray
TIGR; MT0011; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PPO0160; Pro_isomerase; 1.
PRINTS; PRO0153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00172; CSA_PPIASE_2; 1.
PROSITE; PS00772; CSA_PPIASE_2; 1.
3D-structure; Complete proteome; Isomerase; Rotamase.
3D-structure; Complete proteome; Isomerase; Rotamase.
DOMAIN 13 181 PPIase cyclophilin-type.
DOMAIN 13 181 PPIASE CYCLOPHILIN-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                               PPIA MYCLE
Q9CDE9;
           Barrell B.G.;
"Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-I- FUNCTION: PPIases accelerate the folding of proteins.
                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuberculist; Rv0009; -. Tuberculist; Rv00009; CSA_PPIase. InterPro; IPR002130; CSA_PPIase. 1.
                                                                                                                                                                                                                                                                         Corynebacterineae;
NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                               SEQUENCE
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Pred. No. 3.7e-84;
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Matches 164
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Pfam; PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSAPPIASE.1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Complete proteome; Isomerase; Rotama DOMAIN

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05-JUL-2004
05-JUL-2004
Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 PPIase cyclophilin-type domai EMBL; AE017227; AAS02328.1; -; Genomic_DNA.
HSSP; Q27450; 1A58.
SMR; Q794Q3; 14-182.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase ac GO; GO:0006457; P:protein folding; IEA.
                                                                                                                                                                       Name-ppiA; Orderediocuswamco-ren.
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinom
                                                                                                                                                                                                                                                                                Q744Q3 MYCPA PRELIMINARY;
Q744Q3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrues as long as its content is in no way modified and this s
                                                                                                                 STRAIN=k10;
                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                  NCBI_TaxID=1770;
                                                                                                                                                                   Mycobacterium avium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR; Q9CDE9; 12-182.
Leproma; ML0011; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 removed.
                                                                                                                                                                                                                                                                                                          MYCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (omega=0).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
SIMILARITY: Belongs to the cyclophilin-type PPIas
SIMILARITY: Contains 1 PPIase cyclophilin-type do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL583917; CAC29519.1;
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90.1%;
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                                                                                                                                                                                                                                          Created)
Last seq
Last ann
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PPIase cyclophilin-type.
7 6A6D8004348A9544 CRC64;
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Pred. No. 1.8e-76;
9; Mismatches 9
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                                                                                                    Kapur V.;
               activity; IEA
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MBL outstation -
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Matches 136
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Matches 163
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Pfam; PF00160; Pro_Isomerase; 1.
PRINTS; PR00153; CSAPPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Complete proteome; Isomerase; Rotama
SEQUENCE 182 AA; 19327 MW; 7FBE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4JYC5_CORJK
Q4JYC5;
13-SEP-2005
                                                                                                                                                                                                                                 Linke B., Tauch A.;
Submitted (DEC-2004) to the
EMBL; CR931997; CAI36182.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K411;
PubMed=15968079; DOI=10.1128/JB.187.13.4671-4682.2005;
Tauch A., Kaiser O., Hain T., Goesmann A., Weisshaar B.,
Tauch A., Exiser O., Bischoff N., Brune I., Chakrabor
Albersmeier A., Bekel T., Bischoff N., Schneiker S., Viehoever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i3-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8).
Name=ppiA; ORFNames=5k003;
Corynebacterium jelkeium (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                       Nosocomial Pathogen Corynebacterium Bacterium of the Human Skin Flora."; J. Bacteriol. 187:4671-4682 (2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae;
NCBI_TaxID=306537;
                                                                                                                                                                                                                                                                                                                     STRAIN=K411
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182 AA; 19327 MW; 7FBB403D7091A12E
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MTNK---TATAILHTNQGDIAIDLFGNHAPETVANFVGLAQGTKEYSQPNASGTNEGPFY
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                                                                                                Conservative
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77.78;
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89.6%;
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Pred. No. 4.4e
11; Mismatches
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                                                                                                                       Score 717.5;
Pred. No. 9.
                                                                                             Pred. No. 9.20
2; Mismatches
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Viehoever P.,
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RESULT

OCCUPANT

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QBNUA5 CORGL
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STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;

STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;

PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;

Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat I Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat I Gossmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A., McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A., McHardy A.C., Meyer F., Moeckel B., Sahm H., Wendisch V.F., Wiegra
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HSSP;
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05-JUL-2004 (TREMBLrel. 27, Last seq
05-JUL-2004 (TREMBLrel. 27, Last ann
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00160; Pro isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS50072; CSA PPIASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=ppiA; OrderedLocusNames=cg0048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isomerase;
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EMBL; BX927148; CAP18602.1; -;
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J. Biotechnol. 104:5-25(2003).
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its impact on the production of L-aspartate-derived amino acids
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GO; G0:0003755; F:peptidyl-prolyl cis-trans is
GO; G0:0006457; F:protein folding; IEA.
R GO; G0:0006457; P:protein folding; IEA.
InterPro; IPR002130; CSA_PPIase.
InterPro; IPR002130; CSA_PPIase.
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Matches 135; Conser
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T Pallen M.J., Bentley S.D., Beera G.S., Churcher C.M., James De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch B., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J., "The complete genome sequence and analysis of Corynebacteriu diphtheriae NCTC13129.", Nucleic Acids Res. 31:6516-6523(2003).

-i-SIMIIARITY: Contains 1 PPTase cyclophilin-type domain. EMBL; BX248354; CAE48536.1; -; Genomic_DNA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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PRINTS; PR00153; CSA.PPISWAASE.
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PROSITE; PS50072; CSA.PPIASE_2; 1.
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(EC 5.2.1.8).
OrderedLocusNames=Cgl0034;
Corynebacterium glutamicum
Bacteria; Actinobacteria; A
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-i-SIMILARITY: Contains 1 PPIase cyclophilin-type domair EMBL; BA00036; BAB97427.1; -; Genomic_DNA.
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Best Local
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Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q27450; 1A33.

SNR; Q6NKJ3; 9-179.
GO; GO:0016853; F:!somerase activity; IEA.
GO; GO:0016853; F:!somerase activity; IEA.
GO; GO:0016857; P:peptidyl-prolyl cis-trans isomer;
GO; GO:0006457; P:protein folding; IEA.

InterPro; IPR002130; CSA, PPIASE.

InterPro; IPR000215; Prot inh serpin.
Pfam; PP00160; Pro_isomerase; 1.
PARINTS; PR00153; CSA,PPIASE.
PROSITE; PS00170; CSA_PPIASE 1; 1.
PROSITE; PS00170; CSA_PPIASE 1; 1.
PROSITE; PS00170; CSA_PPIASE 7; 1.
PROSITE; PS00284; SERPIN; UNKNOWN_1.
Complete proteome; Isomerase; Rotamase.
SEQUENCE 180 AA; 19442 MW; F04683573BDDF598 CR0
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Genome Bor
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                                                                                                           Pfam; PF00160; Pro isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS50072; CSA PPIASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gojobori T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=YS-314 / AJ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium efficiens. Bacteria; Actinobacteria;
                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                          Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=CE0029;
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COREF
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    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteome; Isomerase; Rotamase.
202 AA; 21829 MW; 814495B2E7C3A818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRVIQGFMIQGGDFTGTGRGGFGYKFADEFHFELQFDKFYLLAMANAGFGTNGSQFFITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPTPHLNNHHTI FGEVTDAASQKVVLDIAQTATDRMDR PVE PVVI ESVEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRVIDGFMIQGGDPTGTGRGGPGYMFADBFHPBLQFDRPFLLAMANAGPGTNGSQFFITV
                                                                                                                                                                                                                                                                                                                                                                                            13:1572-1579(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.9%;
78.4%;
  73.7%;
76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       the therm
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Pred. No. 5e-60;
1; Mismatches
  Score 708;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                       thermostability
                                                                                                                                                                                                                                                                                                                                             cyclophilin-type nomic_DNA.
9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium
                          В
                       2;
                                                                                                                                                                                                                                                       isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                          Length
                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       the amino acid of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                       activity; IEA
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RESULT 11
Q82FC6 STRAW
ID Q82FC6 STRAW 1
AC Q82FC6;
DT 01-JUN-2003 (7
DT 01-JUN-2003 (7

PRELIMINARY;

PRT;

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(TrEMBLrel.

24,

Created) Last seq

sequence update)

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RESULT 10
QGA9U1 PROAC
ID QGA9U1,
AC QGA9U1,
DT 25-OCT-
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                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00160; Pro isomerase; 1.
PFAM; PF00153; CSAPPISMRASE.
PROSITE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS50072; CSA_PPIASE 2; 1.
Complete proteome; Isomerase; Rotama.
Complete proteome; 18078 MW; EADFB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINERAI71202 / DSM 16379;
STRAINERAI71202 / DSM 16379;
PubMed=15286373; DOI=10.1126/science.1100330;
Brueggemann H., Henne A., Hoster P., Liesegang H.,
Strittmatter A., Hujer S., Duerre P., Gottschalk G.
Strittmatter A., Hujer S., Duerre P., Gottschalk G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- SIMILARITY: Contains 1 PPIase cyclophilin-type EMBL, AB017283; AAT82475.1; -; Genomic DNA. GO; GO:001653; F:isomerase activity; TEA. GO; GO:0000755; F:peptidyl-prolyl cis-trans isomera GO; GO:0006457; P:protein folding; IEA. InterPro; IPR002130; CSA PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase A (EC OrderedLocusNames=PPA0718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterineae;
NCBI_TaxID=1747;
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Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 305:671-673(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of human skin.";
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                                           135
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123
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                                                                                                                                                                                                                                                                                                                 Similarity
                              PHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITIS
                                                                                                                    IQGFMIQGGDFTGTGRGGGGGYKFADEFHPELQFDKFYLLAMANAGFGTNGSQFFITVGKT
                                                                                                                                                                                       STATLRTNHGDIVVNLFADQAPKTVDNFVGLAGGTKEYVDPHTGQPTTGKFYDGLTFHRV
                                                                                                                                                                                                                                         ATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGAVFHRVIQGEMIQGGDFTGTGRGGFGYKFADSFHPELQFDKFYLLAMANAGPGTNGSQ
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PHLNRRHTIFGEVADEESRRVVDBIAQVRTGRMDRPVEPVVIBSVELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
10379;
1126/
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                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eria; Actinobacteridae;
Propionibacteriaceae; l
                                                                            11;
                                                                                                                                                                                                                                                                                       Score 611; DB
Pred. No. 1.6e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Rotamase.
EADFB1A883EE6546
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                                                                                                                                                                                                                                                                                                                                     Length 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 109;
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Nat. Biotechnol. 21:526-531(2003).

-!- SIMILARITY: Contains 1 PPIASE cyclophilin-type domain.

EMBL; BA000030; BAC72041.1; -; Genomic_DNA.

REMSP; Q27450; 1A58.

RGO; G0:0016653; F:180nmerase activity; IEA.

RGO; G0:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.

RGO; G0:0006457; P:protecin folding; IEA.

RGO; G0:0007130; CSA_PPIASE.

RFANNTS; PRO0153; CSA_PPIASE.

RPACSITE; PS00170; CSA_PPIASE 1 1.

PROSITE; PS00170; CSA_PPIASE 2; 1.

Complete protecome; Isomerase; Rotamase.

SEQUENCE 186 AA; 20307 MW; 80BB7CC577A5EE05 CRC64;
                                                                                                                                                            25-OCT-2004 (TRRMBLrel. 28, Last sequence update)
25-OCT-2004 (TRRMBLrel. 28, Last sequence update)
25-OCT-2004 (TRRMBLrel. 28, Last annotation update)
25-OCT-2004 (TRRMBLrel. 28, Last annotation update)
Peptidyl-prolyl cis-trans isomerase.
Peptidyl-prolyl cis-trans isomerase.
Name=ppiB; OrderedLocusNames=Lxx00160;
Leifsonia xyli (subsp. xyli).
Leifsonia xyli (subsp. xyli).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-2147403; PubMed-11572948; DOI-10.1073/pnas.211433199
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis; deducing the ability of producing secondary
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IS_LEIXX
Q6AHM5_LEIXX PRBLIMINARY;
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STRAIN=MA-4680 / ATO
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NCBI_TaxID=33903;
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Putative peptidyl-prolyl cis-trans isomerase.
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; Pred. No. 5.4e-44;
17; Mismatches 38
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RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorry H.A.,
RA Ferro M.I.T., Gagliardi P.R., Giglioti B., Goldman M.H.S.,
RA Ferro M.I.T., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Taxi S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
RT Tifhe genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT Xyli subsp. xyli.";
RI Mol. Plant Microbe Interact. 17:827-836(2004).
RL Mol. Plant Microbe Interact. 17:827-836(2004).
RL Mol. Plant Microbe Interact. 17:827-836(2004).
RL Mol. SMILARITY: Contains 1 PPIase cyclophilin-type domain.
RMBL; AE016822; AAT88120.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; TEA.
DR GO; GO:0016853; F:isomerase activity; TEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:000657; P:protein folding; IEA.
DR GO; GO:000657; P:protein folding; IEA.
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PRINTS; PR00153; CSAPPISWAASE
PROSITE; PS00170; CSA PPIASE 1; 1.
PROSITE; PS50072; CSA_PPIASE 2; 1.
Complete proteome; Isomerase; Rotan
                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND CHARACTERIZATION.
MEDLINE=9711779; PubMed=9025285;
Pahl A., Gewies A., Keller U.;
Pahl A., Gewies A., Keller U.;
"SCCYyB is a novel second cytosolic cyclophilin from Streptomyces obrysomallus which is phylogenetically distant from ScCypA.";
Microbiology 143:117-126(1997).
-!- FUNCTION: ppitases accelerate the folding of proteins. It catal the cis-trans isomerization of proline imidic peptide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8)
(Rotamase B) (Cyclophilin ScCypB) (S-cyclophilin).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIIPGEMIQGGDPIGQGIGGPGYQEDDEINBELDFAQPYMLAMANAGSPGGRGTNGSQEF
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179 AA; 19233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAVATLYTNYGDIKVNLFGNHVÞKTVRNFAGLATGEIEW-THPATGEKTNTPLYDGVIFH
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    LOCATION: Cytoplasmic
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                                          Inhibited by
                                                                                                                            Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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Pred. No. 1.6e
21; Mismatches
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4204C1783128784F
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                                               cyclosporin A (CsA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175
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                                                                                                                            (omega=180) =
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YB R.,
YB R.,
YB C.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                peptidylproline
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RESULT
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Best Local S
Matches 104
                                                                             "Complete genome sequence of coelicolor A3(2).",
Coelicolor A17(2).",
Nature 417:141-147(2002).
-|- SIMILARITY: Contains 1 PP
EMBL; AL939118; CAB45223.1; -
PIR; T36725; T36725.
                                                                                                                                                                                                                                                            Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.R., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative peptidyl-prolyl cis-trans isomerase.
OrderedLocusNames=SCO3856; ORFNames=SCH69.26c;
Streptomyces coellcolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; UG
PIR; T51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002130; CSA PPIas
Pfam; PF00160; Pro isomerase;
PRINTS; PR00153; CSAPPISWASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collabor between the Swiss Institute of Bioinformatics and the EMBL outstet the European Bioinformatics Institute. There are no restrictions cuse as long as its content is in no way modified and this statement
HSSP; P30412; 2RMC.
GO; GO:0016853; P:isomerase activity; IEA.
GO; GO:0003755; P:peptidyl-prolyl cis-trans
                                                                                                                                                                                                                                           Hopwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XA08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclosporin; Isomerase; Rotamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
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T51359; T51359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                         PPIase cyclophilin-type
; -; Genomic_DNA.
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Pred. No. 1.7e
l6; Mismatches
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; B77616D34EFA5791 CRC64;
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        activity;
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LATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSG-PFYDGAV

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Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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Arthrobacter sp. FB24.
Bacteria; Actinobacteria;
                                                                                                                                                         Larimer F., Land M.; "Annotation of the draft genome Submitted (JUN-2005) to the EMBL
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13-SEP-2005
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Q4NK35;
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182; s 0; Gaps GGTKDYSTQNASGG             GGTKDYSTQNASGG               FDKPYLLAMANAGP                FDKPYLLAMANAGD FDKPYLLAMANAGD FDKPYLLAMANAGD FDKPYLLAMANAGD	POLYPEPTIDE FRAGMENTS	Sequence 10, Appl Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 11, Appl Sequence 11, Appl Sequence 12, Appli Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
60 60 120 120		ם סקרורות הרקה היים היים היים היים היים היים היים הי

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Hiegand, Roger C.
FILE OF INVENTION: Myxococcus xanthus Genome Secours relies of the Myxococcus and the Genome Secours relies of the Myxococcus and Genome Secours relies of the Myxococcus relies of the Myxococcu
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US-09-583-110-3345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                      ; ORGANISM: Streptococcus pneumoniae US-09-583-110-3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Myxococcus xanthus US-09-902-540-13998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                     Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SEQ ID NO 3345
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APPLICANT: Lynn Dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3345,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13998, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6699703
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al.

IITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                            LENGTH: 466
TYPE: PRT
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                                                                                                 ch 42.0%; Score 403.5; DB 2; Similarity 44.5%; Pred. No. 5.1e-36; 93; Conservative 23; Mismatches 42;
3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSG-PFYDGAVFHRVI
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Pred. No. 1.3e-46;
L2; Mismatches 51;
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                                                                                                                                                                    Length 466;
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                                                                                                        Indels 51;
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; NAME/KEY: misc feature; LOCATION: (B) LOCATION 1...472; SEQUENCE DESCRIPTION: SEQ ID NO: 447
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US-09-107-433-4470
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Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4470:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/107,433
PILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
PILING DATE: May 12, 1998
APPLICATION NUMBER: 60/551553
PILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECHOME: (781)893-5007
TELEPHONE: (781)893-5077
                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 YAVLDVIAAVETGAMDKPVEDVVIETIEI 464
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                                                           93;
3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
                                                       h 42.0%; Score 403.5; DB 2;
Similarity 44.5%; Pred. No. 5.2e-36;
93; Conservative 23; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: GENOME THERAPEUTICS STREET: 100 Beaver Street
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                                                                                                                                                                                                                                                                                                                   LENGTH: 472 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                    4470:
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                                                           Indels
                                                                                          Length 472;
                                                           51;
                                                           Gaps
                       62
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US-09-270-767-49073
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US-09-270-767-33856
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                                                                                                                                   ORGANISM: Drosophila melanogaster US-09-270-767-49073
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                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTMANE: Batentin Ver. 2.0
SEQ ID NO 33856
LENTENCETTION: TOTAL APPLICATION AND APPLICATION OF SEQ ID NO 33856
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49073, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33856, Appropriate Patent No. 6703491
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                               LENGTH: 186
TYPE: PRT
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  18 TLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FMIQGGDPTGTGRGGP---GYKPADEPHPELQFDKPYLLAMANAGPGTNGSQPFITVGKT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHINRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAVLDVIAAVETGAMDKPVEDVVIETIEI 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTNGSQPFI------------------TVGKTPHLNRRHTIFGEVIDAES 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FMIQGGDPTGTGRGGASIYGSEFADELHGDLRHTGAGILSMANSGPDTNGSQFFITLAPT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAG 119
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                                              Conservative
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                                                                37.4%; Score 359; DB 2; Length 186; 46.9%; Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.4%; Score 359; DB 2; Length 186; 46.9%; Pred. No. 1.2e-31; ative 21; Mismatches 45; Indels
                                           21; Mismatches
                                           Indels
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US-09-440-828-1
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; PEATURE: -
; OTHER INFORMATION: 2925455
US-09-136-442-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-136-442-1
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                SOFTWARE: PERL Program SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09440828 Patent No. 6458575
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SEQ ID NO 1
LENGTH: 161
TYPE: PRT
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                                                                                                       CURRENT APPLICATION NUMBER: US/09/440,828
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 09/136,442
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                   APPLICANT: Patterson, Chandra
TITLE OF INVENTION: CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS/TRANS ISOMERASE
FILE REFERENCE: PF-0582 US
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CURRENT FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 4
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APPLICANT: Patterson, Chandra
TITLE OF INVENTION: CYCLOPHILIN-TYPE PEPTIDYL-PROLYL CIS/TRANS ISOMERASE
FILE REFERENCE: PF-0582 US
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APPLICANT: Corley, Neil
  ORGANISM: Homo sapiens
                         LENGTH: 161
TYPE: PRT
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44.4%; Pred. No. 1.8e-30;
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; OTHER INFORMATION: 2925455
US-09-440-828-1
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US-09-134-000C-3739
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3111
LENGTH: 203
TYPE: PRT
              Sequence 3739, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPBUTICS
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Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BUILDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
  FILE
REFERENCE:
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                                                                                                                                                                                                                                                                                                                                       ------VGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGN 167
                                                                                                                                                                                                                                                                                                                                                                            MVQGGDPTATGMGGESIYGSAFEDEFSLE-AFNLYGALSMANAGPNTNGSQFFIVQMKEV
                                                                                                                                                                                                                      DKPVYDVVIESIDV 201
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ilarity 44.4%;
Conservative 2
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; Pred. No. 1.8e-30;
26; Mismatches 49
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PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3739
LENGTH: 175
TYPE: PRT
ORGANISM: Enterococcus faecalis
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BANDMAN, OLGA
APPLICANT: LAL, PREETI
APPLICANT: COLLEY, NEIL C.
APPLICANT: PATTERSON, CHANDRA
APPLICANT: BAUGHN, MARIAH R.
APPLICANT: BAUGHN, MARIAH R.
TITLE OF INVENTION: HUMAN ISOMERASE-LIKE PROTEINS
NUMBER OF SEQUENCES: 4
                                                                  NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,425
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COOPERATING SYSTEM:
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                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                    TELEFAX:
                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 DPVVIESITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 MMSQLEDAGFPEEIIEAYKQGGTPWLDFRHTVFGHVVD--GMDVVDEIGGVQRDAQDRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 NRGDIKIALEGNHAPKTVANEVGLAQGTKDYSTQNASGGPSGPFYDGAVEHRVIQGEMIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              B: Incyte Pharmaceuticals,
3174 Porter Drive
                                    650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                         650-855-0555
                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.8%; Score 334; DE 42.6%; Pred. No. 6.46 tive 17; Mismatches
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                                                                                         PF-0529
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, DB 2; Length 175;
6.4e-29;
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RESULT 13
US-09-999-833A-245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Applicati
Patent No. 6524838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Corley, Neil. C.
APPLICANT: Patterson, Chandra
APPLICANT: Baughn, Wariah R.
TITLE OF INVENTION: HUMAN PEPTIDYL-PROLYL ISOMERSASES
FILE REFERENCE: PF-0539-1 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/639,378A CURRENT FILING DATE: 2000-08-15 PRIOR APPLICATION NUMBER: US 09/088,425 PRIOR FILING DATE: 1998-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOR
CLONE: 2291164
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6524838 2291164CD1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 34.7%; Score 333.5; DB 2 Local Similarity 40.8%; Pred. No. 2.8e-28;
                                                                                                                                                                                                                                                                                       Local Similarity
mes 71; Conserv
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                                                                       FFTLGRADELNNKHTIFGKVTGDTVYNMLR-LSEVDIDDDERPHNPHKIKSCEV 166
                                                                                            FITVGKTPHLNRRHTIFGEVIDAESQRVVBAISKTATDGNDRPTDPVVIESITI
                                                                                                                                                                   FHRVIQGFMIQGGDPTGTGRGGP---GYKFADBFHPELQFDKPYLLAMANAGPGTNGSQF 127
                                                                                                                                                                                                                                                      PLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAV 70
                                                                                                                                              PHRVVPGFIVQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
                                                                                                                                                                                                                  PPTNGKVLLKTTAGDIDIELWSKBAPKACRNFIQLCLEA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEA--
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                                                                                                                                                                                                                                                                                      Score 333.5; DB 2
Pred. No. 2.8e-28;
4; Mismatches 60
                                                                                                                                                                                                                                                                                                                         DB 2; Length 472;
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Sequence 245, Application US/09999833A Patent No. 6916648 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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APPLICANT: Baker Kevin P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                            OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078939
OR APPLICATION NUMBER: 60/078939
                                                                                                                                                                                                                                                                                                                                     OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
OR PILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077641
OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077649
OR APPLICATION NUMBER: 60/077791
OR APPLICATION NUMBER: 60/077791
OR APPLICATION NUMBER: 60/077791
OR FILING DATE: 1998-03-12
                                                                                   FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
                                            APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Stewart, Timothy A.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baton, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James;
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APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT PILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06249
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Sequence 245, Application US/10020445A
Patent No. 6967297
GENERAL INFORMATION:
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Kuo, Sophia S.
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Gerritsen, Mary E.
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Filvaroff,
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                          PITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
FFTLGRADELNNKHTIFGKVTGDTVYNMLR-LSEVDIDDDERPHNPHKIKSCEV 166
                                                                          PHRVVPGPIVQGGDPTGTGSGGESIYGAPPKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
                                                                                              FHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKFYLLAMANAGFGTNGSQF
                                                                                                                                                    PPTNGKVLLKTTAGDIDIELWSKEAPKACRNPIQLCLEA------YYDNTI
                                                                                                                                                                                          PLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAV
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40.8%; Pred. No. 2.8e-28;
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                                                                                                                                                                                                                                                                 DB 2;
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Search completed: April 14, Job time: 17.829 secs

2006, 17:37:58

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GENERAL INFORMATION:
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61
TELECHMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Fisher, Jonald
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION NUMBER: US/08/482,728A
APPLICATION NUMBER: US/08/482,728A
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ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                 Local
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                             141 HTIFGEVIDAESQRVVEAIS 160
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                                                                                          84 DPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRR
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: California
                                                              DPTGTGMGGESIWGGEFEDEFHSTLRHDRPYTLSMANAGSNTNGSQFFITVVPTPWLDNK 105
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HTVFGRV--TKGMEVVQRIS
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Fisher, Joseph
Payan, Donald
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Pred. No. 6.5e-28;
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Maximum Match 100%
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Maximum DB seq length: 200000000
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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US-10-477-76-94
US-10-477-928-3150
US-10-477-932-44839
US-10-437-963-144839
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US-10-425-115-237088
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US-10-158-057-327
US-10-158-057-327
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US-10-501-282-5678
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Sequence 14470, Ap
Sequence 19256, A
Sequence 168022,
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4 US-10-123-994 4 US-10-140-479- 4 US-10-176-918- 4 US-10-176-921- 4 US-10-137-865- 4 US-10-137-865- 4 US-10-142-431- 4 US-10-142-431- 4 US-10-123-262- 4 US-10-123-262- 4 US-10-121-050- 4 US-10-121-050- 4 US-10-121-051- 4 US-10-123-236- 4 US-10-123-236- 4 US-10-123-236- 4 US-10-123-236-	٠										٠							
US-10-123-904 US-10-140-477 US-10-175-746- US-10-176-918- US-10-176-921- US-10-142-131- US-10-142-141- US-10-142-141- US-10-142-141- US-10-142-141- US-10-142-141- US-10-142-131- US-10-143-13-262- US-10-143-13-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	
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	4	-10-123-108	-10-143-032-	-10-141-755-	-10-121-050-	-10-142-423-	-10-123-262-	-10-142-419-	-10-143-114-	-10-142-431-	-10-140-474-	-10-137-865-	-10-176-921-	-10-176-918-	-10-175-746-	-10-140-470-	-10-123-904-	100
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ALIGNMENTS

#### GENERAL INFORMATION: APPLICANT: ADDRESSN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: OETTINGER, Thomas APPLICANT: RASMUSSEN, Peter Birk APPLICANT: RASMUSSEN, PETER APPLICANT: ROSENKRANDS, Ida APPLICANT: WELDINGH, KARIN APPLICANTON WINGER: US/09/791,171 CURRENT FILING DATE: 1900-02-20 PRIOR APPLICATION NUMBER: US/09/791,171 CURRENT FILING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 0376/97 PRIOR APPLICATION NUMBER: 0376/97 PRIOR APPLICATION NUMBER: 1277/97 PRIOR APPLICATION NUMBER: 1277/97 PRIOR APPLICATION NUMBER: 60/044,624 PRIOR APPLICATION NUMBER: 60/044,624 PRIOR APPLICATION NUMBER: 60/070,488 PRIOR FILING DATE: 1997-04-18 PRIOR FILING DATE: 1997-04-18 PRIOR FILING DATE: 1998-01-05 NUMBER OF SEQ ID NOS: 173 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 12 LENGTH: 182 TYPE: PRI TYPE: PRI COCANITSM: MYCChacterium tuberculosis ; ORGANISM: Mycobacterium tuberculosis US-09-791-171-12 RESULT 1 US-09-791-171-12 Sequence 12, Application US/09791171 Patent No. US20020094336A1 GENERAL INFORMATION: Matches Best Query Match Local 121 121 GTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESIT al Similarity 182; Conserv 61 PSGPFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGP 61 PSGPFYDGAVFHRVIQGFMIQGGDFTGTGRGGPGYKFADEFHPELQFDKPYLLAMANAGF $\vdash$ GTNGSOFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESIT MADCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGG MADCDSVTNS PLATAT LITTNRGD I KI AL FGNHAPKTVAN FVGLAQGTKD YSTQNASGG 100.0%; Score 961; DB 3 ilarity 100.0%; Pred. No. 6e-94; Conservative 0; Mismatches 3; Length 182; 0 Indels 0, Gaps 180 120 120 60 180 0

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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 182
TYPE: PRT
APPLICANT: ORTTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: RELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
FILLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
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Best Local Similarity 100.0%; Pred. No. 6e-94;
Matches 182; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: OETTINGER, Tho
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US-09-738-626-3539
                                                                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2002-05-02
PRIOR PELICATION NUMBER: 09/791,171
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR FILING DATE: 1999-01-21
PRIOR PELICATION NUMBER: 1281/98
PRIOR PILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
                                                                                  SOFTWARE: PatentIn ver. SEQ ID NO 3539
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                                                                                                                          PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
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TYPE: PRT
                    ORGANISM: Corynebacterium glutamicum
                                          TYPE: PRT
                                                            LENGTH: 187
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Local Similarity 100.0%; Pred. No. 6e-94;
Les 182; Conservative 0; Mismatches
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Query Match

74.5%;

Score 716;

DB 3;

Length 187;

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317

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RESULT 6
US-10-474-776-694
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
              Sequence 694, Application US/10474776

Publication No. US20040110181A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REPERENCE: AM10649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
NUMBER OF SEQ ID NOS: 752
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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Best Local :
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LENGTH: 186
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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hes 135; Conserva
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                                                                                                                                                                                                                                                                                                                 HLNRRHTIFGEVIDAESQRVVEAISKTATD-GNDRFTDFVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                   SGFMIQGGDFLGNGTGDFGYQFQDEFHPDLRFDKFYLLAMANAGFGTNGSQFFITVAFTA 125
                                                                                                                                                                                                                                                                                                                                                                                         QGFMIQGGDPTGTGRGGPGYKFADBFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ATLKTSQGDIAVRLLPNHAPKTVRNFVELATGEREW-TNPATGEKSKDKLYDGTVFHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS-GPFYDGAVFHRVI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPHLNNAHTIFGEVTDAESQKVVDAIATTATDRYDRPADAVVIESVEIT 186
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; Pred. No. 1.9e-49;
17; Mismatches 38
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1; Mismatches
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SOFTWARE: SegWin99, version 1.03
SEQ ID NO 3150
                                                                                                                                                                                                                                                                                                                                           Query Match 42.4%; Sci
Best Local Similarity 45.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHIRON SPA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE I
FILE REFERENCE: P026926W0
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
FRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: cof family protein/peptidyl-prolyl cis-trans isomerase, cyclophi OTHER INFORMATION: Cellular location: cytoplasm OTHER INFORMATION: Similar to strain R6 sequence 15903436 (0.E+01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Streptococcus pneumoniae FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                      436
                                                                                                                                                                                          318
                                                                                                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD-------
                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                           3 DCDSVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DCDSVTNSPLATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                      YAVLDAIAAVETGAMDKPVEDVVIETIEI 464
                                                                          QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                              -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                              GPFYDGAVFHRVIQGFMIQGGDPTGTGRGGP---GYKFADBFHPBLQFDKPYLLAMANAG 119
                                                                                                                                                                                                                                                                       DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRVVEAISKTATDGNDRPTDPVVIESITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNTNGSQFFIVQNQHLPYSKKBITRGGWPEPIABIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGTNGSQFFI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GYYDGVIPHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPFYDGAVFHRVIQGFMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Score 407.5; DB Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 407.5; DB Pred. No. 2e-34;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TVGKTPHLNRRHTIFGEVIDAES 152
                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND
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                                                                                                                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                       317
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US-10-617-320-4470

I Sequence 4470, Application US/10617320

Publication No. US20050136404A1

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4470:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...472
SEQUENCE DESCRIPTION: SEQ ID NO: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/ 08513:
PILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
PILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/617,320 FILING DATE: 10-Jul-2003 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                  382
                                                                                                                         120
442
                                                                                                                                                                  324 -GYYDGVIFHRIIKDFMIQGGDPTGTGMGGESIYGESFEDEFSEEL-YNIRGALSMANAG
                                    153 QRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                    283 DIETV-EGPL----ATIKTNHGDLRIKLFPEHAPKTVANFVSL---SKD------
                                                                                                                                                                                          63 GPFYDGAVFHRVIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKFYLLAMANAG
:||| :||| :| || :|||||| || || || || || :: || :|||||
                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                            3 DCDSVTNSPLATATATHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPS
YAVLDVIAAVETGAMDKPVEDVVIETIEI 470
                                                                                  PNTNGSQFFIVQNQHLPYSKKEITRGGWPBPIABIYANQGGTPHLDRRHTVFGQLADEAS
                                                                                                                           PGTNGSQFFI ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (781) 893-8277
                                                                                                                                                                                                                                                                                                                                                       42.0%;
                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                  Score 403.5; DB 5
Pred. No. 5.4e-34;
3; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           085131
                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                         -TVGKTPHLNRRHTIFGEVIDAES 152
                                                                                                                                                                                                                                                                                                                                    Indels 51;
                                                                                                                                                                                                                                                                                                                                                                           Length 472;
                                                                                                                                                                                                             119
                                                                                  441
                                                                                                                                                                    381
                                                                                                                                                                                                                                                    323
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                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_45616C.1.pep
US-10-437-963-144839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-437-963-144839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10248_1.pep
US-10-767-701-39256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39256, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Koyalic, David K.
                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144839
LENGTH: 651
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 39256
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 144839, Application US/10437963
Publication No. US20040123343A1
                                           Matches
                                                                Query Match
Best Local Similarity
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Best Local S
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Sorghum bicolor PEATURE:
                                                                                                                                                                                                 ORGANISM: Oryza sativa
                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 SOFFITTVATPWLDNKHTVFGRVV--KGMDVVQQIEKVKTDKNDKPYQDVKILNVTV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 SQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 GAVFHRVIQGEMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 TATTSLPDNLVLHTSMGDIHLKLYPBECPKTVBNF-----TTHCRNG----YYD
14 TATATL-----HTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYD
                                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 NLIFHRVIKGFMIQTGDPLGDGTGGQSIWGTEFEDEFHKSLRHDRPFTLSMANAGPNTNG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 TATAT-----LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 40.2%; So
Similarity 46.3%; Pr
82; Conservative 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbazuk, Brad
                                             Conservative
                                                                46.3%;
                                             23,
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Pred. No. 1.2e-32;
3; Mismatches 46
                                           Score 386; DB 4;
Pred. No. 6.1e-32;
3; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 195;
                                                                                       Length 651;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                             26;
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                                             Gaps
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US-10-424-599-168022
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-10-437-963-196266
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        APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li Ping
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 196266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                        Sequence 196266, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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LENGTH: 160
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APPLICANT: Cao Yongwei
TITLE OP INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OP INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION UMBER: 39/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                       APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGEMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKFYLLAMANAGPGTNGSQFFITVG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVTLHTNLGDIKCEIFCDEVPKTSENFLALC------ASG-----YYDGTIFHRNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQPHLNGLYTVFGKVI--HGFEVLDLMEKTQTGAGDRPLABIRLNRVTI
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RESULT 14
US-10-739-930-8097
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US-10-767-701-61368
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Sequence 8097, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)B
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 61368
LENGTH: 166
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OP INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OP INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)B
CURRENT FILING DATE: 2004-01-29
RUMBER: OF SEQ ID NOS: 63128
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ORGANISM: Sorghum bicolor
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ORGANISM: Oryza sativa
FEATURE:
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Local Similarity 47.3%;
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47.3%; Pred. No. 2e-32;
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Pred. No. 3.4e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 166;
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285884
SEQ ID NO 212565
LENGTH: 616
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
FEATURE:
FEATURE:
FEATURE:
FEATURE:
FORMATION: Clone ID: PAT_MRT3847_33973C.1.pep
US-10-424-599-212565
Search completed: April 14, 2006, 18:40:38 Job time : 64.9683 secs
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US-10-424-599-212565
; Sequence 212565, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-10-739-930-8097
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LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.5%; Score 380; DB 4; Length 616; Best Local Similarity 46.4%; Pred. No. 2.5e-31; Matches 83; Conservative 21; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.6%; Score 381; DB 5; Length 639; Best Local Similarity 45.8%; Pred. No. 2e-31; Matches 81; Conservative 23; Mismatches 47; Indels
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1).. (639)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FEATURE:
                                                                                                 557
                                                                                                                                123 NGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                             497 YDNLIFHRVIKGFMIQTGDPLGDGTGGQSIWGREFEDEFHKSLRHDRPFTVSMANAGPNT 556
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                                                                                                                                                                                                                                                                                               454 SVITS--LPDNVILHTIMGDIHMKLYPEECPKIVENF-----TTHCRNG----Y 496
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                                                                                                                                                                                                                            66 YDGAVFHRVIQGFMIQGGDFTGTGRGGF---GYKFADEFHPELQFDKFYLLAMANAGFGT 122
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                                                                                                                                                                                                                                                                                                                                6 SVTNSPLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPF 65
                                                                                              ID NOS: 11088
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Maximum Match 100%
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Perfect score:
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                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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seq length: 2000000000
                                                                                                                                                                                       Published Applications AA_New:*

1: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Gapop 10.0 ,
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egult No.	Score 352	Match Match	Length	6 B	ID	Description Sequence 8
ωι	UT (	٠.	166	σ (	-10-973-115B	Sequence
4	352	٥,	166	7	-11-290-153-8	Sequence
UI	348	٥.	164	7	-11-024	Sequence
6	4		164	7	-11-096-568A-2	Sequence
7	345	35.9	163	7	-11-024-959-435	Sequence
œ	333.5		472	σ		Sequence
9	333.5	٠	472	6	US-10-195-883-98	Sequence
10	333.5		472	σ	-10-195-888-9	Sequence
11	333.5		472	σ	-889-9	Seguence
12	332	•	164	7	-11-096-	Seguence
13	332	•	373	7	-11-024-	Sequence
14	330	34.3	147	7	US-11-096-568A-21481	Sequence
15	321	33.4	140	7	-11-096-568A-2148	Sequence
16	318	٠	147	7	-568A-3315	Seguence
17	315	•	493	7	90	Sequence
18	312	32.5	140	7	-11-096-568A-331	Sequence
19	312	٠	502	7	US-11-024-959-301	Sequence
20	308	٠	504	7	US-11-096-568A-29206	Sequence
21	297.5		361	7	US-11-024-959-438	Seguence
22	•	30.4	252	7	-11-096-568A	Seguence
23	292.5	30.4	257	7	-11-096-568A-14	Seguence
24	•	30.4	264	,	-11-096-568A-149	Sequence
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Prior Application data removed - See File Wrapper or PALM.

291 30.3 208 7 US-11-227-238-44 28 288 30.0 257 7 US-11-024-959-303 29 287.5 29.9 262 7 US-11-024-959-313 30 283.5 29.5 361 7 US-11-024-959-313 31 282.5 29.4 172 7 US-11-024-959-313 32 282.5 29.4 172 7 US-11-024-959-323 34 281 29.2 663 7 US-11-024-959-323 35 278.5 29.0 20.4 7 US-11-024-959-323 36 276.5 28.6 172 6 US-10-024-959-433 36 276.5 28.6 172 6 US-10-91-285-879 37 274.5 28.6 213 7 US-11-024-959-328 38 274.5 28.6 233 7 US-11-024-959-329 39 274.5 28.6 233 7 US-11-096-568A-21249 40 272.5 28.6 239 7 US-11-096-568A-21249 41 273.5 28.5 172 7 US-11-024-959-317 42 273.5 28.4 172 7 US-11-024-959-317 43 272.5 28.4 172 7 US-11-024-959-426 45 272.5 28.4 172 7 US-11-024-959-426																				
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7	28.4	28.4	28.4	28.5	28.5	28.6	28.6	28.6	28.6	28.8	29.0	29.2	29.4	29.4	29.4	29.5	29.9	30.0	30.3	
	172	172	172	172	172	242	239	213	203	172	204	663	172	172	172	361	262	257	208	
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	US-11-024-959-426	US-11-024-959-424	US-11-024-959-317	US-11-024-959-425	US-11-024-959-306	US-11-096-568A-21248	US-11-096-568A-21249	US-11-096-568A-21250	-11	US-10-991-285-879		-11	1		-11	-11	US-11-024-959-430		Ë	
	426,	424,	317,	425,	306,	2124	2124	2125	308,	879,	433,	314,	323,			•	•	•		
303, App 430, App 430, App 430, App 313, App 315, App 323, App 323, App 323, App 323, App 323, App 323, App 324, App 879, App 870, App 870, App 871, App 871, App 872, App 873, App 874, App 875, App 875, App 875, App 876, App 877, App 877, App 877, App 877, App 878, A	Ą	Apr	App	App	App	8 A	9, A	0, A	App	App	App	App	App	App	App	App	App	App	Appl	

ALIGNMENTS

### RESULT 1 US-10-131-826A-8 PRIOR APPLICATION NUMBER: 60/049911 PRIOR FILING DATE: 1997-06-18 PRIOR APPLICATION NUMBER: 60/056974 PRIOR PILING DATE: 1997-08-26 PRIOR APPLICATION NUMBER: 60/059113 PRIOR PILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059122 PRIOR APPLICATION NUMBER: 60/059184 PRIOR APPLICATION NUMBER: 60/059263 PRIOR PILING DATE: 1997-09-18 PRIOR APPLICATION NUMBER: 60/059263 PRIOR PILING DATE: 1997-09-18 PRIOR APPLICATION NUMBER: 60/059263 PRIOR APPLICATION NUMBER: 60/059263 PRIOR APPLICATION NUMBER: 60/059263 PRIOR APPLICATION NUMBER: 60/059268 PRIOR APPLICATION NUMBER: 60/059268 PRIOR APPLICATION NUMBER: 60/059352 PRIOR APPLICATION NUMBER: 60/059268 PRIOR APPLICATION NUMBER: 60/059268 PRIOR APPLICATION NUMBER: 60/059268 PRIOR PILING DATE: 1997-09-19 PRIOR PILING DATE: 1997-09-19 GENERAL INFORMATION Sequence 8, Application US/10131826A Publication No. US20050245730A1 APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K APPLICANT: Wood, William APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C128 CURRENT APPLICATION NUMBER: US/10/131,826A CURRENT FILING DATE: 2002-04-24 APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maux Stewart, Timothy A Tumas, Daniel Watanabe, Colin K Wood, William Goddard, Audrey Godowski, Paul J. Sherwood, Steven Gurney, Austin L. Gerritsen, Mary B. Gao, Wei-Qiang DeForge, Laura Beresini, Maureen Filvaroff, Ellen

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APPLICANT: NAKAMURA, YUSUKE
APPLICANT: PURUKAWA, YOICHI
APPLICANT: Oncotherapy Science, Inc.
APPLICANT: The University of Tokyo
TITLE OF INVENTION: Genes and Polypeptides Rela
TITLE OF INVENTION: Colorectal Carcinoma
FILE REFERENCE: 082379-000400US
CURRENT APPLICATION NUMBER: US/10/517,151
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/386,985
PRIOR FILING DATE: 2002-06-06
PRIOR PILING DATE: 2002-06-06
PRIOR PILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 166
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SEQ ID NO 8
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
                                                                                                        RESULT 3
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                 Sequence 8, Application US/10973115B Publication No. US20060040351A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 75
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Best Local S
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APPLICANT: Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                            36.6%; Score 352; DB 6; Length 166; llarity 46.6%; Pred. No. 2.5e-28; Conservative 20; Mismatches 46; Indels
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Sequence 8, Application US/11290153
Publication No. US20060073568A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Pilvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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FURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 10/028,072
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
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SEQ ID NO 8
LENGTH: 166
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PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/123,090
PRIOR FILING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/581,742
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: PCT/US00/05746
PRIOR FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SACRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                              61 MIQGGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLAPTQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                           79 MIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGFGTNGSQFFITVGKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LETSMGIIVLELYWKHAPKTCKNFAELAR------RGYYNGTKFHRIIKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 LHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beresini, Maur
DeForge, Laura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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46.6%; Pred. No. 2.50
tive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
.5e-28;
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                                                                                                                                                                                                                                                                                                                    159
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US-11-024-959-310
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Best Local S
Matches 75
                                                                                                                                                                  Sequence 310, Application US/11024959
Publication No. US20060010516A1
GENERAL INFORMATION:
APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
                                        APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/290,153
CURRENT FILING DATE: 2005-11-30
PRIOR APPLICATION NUMBER: US/10/146,728
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
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FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059117
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                                                                                                                                                                                                                                                                                                                                                                    121 WLDGKHTIFGRV--CQGIGMVNRVGMVETNSQDRPVDDVKI
                                                                                                                                                                                                                                                                                                                                                                                                             136 HLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRFTDFVVI 176
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T: KODRZYCKI, BOB
INVENTION: CELL CYCLE GENES AND RELATED METHODS
ERENCE: 044463-0360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 36.6%; Score 352; DB 7; Length 166; Similarity 46.6%; Pred. No. 2.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIQGGDPTGTGRGGP---GYKPADEFHPBLQFDKPYLLAMANAGPGTNGSQFFITVGKTP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LETSMGI I VLELYWKHAPKTCKNFAELAR------RGYYNGTKFHR I I KDF
                                                                                                       CONNETT, MARIE B.
EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
                                                                                                   HIGGINS,
                                                            LUND, STEVEN TROY MAGUSIN, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood, William
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RESULT 7
US-11-024-959-435
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US-11-096-568A-21480
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Matches
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21460
LENGTH: 164
Sequence 435, Applic Publication No. US20 GENERAL INFORMATION:
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SOFTWARE: PatentIn version
SEQ ID NO 310
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CURRENT FILING DATE: 2004-12-30
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PRIOR FILING DATE: 2003-12-30
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LOCATION: (1)..(164)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Zea mays subsp. FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                        131 VGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI
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                                                                                                                                                                                                            54 IIKDFIVQGGDFTGTGRGGESIYGAKFEDEIKTELKHTGAGILSMANAGPNTNGSQFFIT 113
                                                                                                                                                                                                                                      74 VIQGEMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFIT 130
                                                                                                                                                                                                                                                                                                                           14 TATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHR 73
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                                                                                                                                   LAPCQSLDGKHT1FGRV--CRGME1VKRLGSVQTDKNDRPIHEVKI
                                                                                                                                                                                                                                                                                           TPEVTLETSMGAVSVEMYYRHAPKTCRNFVELAR------RGYYDNVIFHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLETSMGSFTVELYFKHAPRTSRNFIELSR------RGYYDNVKFHRIIKD
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                  Application US/11024959
o. US20060010516A1
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43.8%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 347; DB 7;
Pred. No. 7.9e-28;
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Pred. No. 6.2e-28
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98, Application US/10194487 Publication No. US20060074226A1
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Best Local
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APPLICANT:
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PRIOR TLING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/194,487
CURRENT FILING DATE: 2002-07-12
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93430R1C312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
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TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
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                                                                                                                    APPLICATION NUMBER: 60/059266
FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/062250
                                                                                                FILING DATE: 1997-10-17
                 FILING DATE:
                                      APPLICATION NUMBER: 60/063121
                                                            FILING DATE:
                                                                             APPLICATION NUMBER: 60/063120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 VGKTPHLNRRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVIESITI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LAPTPWLDEKHTIFGRV--CKGMDVVKRLGNVQTDKNDRPIHDVKILRTTV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 VIKDEMVQGGDPTGTGRGGESIYGPRFEDEITRDLKHTGAGILSMANAGPNTNGSQFFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 VIQGFMIQGGDFTGTGRGGP---GYKFADEFHPELQFDKFYLLAMANAGFGTNGSQFFIT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 TATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHR
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75; Conserv
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EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
LUND, STEVEN TROY
MAGUSIN, ANDREAS
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Godowski, Paul J.
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                     1997-10-24
                                                            1997-10-24
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43.9%; Pred. No. 1.2e-27;
ative 23; Mismatches 53; Indels
60/063486
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PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-883-98
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Best Local Simi
Matches 71;
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 98
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Publication No.
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Best Local 9
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CURRENT APPLICATION NUMBER: US/10/195,883
CURRENT FILING DATE: 2002-07-15
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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ORGANISM: Homo Sapien
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                                       71 FHRVIQGEMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQF 127
                                                                                                                                                                                                       11 PLATATATLHTNRGDIKIALFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAV 70
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Similarity 40.8%;
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PHRVVPGFIVQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
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; Pred. No. 7.4e-26;
24; Mismatches 60;
                                                                                                                                                                                                                                                                        ; Score 333.5; DB 6; ; Pred. No. 7.4e-26; 24; Mismatches 60;
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RESULT 11
US-10-195-889-98
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US-10-195-888-98
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US-10-195-888-98
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Publication No. US20060074227A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                      APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C329
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PA43ORIC324
CURRENT APPLICATION NUMBER: US/10/195,888
CURRENT FILING DATE: 2002-07-15
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                      CURRENT APPLICATION NUMBER: US/10/195,889
CURRENT FILING DATE: 2002-07-15
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Application removed - See File Wrapper or Palm
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FHRVVPGFIVQGGDPTGTGSGGESIYGAPPKDEFHSRLRFNRRGLVAMANAGSHDNGSQF
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Goddard, Audrey
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ilarity 40.8%;
Conservative 2
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Pred. No. 7.4e-26;
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RESULT 13
US-11-024-959-442
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US-11-096-568A-33153
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SEQ ID NO 98
: LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-195-889-98
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                                                                                         Sequence 442, Application No. US200 GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 33153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 164
TYPE: PRT
ORGANISM: Arabidopsis thaliana
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(164)
OTHER INFORMATION: Ceres Seq. ID no. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGOR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
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TITLE OF INVENTION: Sequence-Determined
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 34.5%; Score 332; DB 7; Local Similarity 41.4%; Pred. No. 2.6e-26;
                                                                                                                                                                                                                           118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
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                                                                                                                                                                                                                                                            PHINRHTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI 176
                                                                                                                                                                                                                                                                                                                                      FMIQGGDPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKT 134
                                                                                                                                                                                                                                                                                                                                                                           TLETSMGPFTVEMYYKHSPRTCRNFLELSR------RGYYDNVLFHRIVKD
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                                                                                                                                                                                                                         PSLDGKHTIFGRV--CRGMBVIKRLGSVQTDNTDRPIHEVKI
                                                                                                                                                                                                                                                                                                 FIVOGODFTGTGRGGESIYGSKFEDEINKELKHTGAGILSMANAGPNTNGSQFFITLAPQ 117
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                                                                                                                            Application US/11024959
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40.8%; Pred. No. 7.4e-26;
tive 24; Mismatches 60;
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US-11-096-568A-21481
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; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-442
                                                                                                                                                                                                                                                                                        US-11-096-568A-21481
                                                                                                                                                                                                                 Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21481
LENGTH: 147
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Best Local S
Matches 78
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APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.3 SEQ ID NO 442
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS FILE REFERENCE: 044463-0360
                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(147)
                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Ceres Seq. ID no. 12404719
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays subsp.
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Local Similarity 48.4%;
 107
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                                                                                                                                                                                                                                    Similarity
                               HTIFGEVIDAESQRVVEAISKTATDGNDRPTDPVVI 176
HTIFGRV--CRGMEIVKRLGSVQTDKNDRPIHEVKI 140
                                                                       DPTGTGRGGESIYGAKFEDEIKTELKHTGAGILSMANAGPNTNGSQFFITLAPCQSLDGK 106
                                                                                                        DPTGTGRGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRR 140
                                                                                                                                            GAVSVEMYYRHAPKTCRNFVELAR-------RGYYDNVIFHRIIKDFIVQGG
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                                                                                                                                                                                                                                  Score 330; DB 7;
Pred. No. 3.6e-26;
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Pred. No. 7.7e-26;
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; LOCATION: (1)...(140)
; OTHER INFORMATION: Ceres Seq. ID no.
US-11-096-568A-21482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21482
LENGTH: 140
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21482, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays subsp.
FEATURE:
106
                                          147 VIDAESQRVVEAISKTATDGNDRPTDPVVI 176
                                                                                      46 RGGESIYGAKFEDEIKTELKHTGAGILSMANAGPNTNGSQFFITLAPCQSLDGKHTIFGR
                                                                                                                         90 RGGP---GYKFADEFHPELQFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRRHTIFGE 146
                                                                                                                                                                                                           30 LFGNHAPKTVANFVGLAQGTKDYSTQNASGGPSGPFYDGAVFHRVIQGFMIQGGDPTGTG
                                                                                                                                                                               1 MYYRHAPKTCRNFVELAR-------RGYYDNVIFHRIIKDFIVQGGDPTGTG
V--CRGMEIVKRLGSVQTDKNDRPIHEVKI
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Pred. No. 2.7e-25;
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Search completed: April 14, Job time: 7.79883 secs 2006, 18:42:15

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 A Geneseq_21:*
1: geneseqp1980
2: geneseqp2000
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91	91	91	91	91	91.5	92	92.5	93.5	94.5	94.5	95	96	96	96	96	99.5	100	100	103	108	147	1348	1348	Score	I
6.8	6.8	6.8	6.8		6.8	6.8	6.9	6.9	7.0	7.0	7.0	7.1	7.1	7.1	7.1	7.4	7.4	7.4	7.6	8.0	10.9	100.0	100.0	Match	Query
469	442	441	383	381	2194	728	583	269	853	853	4038	621	614	579	565	755	19	19	8805	1574	287	265	265	Match Length	
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AAG29503	ABU52687	ADM26564	AAG29504	AB061838	AAM40114	ADX92106	ADJ49538	AB071472	ABU62618	AAB26917	ABG99871	ABB66212	ADS28471	ADN26762	ADN26519	ABB91978	AAY21915	AAW72898	ABB67112	AAE37002	ABM95900	AAY21908	AAW72891	ID	
Aag29503 Arabidops	Abu52687 Human sig		Aag29504 Arabidops		Aam40114 Human pol	Adx92106 Plant ful	Adj49538 Oil-assoc	Abo71472 Pseudomon	Abu62618 Pseudomon	Aab26917 Large sub	Abg99871 S. cinnam	Abb66212 Drosophil	Ads28471 Bacterial	Adn26762 Bacterial	Adn26519 Bacterial	Abb91978 Herbicida	Aay21915 N-termina	Aaw72898 Mycobacte	Abb67112 Drosophil	Aae37002 Micromono	Abm95900 M. xanthu	Aay21908 Amino aci	Aaw72891 Mycobacte	Description	

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

africanum or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 140; 163pp; English.

WPI; 1998-542705/46. N-PSDB; AAV63922.

Andersen P, Oettinger T,

Rosenkrands I,

Weldingh'K,

Rasmussen

PB;

(STAT-)

STATENS SERUM INST. Nielsen R, Florio W;

45	44	43	42	41	40	39	38	37	36	35	ω 4	ω ω	32	31	30	29	28	27	26	25
89.5	89.5	89.5	89.5	89.5	89.5	90	90	90	90	90	90	90	90	90.5	90.5	90.5	90.5	91	91	91
6.6	6.6	6.6	6.6	6.6		6.7		6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7					6.8
539	539	530	416	416	268	792	792	792	530	505	505	464	328	1220	526	345	245	702	472	469
ហ	v	v	8	ω	7	σ	σ	4.	7	œ	œ	60	σ	4	œ	8	œ	σ	œ	œ
AAU98656	AAU97744	ABP66019	ADN24843	ADN22084	ABO84045	ABJ18816	ABU38650	AAU36373	AB071541	ADS27020	ADS26629	ADS26263	ABU43515	ABG24318	ADS29018	ADR24079	ADR24082	ABU24332	ADT59335	ADN72195
Aau98656	Aau97744	Abp66019	Adn24843	Adn22084	Abo84045	Abj18816	Abu38650	Aau36373	Abo71541	Ads27020	Ads26629	Ads26263	Abu43515	Abg24318	Ads29018	Adr24079	Adr24082	Abu24332	Adt59335	Adn72195
Mycobacte	Mycobacte	Bifidobac	Bacterial	Bacterial	Pseudomon	Pseudomon	Protein e	Pseudomon	Pseudomon	Bacterial	Bacterial	Bacterial	Protein e	Novel hum	Bacterial	Pyrococcu	Pyrococcu	Protein e	Plant pol	Thale cre

## ALIGNMENTS

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02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                        01-APR-1998;
                                                                                                                                                                  08-OCT-1998.
                                                                                                                                                                              WO9844119-A1
                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                          Mycobacterium tuberculosis; antigen; vaccine;
                                                                                                                                                                                                                    Mycobacterium tuberculosis antigen CFP29.
                                                                                                                                                                                                                                21-JAN-1999
                                                                                                                                                                                                                                            AAW72891;
                                                                                                                                                                                                                                                       AAW72891 standard; protein; 265
                                                                                                                                                                                                     infection.
                                                                                                                                                                                                                                (first entry)
                                                                                                                           98US-0070488P
                                                                                                                                97US-0044624P.
97DK-00001277.
                                                                                                                                            97DK-00000376
                                                                                                                                                        98WO-DK000132
                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                          immunological; immunogen;
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RESULT 2
ANY21908
ID ANY2
XX ANY2
AXC ANY2
XX AMIN
XX IIMNU
XX CPP7
XX WPCC
PN W999
XX W909
PN 05-1
PN 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1997;
05-JAN-1998;
01-APR-1998;
The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis; fusion polypeptide; pharmaceutical; vaccination; M. af CFP7B; CFP19; CFP27; CFP3OA; RD1-C
                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                         New immunogenic fragment of Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                            WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9924577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of antigen CFP29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY21908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP3OA; cFP7B; CFP19; CFP23;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (STAT-) STATENS SERUM INST
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98US-0070488P.
98WO-DK000132.
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Pred. No. 2.3e-130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second condifferent amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo concentration or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid fragment care useful as pharmaceuticals, for diagnosis of and as antigens for care useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or povis. The polypeptides are also useful for diagnosing or previous sensitization in an animal with bacteria belonging to the cuberculosis complex. The invention also describes the use of CFP7A or CFP3OA or T-cell epitope of for the induction of a strong immune cresponse in a mammal; use of CFP7B, CFP19 or MPT59-8SAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP3OA, RDI-ORF2, RDI-ORF3, RDI-ORF3, MPT59-SSAT6, CESAT6-MPT59, CFP1OA, CFP1OA, RDI-ORF3, RDI-ORF3, RDI-ORF3, RDI-ORF3, MPT59-SSAT6. CESAT6-MPT59, CFP1OA, CFP1OA, RDI-ORF3, RDI-ORF3, RDI-ORF3, RDI-ORF3, ADT59-SSAT6. CESAT6-MPT59-SCAT6, CFP1OA, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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TERLYLOSTLTFLCYTABASVALSH
                                      TERLYLQETLTFLCYTAEASVALSH 265
                                                                                                                       VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD
                                                                                                                                                          VSETSDHGYPIREHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD
                                                                                                                                                                                                                                                 EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK
                                                                                                                                                                                                                                                                                        EGYSAAS IEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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100.0%; Pred. No. 2.3e-130;
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Transgenic plant; DNA replication; gene regulation; gene expression
                                                                                                                    M. xanthus protein sequence, seq id 15099
                                                                                                                                 02-JUN-2005
                                                                                                                                             ABM95900;
                                                                                                                                                         ABM95900 standard;
                                                       10-JUL-2001; 2001US-00902540
                                                                    21-DEC-2004.
                                                                                 US6833447-B1
                                                                                            Myxococcus xanthus.
                                                                                                                                 (first entry)
                                                                                                                                                         protein;
                                                                                                                                                          287
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Goldman BS, Hinkle GJ,

Slater SC,

Wiegand

RC;

10-JUL-2000;

2000US-0217883P.

(MONS)

MONSANTO TECHNOLOGY LLC.

WPI; 2005-028716/03

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RESULT 4
AAE37002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDs 9692-16825 represent a group of 7134 Mayococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                     23-OCT-2003
07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing
WPI; 2003-343556/33
                                                                                     26-JUL-2001; 2001US-0307629P.
                                                                                                                   26-JUL-2002; 2002CA-02391131
                                                                                                                                                 19-NOV-2002
                                                                                                                                                                                                           Micromonospora
                                                                                                                                                                                                                                           Macrolide;
                                                                                                                                                                                                                                                                      Micromonospora carbonacea polyketide synthase (PKS) type I
                                                                                                                                                                                                                                                                                                                                                   AAE37002;
                                                                                                                                                                                                                                                                                                                                                                              AAE37002 standard; protein; 1574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                        ECOPIA BIOSCIENCES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIFYGDARLGYEGLMTA--NGRLTVPLGDWTSPGGGFQAIVEATRKLNEQGHFGPYAVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SADVYTKVSETSDH-GYPIREHLNRLVDGDIIWAPAIDG--AFVLTTRGGDFDLQLGTDV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIFEGYSAASIEGIRSASSNPALTLPEDPREIP----DVISQALSELRLAGVDGPYSVLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVTEAAWABIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVST------GRLIDV-
                         Staffa A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KAPTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVBRGSKDSDWBPVKBAAKKLAFVBDR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLREEEWARLNETVIQVARRSLVGRRILDIY----GPLGAGVQTVPYDEFQNVSPGAVDIV
                                                                                                                                                                                                                                        rosaramicin; polyketide; polyketide synthase; PKS; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO
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                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                             carbonacea
                            Parnet
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Pred. No. 4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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Drosophila; developmental

26-MAR-2002 Drosophila r

melanogaster polypeptide SEQ ID NO 28128

biology; cell signalling; insecticide;

(first entry)

ABB67112 standard; protein; 8805

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ABB67112

23-MAR-2001; 2001WO-US009231.

WO200171042-A2

27-SEP-2001.

Drosophila melanogaster.

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of macrolides by microorganisms. In particular it relates to the nucle: acids forming the biosynthetic locus for rosaramicin (a 16-member macrolide antibiotic) from Micromonospora carbonacea. The invention is useful for the biosynthesis of macrolides by microorganisms. It allows direct manipulation of macrolides and related chemical structures by chemical engineering of the proteins involved in the biosynthesis of rosaramicin. It is useful to catalyse certain biochemical reservices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rosaramicin. It is useful to catalyse certain biochemical reactions, in vitro or in vivo, to direct or enhance the synthesis or modification of polyketide, polyketide substrate or its prescursor. The present sequence is M. carbonacea polyketide synthase (PKS) type I protein. (Updated on -OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 158-163; 206pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptide involved in biosynthesis of macrolides by microorganisms, useful for biosynthesis of macrolides by microorganisms, preferably for biosynthesis of rosaramicin.
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775
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                                                                                                                                                                           140 LTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIREHLNRLV 199
                                                                                                                                                                                                                                                                                    565 ---VAAPTGRTVFVFPGQGTHWAGMGADLLDQSPVFAESMRRCEQALSAHTDWKLGEVIR
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                               TATOELTLEP
                                                                                                       DGDIIWAPAIDGAFV-----LTTRGGDFDLQL-----GTDV-----AIGYASHDTDTER
                                                                                                                                                                                                              GAAGSPPLDRVDVLQPVSWAVMVSLAQVWRSLGVBPDAVV-
                                                                                                                                                                                                                                                                                                                       LIDVKAPTN-----
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                                                                                                                                                                                                                                                                                                                                                                                           RDL---APVTEAAWAEIELEAARTFKRH-----IAGR-RVVDVSD--PGGPVTAAVSTGR
L-RABLLTVL
                                                                                                                                                                                                                                                   GSKDSD-----WEPVKEAA-----KKLAFVEDRTIFEGYSAASIEGIRSASSNPA
                                                                                                                                          LTLPDAARVVA-LRSQVIGRV-LSGRGGMASVQL-----
                                                                    ---AWAGRLDVAAVNGPQSTVVSGAADAVTELVEAFAAEDVRVRRIPVDYASHSTQVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                 253
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27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                       -GVIAHLRASKPLV---RLRVPFTLSRN----EIDDVER
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 100;
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                                                                                                                                                                                                                -GHSQGE---IAAAVVCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                94;
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                                                                                                                                          PAREVAGRLA
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o the nucleic
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Best Local S
Matches 64
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                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                          21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW72898 standard; peptide; 19
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11-JUL-2000; 2000US-00614150.
                                                                                WO9844119-A1
                                                                                                                                  Mycobacterium
                                                                                                                                                                                    infection.
                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSADVYTKVSETSDHGYPIREH-----LNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----APTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVBRGSKD-SDWBPVKBAAKKLA
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                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                  tuberculosis antigen CFP29 N-terminal peptide.
                                                                                                                                  tuberculosis
                                                                                                                                                                                                                tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
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23.4%;
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a and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           드
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QTSGELGSPENPRNIADAITAGSVDTK----TGLYRVK 1635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated nucleic acid detection
                                                                                                                                                                                                                antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 103; D
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                   $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 108;
                                                                                                                                                                                                                vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                immunological; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reagent
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                                                                          10-NOV-1997;
05-JAN-1998;
01-APR-1998;
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18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                                                                                 Immunogenic; Mycobacterium tuberculosis; immune response; infectio tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; T pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP3OA; CFP7B; CFP1B; CFP1B; CFP1B; CFP23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Mycobacterium tuberculosis N-terminal peptide. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from Atuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the dispnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated mycobacteria polypeptides and nucleic acids developing products for the diagnosis of or vaccination a mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                     N-terminal sequence of antigen
                                                                                                                                                                                                                                                                                            06-SEP-1999
                                                                                                                                                                                                                                                                                                                 AAY21915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 144; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersen P,
Oettinger T,
                                                                                                                    08-OCT-1998;
                                                                                                                                          20-MAY-1999.
                                                                                                                                                               WO9924577-A1
                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                       AAY21915 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1998;
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                                                                                                                                                                                                        CFP30B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Florio
                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                    tuberculosis.
                                                                          97DK-00001277.
98US-0070488P.
98WO-DK000132.
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97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                     98WO-DK000438
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                                                                                                                                                                                                        CFP7B.
                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%;
                                                                                                                                                                                                                                                                                                                                      peptide;
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Pred. No.
                                                                                                                                                                                                                                                                        CFP29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0044;
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                                                                                                                                                                                                                                                 immune response; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 19
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                                                                                                                                                                                                                              ; MPT59; TB
7A; CFP30A;
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WPI; 1999-347282/29

Andersen P,

Skjot R;

(STAT-) STATENS SERUM

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RESULT 8
ABB91978
ID ABB9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a substantially pure immunogenic polypeptide CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a CC protective immune response against infections by mycobacteria belonging CC to the tuberculosis complex. The invention provides a (1) fusion CC polypeptide comprising at least one polypeptide fragment (I) and at least CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell CC epitope from M. tuberculosis protesin SBAT-6, or MPTS9 and a second CC different amino acid sequence from M. tuberculosis, and/or including a CC sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment CC that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or CC waccination against TB caused by Mycobacterium tuberculosis, africanum or CC covis. The polypeptides are also useful for diagnosing ongoing or CPP70 or CC covis. The polypeptides are also useful for diagnosing ongoing or CPP70 or CC covis. The polypeptides are also useful for diagnosing ongoing or the CC cuberculosis complex. The invention also describes the use of CPP70 or CC cP30A or a T-cell politope of for the pitope of for the induction of a strong immune CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin C est; use of CPP27, CPP30A, RDI-ORP2, RDI-ORP3, RDI-ORP5, PCP30B, CPP7B or a T-cell epitope of for the preparation of an immunological composition; and CC cell epitope of for the preparation of an immunological composition; and
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Best Local (
                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002
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                                                                                                                                                                                                                                                                                                    Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                         (FARB )
                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB91978 standard;
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                                                                                                                                                                                                                                         2002-269010/31
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                                                                                                                                                                                                                                                                                                                                                                     BAYER
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                                                                                                                                                                                                                                                                                                       Weidler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; 500
100.0%; Pr/
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Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 755
363
                                                                                                  185
                                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
CFHTRRVMYGLSLDDLGDDGSLSSIA----TRKYLAEESLT
                                VLTTRGGDFDL---QLGTDVAIGYASHDTDTERLYLQETLT
                                                                                                                                    VGDEKEVPHVVYISREKRPNHFHHYKAGAMNFLVRVSGLMTNAPYMLNVDCDMYVNEADV
                                                                                                                                                                                                                                                                          PANKLACYVSDDGCSPLTYFSLKEASKFAKIWVPFCKKYNVRVRAPFMYFRNSPEAAEGS 184
                                                                  VRQAMCIFLQKSMDSNHCAFVQYPQDFYDSNVGBLTVLQLYLGRGIAG--IQGPQYAGSG
                                                                                                                                                                    --DPREIPDVI-------SQALSEL-RLAGV--DGPYSVLLSADVYTKVSET
                                                                                                                                                                                                      EFSKDWEMTKREYEKLSQKVEDATGSSHWLDAEDDFEAFLNTKSNDHSTIVKVVWENKGG
                                                                                                                                                                                                                                        SKDSDWEPVKEAAKKLA-FVEDRTIFEGYSAA--SIEGIRSASSNPALTLPE-----
                                                                                                                                                                                                                                                                                                            PTNGVIAHL-----RASK----PL----VRLRVPFTLSRNEIDDVERG
                                                                                                                                                                                                                                                                                                                                              ITNIKWSPADY----KTYPERLDERVHELPPVDMFVTTADPVRBPPLIVVNTVLSLLAVNY
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%;
                                                                                       SDH----GYP------IRBHLNRLVDGDIIWAPAIDGAF
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99.5;
Pred. No. 1
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                                251
399
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bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria.
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(HINK/)
                                                                                                                                                                                            21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                     20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003233675-A1
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                                                                                                   (CAOY/) CAO
HINKLE
SLATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorus; photosynthesis; lignin; galactomannan; polypeptide.
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Claim 5;

SEQ ID

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1189;

261pp + Sequence Listing; English

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RESULT 10
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AC ADN26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC microbial source: The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant is maize or soybean. The method of producing a transformed plant CC recombinant DNA construct and growing the transformed plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC ingrance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC content, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan CC growding improved plant growth and development under at least one stress condition. Note: The sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence aspecification but was obtained in electronic cormat from USPTO at sequence aspecification but was obtained in electronic cormat from USPTO at sequence aspecification but was obtained in electronic cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat from USPTO at sequence data for this patent did not cormat
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Matches 68
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                          02-DEC-2004
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                                                                       ADN26762;
                                                                                                                   ADN26762 standard;
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(GOLD/) GOLDMAN B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ention relates to a recombinant DNA construct comprising a r functional in a plant cell, where the promoter is positioned for expression of a polynucleotide encoding a polypeptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinkle GJ,
                                                                                                                                                                                                                                                                               DLQLGTDVAIGYASHDTDTERL
                                                                                                                                                                                                                                                                                                                                                                          TKVSETSDHGYPI-----REHLNRLVDGDIIWAPAIDGAF-----VLTTRGGDF
                                                                                                                                                                                                                                                                                                                                                                                                                     ATMPPQIRRI-----AQTYLQDPIB----VTIATKTTTAANIRQRYWWVSGLHKLDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPY---SVLLSADVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAPVTEAAWAEIELEAARTFKRH---IAGRRVVDV--SDPGGPVTAAVSTGRLIDVKAPT
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                          (first entry)
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Pred. No. 2.2;
31; Mismatches
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63 NGVIAHL-RASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFE

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CC prowder functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC comprising the recombinant DNA construct and a method of producing a comprising the recombinant DNA construct and a method of producing a comprising the recombinant DNA construct and a method of producing a comprising the recombinant DNA construct and a method of producing a comprise sing the plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property. The plant is a crop plant crombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic cormat from USPTO at sequence approved sequence.html.
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(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA construct; transformed plant; improved plant cold tolerance; heat tolerance; drought tolerance; herbicide;
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-061375/06
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73
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HINKLE G J
SLATER S C
CHEN X.
GOLDMAN B
                                                                                   Similarity
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LAPTRELA-----IQVAEAFQRYAASISGFRVLPVYGGQSYGQQLAALKRGVHVIVGTP-
                                LAPVTEAAWAEIELEAARTFKRH---IAGRRVVDV--
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                                                                   7.1%;
llarity 26.0%;
Conservative 3:
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Pred. No. 2.2;
31; Mismatches
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                                  SDPGGPVTAAVSTGRLIDVKAPT
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property attansforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties, improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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(SLAT/)
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bacterial
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SLATER S
CHEN X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 17504; 122pp; English.
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polypeptide.
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                                                              N-PSDB;
                                                                                                   Venter JC,
                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                       27-SEP-2001.
                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                              ABB66212
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                                                                                                   Adams M,
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2000US-00614150
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26.0%;
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                                                                                                     PWD,
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Best Local S
Matches 61
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   New DNA sequence encoding polyketide synthase, useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. cinnamonensis MonAIV/polyketide synthase multi-enzyme MONS4.
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                                                                           WPI; 2001-611393/70
N-PSDB; ABX04971.
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                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                      PF,
                                                                                                                                                                                                                                                          BIOTICA TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVIPISALKGTNLELLAEAVSTQATLMGLKADPTGLVEGIVVESKTDPRRGKLSTAIVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTLRKGSVLLSGLAHAKVRGLFDHNGQPLSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVDGPYSVLLSADVYTKVSETSDH-GYPIREHLNRLVDGDIIWAPAIDGAFVLTTR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TIFEGYSAASIEGIRSASSNPA--LTLPEDPREIPD-VISQALSELRLA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGVMAQTREVIQLAKEAQVPIIVALNKIDKPEANIEKSK----RELAQMGLALEEHGGDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGDLILEVETEKKAHAVLKYREHESQQEKI 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene cluster; polyketide synthase; antibiotic; antihelminthic;
de; immunosuppressant; antifungal; antibacterial; polyether;
on BII; mon CI; mon CII; mon H; mon RI; mon RII; mon T; mon AIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                      Staunton
                                                                                                                                                                                                                                                                                                                                      99GB-00012563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.1%;
22.6%;
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                                                                                                                                                                                         Oliynyk M;
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Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mon AIX;
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of polyketides such as antibiotic monensin

CC cluster (and is capable of expressing a corresponding polypeptide), and CC hybridization probe derived from the gene cluster (for identification and CC isolation of the same or analogous gene cluster, e.g. one which binds gpecifically to a region of the monensin gene cluster selected from mon CC BI, mon BI, mon CI, mon CI, mon H, Mon RI, mon RII, mon T, mon AIX and CC mon AX), the use of the mon RI gene or variant and a monensin promoter to CC control expression of a heterologous gene in Streptomyces cinnamonensis, CC a polypeptide encoded by a portion of the monensin gene cluster (preferably comprising mon BI, mon BI, mon AIX or mon AX or their control expression of a heterologous gene in Streptomyces cinnamonensis, CC enhanced levels of production of monensin comprising engineering it to cyclase enzyme encoded by mon CII, producing S. cinnamonensis capable of coverexpress the mon RI gene, S. cinnamonensis capable of coverexpress the mon RI gene, S. cinnamonensis capable of containing a heterologous gene and expressing a gene heterologous to S. cinnamonensis comprising transforming S. cinnamonensis with DNA CC containing a heterologous gene and expressing the gene under control of the activator gene mon RI or actil/orf4 and 13-propyl erythromycin A. The corresponding antibacterials (enzyme systems, nucleic actids and vectors) are useful for preparing polyketides by recombinant synthesis. The corresponding antibacterials or or other pharmaceuticals. In particular the gene is useful for the production of monensin, an antibiotic polyether contain capable or polyketides. The present sequence represents a protein encoded by the The invention relates to a DNA sequence which is a fully defined sequence of 103551 base pairs appearing as ABX04971, or its variant, that it is not a sequence encoding all or part amino acids 1-920 encoded by mon AI as given in the specification. The DNA is the S. cinnamonensis polyketide antibiotic momensin biosynthetic gene cluster. Also included are a recombinant cloning or expression vector comprising the gene cluster, a transformed host cell which has been transformed to contain the gene Sequence 4038 AA; monensin gene cluster

Matches Query Match Best Local 1176 LLPPTDAEQVWLPFAWNDVALHAVRATTVRVRLTPLGERI----DQGLRITVADAVG---1229 ---APVL-TVRDLR-SRPTDTGRLAAAATRD-----RHGLFDLEWIAPENAAENAA----177 60; 57 DVKAPTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVBRGSKDSDWBPVKBAAKKLAFVBD 8 LAPVTEA-----AWABIBLEAARTFKRHI----AGRRVVDVSDPGGPVTAAVSTGRLI Similarity V---EPDRTDDGLALATHVLDLVQ---TWLASPLHDSRLVLVTRGAVTDADV--DVA VYTKVSETSDHGYPIREHLNRLVDGDIIW--APAIDGAFVLTTRGGDFDLQLGTDVA 231 RTIFEGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSAD Conservative 7.0%; -GPARDASEGWVTLGEDAASLADLLASV-----EAGAPAPQ--LVAAP 1314 29, Score 95; DB 4; Length 4038; Pred. No. 57; 9; Mismatches 86; Indels 62; Gaps 1363 1274 1228 56 176 14;

# RESULT 14 AAB26917

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AAB26917 standard; protein; 853

## SXAXBXBXAXB AAB26917;

12-JAN-2001 (first entry)

Large subunit of periplasmic nitrate reductase NapA

NapA; toxic periplasmic nitrate reductase; enzyme; transgenic organism; waste denitrification; denitrifying bacteria.

Pseudomonas sp.

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is NapA from Pseudomonas sp. strain G-179. This sequence is the large subunit of periplasmic nitrate reductase. The NapA gene can be used to create transgenic organisms that can denitrify toxic waste. In addition, the present sequence may be used to produce probes and primers for identification of new denitrifying bacteria. Residues 20 to 853 of the present sequence are encoded by the accuracy in processions 20 to 853 of the present sequence are encoded by the accuracy.
                                                                                           Periplasmic nitrate reductase subunit; enzyme; NapA; NapB; NapC; denitrification; water purification; industrial waste purification; denitrifying bacteria; nitric oxide reductase subunit; NorB; NorC;
                                                                                                                                                                 23-OCT-2003
02-SEP-2003
             06-AUG-2002
                                   US6429003-B1
                                                                                                                                           Pseudomonas
                                                                                                                                                                                                     ABU62618;
                                                                                                                                                                                                                             ABU62618 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 853 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Col 35-40; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding bacterial nitric for preparing transgenic organisms able to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999;
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                                                          Pseudomonas
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                                                                                                                                                                                                                                                                                       272
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                                                                                                                                                                                                                                                                                                    GGDP-DLQL----GTDVAI-GY-ASHDTDTERL---YLQETLTFLCYTAEASVAL 263
                                                                                                                                                                                                                                                                                                                                                                                   GQWTTFEGYAATKLMRAGFRSNNL-----DPNARHCMASAAYGFMRTFGMDEPMGCY
                                                                                                                                                                                                                                                                                                                                                                                                         ---TIFEGYSAASI--EGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGP---Y 169
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMDLADIPLVFKPGTDLAILNY IÄNHIIQTGRVNQEFIDKNTKFMQATTDIGYGL
                                                                                                                                                                                                                                                                                                                                      DDFEHADAFVLWGSNMAEMHP----
                                                                                                                                                                                                                                                                                                                                                            SVLLSADVYTKVSETSDHGYPIREHLNRLVDGDIIWAPAIDGAF------VLTT---R 218
                                                                                                                                                                                                                                                                                                                                                                                                                                 RLTTPLLRKRNGVFD-----KEGEFEPVTWEEAFDIMAEKAKKT--LKEKGPTALGMFGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PONT DB
                                                          яþ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ye RW;
                                                                                                                                           nitrate reductase
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                                                           strain
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                                                                                                                                                                   entry)
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                                                           G-179
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Pred. No. 5.8;
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                                                                                                                                                                                                                                                                                                                                      ---ILWTRLADRRLGHEHVKVSVLSTFTHR
                                                                                                                                         NapA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxide reductase, useful detoxify wastes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                             NorQ;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                 subunits. Also included are a chimaeric gene comprising the Map nucleic acid linked to regulatory sequences, a transformed cell comprising the chimaeric gene and a nucleic acid fragment encoding an enzymatically active bacterial periplasmic nitrate reductase subunit, obtained by probing a library with the Map nucleic acid and sequencing the isolated clone. The Map nucleic acid is useful for producing enzymes useful in denitrifying reactions (for water purification and industrial waste purifying) and for identifying other denitrifying bacteria. Also disclosed are the nucleic acid and protein sequences for the nitric oxide reductase subunit genes NorE, NorC, NorQ and NorD. The present sequence represents the Mapa protein. Note: The present sequence is stated to be encoded by the DNA appearing as ACD26043 but is not encoded by it.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid fragment encoding enzymatically active bacterial periplasmic nitrate reductase subunit perupomonas sp. strain G-179, which comprises NapA, NapB and NapC subunits. Also included are a chimaeric gene comprising the Nap nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 35-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bedzyk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998;
15-JUL-1999;
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                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas bacterial periplasmic nitrate reductase subunit nucleic , for producing enzymes used in water purification.
272
                                                                     224
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                                                                                                                                                                                     118
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                                                                                                                                                                                                                                                                                               Similarity 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACD26043
SMDLADIPLVEKPGTDLAILNYIANHIIQTGRVNQEFIDKNTKFMQATTDIGYGL 326
                     GGDF-DLQL----GTDVAI-GY-ASHDTDTERL---YLQETLIFLCYTAEASVAL
                                                                     DDFEHADAFVLWGSNMAEMHP------ILWTRLADRRLGHEHVKVSVLSTFTHR
                                                                                                                                                GOWTIFEGYAATKLMRAGFRSNNL-----
                                                                                                                                                                                                                         RLTTPLLRKRNGVFD-----KEGEFEPVTWEEAFDIMAEKAKKT--LKEKGPTALGMFGS 171
                                                                                                                                                                                                                                                          RLRVPFTLSRNEIDDVERGSKDSDWEPV-----KEAAKKLAFVEDR------
                                                                                                        SVLLSADVYTKVSETSDHGYPIREHLNRLVDGDIIWAPAIDGAF-----VLTT---
                                                                                                                                                                                 ---TIFEGYSAASI--EGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGP---Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ϋ́e
                                                                                                                                                                                                                                                                                             7.0%; Score 94.5; Dilarity 25.1%; Pred. No. 5.8; Conservative 27; Mismatches
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A
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Qy 241 7 Db 241 7	Qy 181 V	Qy 121 E Db 121 E	Qy 61 I Db 61 I	Qy 1 N	Query Match Best Local Similarity Matches 264; Conser	30 89 6.6 1772 2 T3611 31 88.5 6.6 281 2 AE35. 32 88.5 6.6 3149 1 QOBE 32 88.5 6.6 3149 1 QOBE 33 88 6.5 6.6 3149 1 QOBE 34 88 6.5 6831 2 A8881 35 88 6.5 6831 2 A8881 36 88 6.5 6831 2 T505. 37 87.5 6.5 371 2 T505. 38 87.5 6.5 712 2 A632. 40 87.5 6.5 72 2 A632. 40 87.5 6.5 72 2 A831. 41 87.5 6.5 72 2 T329. 40 87.5 6.5 1220 2 T329. 41 87.5 6.5 1220 2 T329. 44 86.5 6.4 740 2 C8311 42 87 6.5 1220 2 T329. 43 87 6.5 1220 2 T329. 44 86.5 6.4 937 2 D8741 45 86.5 6.4 937 2 D8741 45 86.5 6.4 937 2 D8741 45 87.5 6.5 1220 2 T329. 46 87.5 6.5 1220 2 T329. 47 88 88 88 88 88 88 88 88 88 88 88 88 88
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	VSETSDHGYPIREHLNRLYDGDIIWAPAIDGAFYLTTRGGDFDLQLGTDVAIGYASHDTD 240 	GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180 	PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF 120 	MNNLYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKA 60 	2; Length 265; 1; Indels 0; Gaps 0;	probable large gly icc protein [impor BPLF1 protein - hu dihydrolipoamide a protein unc-22 [im twitchin [similari hypothetical prote riboflavin-specifi spore germination conserved hypothet siderophore recept nitrate reductase endopeptidase Clp hypothetical prote probable metal-tra ribonucleotide red  #### ###############################

RESULT 2 B72333 bacteriocin - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <ARN>
A;Cross-references: UNIPROT:Q9WZP2; UN
A;Cross-references: Btrain MSB8
C;Genetics:
A;Gene: TM0785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein aq 1760 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1 C;Accession: E70451
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Y.
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A;Title: Bvidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72333
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A; Residues: 1-281 < AQF >
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A; Status: prelimina
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Experimental source: strain VF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaasterland, T.; Young, W.G.; Lenox,
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A; Residues: 1-492 <B
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                                     RVLTVGGGFIS-VEFAGIFNAYKPKDGQVTLCYRGEM---ILRGFDH--TLREELTKQLT
                                                                   BIPDVISQALSBLRLAGV------DGPYSVLLSADVYTKVSETSDHGYPIRBHLNRLVD
                                                                                                              SKNVVNVRESADPASAVKERLETEHILLASGSWPHMPNIPGIEHCISSNEAFYLPEPPR
GDIIWA-----PA----IDGAFVLTTRGG---DFDLQLGTDVAIGYASHDTDTE
                                                                                                                                                    DS-DWEPVKEAAKKLAFVEDRTIFEGYSAAS-----IEGIRSA-SSNPALTLPEDPR
                                                                                                                                                                                         MEHLRESAGFGWEFDRTTLRAEWKNLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSL
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41;

Mismatches

Indels

82;

Gaps

18

KPLVRLRVPFTLSRNE-IDDVER---

-GSK

97 70 65

130

190 147

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A;Molecule type: DNA, A;Molecule type: DNA, A;Molecule type: DNA, A;Molecule type: DNA, A;Residues: 1-94,'K',96-111,'E',113-155,'N',157-352,'N',354-401,'NI',404-440,'V',442-49 A;Residues: UNIPARC:UPI00001378PB; EMBL:M38051; NID:9162316; PIDN:AAA63547.1; PC;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology C;Keywords: NADP; oxidoreductase; redox-active disulfide F;9-468/Domain: dihydrolipoamide dehydrogenase homology F;53-58/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Borges, A.; Fairlamb, A. submitted to the EMBL Data Library, June 1992
A;Description: Mutagenesis of the redox-active cysteines in the trypanothione reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Borges, A.; Cunningham, M.L.; Tovar, J.; Fairlamb, A.H. Eur. J. Biochem. 228, 745-752, 1995
A;Title: Site-directed mutagenesis of the redox-active cysteines A;Reference number: S68968; MUID:95255281; PMID:7737173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Trypanosoma cruzi
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S68968; S24243; S30204
                                                                                                                                                                                                                                                                                                                                                       A;Title: Cloning, sequencing, overproduction and purification A;Reference number: $30204; MUID:91187059; PMID:2011150 A;Accession: $30204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-111,'E',113-139,'A',141-155,'N',157-492
A;Cross-references: UNIPARC:UP100001720C2; EMBL:Z13958
R;Sullivan, F.X.; Walsh, C.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biochem. Parasitol. 44, 145-148, 1991
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25.8%;
Score 111; UB .
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                                        Length 492;
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Data Library,
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January 1995
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A; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; R DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz A; Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: B72639

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <KAW>
A;Cross -references: UNIPROT:Q9YEN2; UNIPARC:UPI00005DBB7; DDBJ:AP000060; NID:g5104188; C;Genetics: APE0546
C;Superfamily: Methanococcus in increase in the complex c
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                                                                                                                  A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Richerence number: A75250; MUID:20036896; PMID:10567266
A;Rccession: E75395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <#HII>
A;Cross-references: UNIFROT:Q9RUF1; UNIPARC:UPI000013AACA; GB:AE00198:A;Experimental source: strain R1
C;Genetics: DR1435
A;Map position: 1
C;Superfamily: uncharacterized conserved protein
                                                                                                                                                                                                                                                                                                                                                                                                             R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, I. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004 C;Accession: E75395
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E75395
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Best Local (
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                                                  Local Similarity
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Similarity 24.5%;
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                         Conservative
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                                                7.8%; Score 105.5; 26.1%; Pred. No. 1.3
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Pred. No. 1;
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Utterback,
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T.; Zalewski,
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R; Barnett, M.J.; Fit
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Matches 65
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                                                                                                                                                                                                                                                                                                                                              65,
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                                                                                                EGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGP---YSVLLSADVYTKVSETS 185
                                                                                                                                                   GAFAKDGEFEPVSWDEAPDVMAEQAKKV--LKDKGPTAVGMFGSGQWTIFEGYAATKLMR
                                                                                                                                                                                                                                              GCGVMVGVKEGQVVATHGDMQAEVNRGLNCIKGYFLSKIMYGTDRLKTPLLRKRN-----
                                                                                                                                                                                                                                                                                         GGPVTAAVSTGRLI----DVKAPTNGVIAHLRA---SKPLV---RLRVPFTLSRNEIDDV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTARHD
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     DHGYPI ---
                                                                                                                                                                                              ERGSKDSDWEPVK------BAAKKLAFVEDR------TIFEGYSAASI--
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23.6%;
                                                DPNARHCMASAAYAFMRTFGMDBPMGCYDDFBHADAFVLWGSNM
                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                         Score 102.5;
Pred. No. 5.1;
37; Mismatches
     -- RLVDGDIIWAPAIDGAFVLTTRGGDF
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21
                                                                            PIREHLNRLVDGDIIWA-----PAI-----DGAFVLTTRGGDFDL----QLGTDVA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARLLLHRFGRGEGLEGHTFGNLLLATLSE-----ERGGLGTAMQDIHEILKVRGRVYPA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRLRVP-----FTLSRNBIDDVBRGSKDSDWEPVKEAAKKLAFV---
                                                                                                                                                                                                                                                                                                                                  TTRPVTLVAELADGRTIRGESRFAEQIRPSRIERVRLEPENPSALTQVLEAVRDAEMIVL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTGLKTHSSNITA--VVTVADDGG-----SSGRLREALDMVAPGDLTDCYAALSESPAL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRL---IDVKAP--TNGVIAHLRASKPL
                                                                                                                                                                                                                                                                                                                                                                                                     EDRTI-----FEGYSAASIEGIRSASSNP-ALT-LPEDPRE-----
                                                                                                                                                                                                                                                 IPDVISQALSELRLAGVDGPYSVLLSADVYTKVSET----SDHGY 189
WVLLSNSKIEPAVQRRYQQEGATVLTLDGAGRDLRGRVRFAPLIQ 434
                                                                                                                                                                     -SPAPVVYVÁSLMTEPGETDGLSLSDHVN 378
                                                                                                                                                                                                                                                                                                                                                                                                                      148
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A;Cross-references: UNIPROT:092236; UNIPARC:UPI00000CB17C; GB:AB006469; PIDN:AAK65332.1 A;Experimental source: strain 1021, megaplasmid pSymA A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorbolter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; E; KAlman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Genome: plasmid C;Superfamily: Alcaligenes eutrophus nitrate reductase A chain apA periplasmic nitrate reductase [imported] - Sinorhizobium meliloti (strain;Species: Sinorhizobium meliloti; Species: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004 A.P.; Barloy-Hubler, ki, R.; Wells, D.H.; entire Sinorhizobium melilot Yeh, 1021) . . Bow!

99;

220

222

168

128 110

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C;Accession: B84331

C;Accession: B84331

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.

A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                           cellulose synthase homolog T26B15.10 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) c;Species: Arabidopsis thaliana (mouse-ear cress) c;Pate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02553; D84734 C;Accession: T02553; D84734 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                A;Description: Arabidopsis
A;Reference number: Z14678
A;Accession: T02553
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C; Genetics:
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A; Residues: 1-694 <S'
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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;Cross-references: UNIPROT:080891; UNIPARC:UPI00000485E0; EMBL:AC004681; NID:g3298532; Experimental source: cultivar Columbia; Experimental source: cultivar Columbia; C.Y.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.S.E.; Umayam, L.; Tallon, L.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Fraser, C.M.; Venter, use, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                      Status: translated from
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                                                                                                                                                             Molecule type: DNA
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                                                                                                                                    1-755 <ROU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDLQLGTDVAI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P---LIDEGFEPAESDGAATNEGHDVSMFVAELIDCLAADGLSAPVLVDGG-----HG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSRSVESLFFPDPVAVTGGQTVVASADSTPLVT----
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                                                           C.Y.;
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acetyl-coenzyme A synthetase [imported] - Nostoc sp. (strain PCC 7120) c;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AB2338
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A;Title: Sequence and ana
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A; Residues: 1-755 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana nce number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PTNGVIAHL------RASK-----PL----VRLRVPFTLSRNBIDDVERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 VTEAAWAEIELEAARTFKRHIAGR-----RVVDVSDP--GGPVTAAVSTGRLIDVKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                       CFHTRRVMYGLSLDDLGDDGSLSSIA----TRKYLABESLT
                                                                                                                                                                                                                                              VLTTRGGDFDL----QLGTDVAIGYASHDTDTERLYLOETLT 251
                                                                                                                                                                                                                                                                                                                                                                         VGDEKEVPHVVY I SREKRPNHFHHYKAGAMNFLVRVSGLMTNA PYMLNVDCDMYVNEADV
                                                                                                                                                                                                                                                                                                                                                                                                                --DPREIPDVI------SQALSEL-RLAGV--DGPYSVLLSADVYTKVSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFSKDWEMTKREYEKLSQKVEDATGSSHWLDAEDDFEAFLNTKSNDHSTIVKVVWENKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKDSDWEPVKEAAKKLA-FVEDRTIFEGYSAA--SIEGIRSASSNPALTLPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANKLACYVSDDGCSPLTYPSLKBASKFAKIWVPPCKKYNVRVRAPFMYFRNSPBAAEGS
                                                                                                                                                                                                                                                                                       VRQAMCIFLQKSMDSNHCAFVQYPQDFYDSNVGELTVLQLYLGRGIAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITNIKWSPADY---KTYPERLDERVHELPPVDMFVTTADPVREPPLIVVNTVLSLLAVNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 99.5;
20.8%; Pred. No. 7
                                                                                                                                                                                                                                                                                                                              SDH----GYP-----IREHLNRLVDGDIIWAPAIDGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112;
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                                                                                                                                                                                                                                                                                           IQGPQYAGSG
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabate DNA Res. 8, 205-213, 2001
A;Ritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 3

A;Accession: AB2338

A;Status: preliminary

A;Molecule type: DNA A;Residues: 1-524 <KUR> A;Cross-references: UNIPROT:Q8YPRO; UNIPARC:UPI00000CEA81; GB:BA000019; PIDN:BAB75956.1 A;Experimental source: strain PCC 7120

Genetics:

Query Match

A; Gene: all4257 C; Superfamily: acetate-CoA ligase; acetate-CoA ligase homology

BB

2;

Length 524;

밁 S Local 149 IPDVISQALSELRLAGVDGPYSVLLSA------DVYTKVSETSDHGY-----PI Similarity MPMIPEAAIAMLACARIGAPHSVVFGGFSAEALRDRLIDAQAKVVVTADGGWRKDAIVPL Conservative 7.2%; Score 96.5; Di 25.8%; Pred. No. 7.8; 25; Mismatches 46; Indels -TDVAIGYASHDTDTERLY 27; Gaps 205 191 245 6

S

REHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLG----

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regulatory protein ppsk [imported] - Rhodobacter sphaeroides C;Species: Rhodobacter sphaeroides C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_char C;Accession: T50734 R;Choudhary, M.; Kaplan, S. Nucleic Acids Res. 28, 862-867, 2000 Nucleic Acids Res. 28, 862-867, 2000 A;Title: DNA sequence analysis of the photosynthesis region c A;Reference number: Z25222; MUID:20115911; PMID:10648776 A;Accession: T50734
                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyketide synthase pksF - Mycobacterium N;Alternate names: L518_F1_8 protein C;Species: Mycobacterium leprae C;Date: 19-Mar-1997 #sequence_revision 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1489 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S72591
A; Accession: S73015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A;Description: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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Matches
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;Reywords: 3-oxoacyl-[acyl-carrier-protein] Synthase I homology <OAS2>;26-436/Domain: 3-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology <AMT>;934-832/Domain: acyl-carrier protein homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
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                                                                                                                                                                                                                                                                                                                LOBTLIFLCYTABASVALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEVGPGGSLTGSAMRHPRWSSGHRAVRLMRHPLQNVDDHDTFLRALGELWSAGIEVDWAP 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNDPGNCVVAGPKDQIRAFSQRLDEVGIPVRRVRATHAFHTSSMEPMLREFSEFLSRQQL 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site: phosphopantetheine
                                                                                                                                                                                                                                                                           EHPTLASLTAAVDASFASS
                                                                                                                                                                                                                                                                                                                                                                                                                                       QRSVMPHL----VSLPGYPFARQRHWVEPRYTIWAQIPGASSGSPVDSSVDSATVEGVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSADVYTKVSETSDHGYPIREHLNRLVDGDIIWA------PAIDGAFVLTTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEGYSAASIEGI-----RSASSNPALTLPEDPR---BIPDVISQALSELRLAGVDGPYSV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVPNTPLLSNLTGTWMSEQQVTDPE-----NW--TRQISSTIRFADELDVVLSQSGRVL 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVPFT-----LSRNBIDDVBRGSKDSDWBPVKBAAKKLAFVBD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDPGGPVTAA-----VSTGRLIDVKAPTNGVIA----HLRASKPLVR------L
                                                                                                                                                                                                                                                                                                                                                          GESQTEATLQRIWSQCLGVSSVDRNANFFD--LGGDSLMAISISMAAANEGMTITPQDMY
                                                                                                                                                                                                                                                                                                                                                                                                   GD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEQVDXALADDAV--PSVENVLVVKRTGQDIYMQLGGRDHWWHDLQKG-ASADCPABPMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQETLTFLCYTA 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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21.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96.5;
Pred. No. 34
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                                                                                                                            21-Jul-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-Apr-1997
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                                                                                                                                                                                                                                                                                                                                                                                                 -FDLQLGTD----VAIGYASHD----TDTERLY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 107;
                                          of Rhodobacter sphaeroides
                                                                                                                                09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                          931
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S

Matches Query Match Best Local :

Similarity

26.0%;

Conservative

31;

Pred. No. 11; 1; Mismatches Score 96; DB Pred. No. 11;

111; Indels Length 614;

52;

Gaps

62

В 2;

```
RESULT 13
[682830]
ATP-dependent RNA helicase XF0252 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82830
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleoti
Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
                                                                                                     A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
A;G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
C.F.G.; Nunes, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
M. Deference number, Ascola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                      A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: G82830
                                                      ;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: UNIPROT:Q9PGP6; UNIPARC:UPI00000C234B; GB:AE003878; GB:AE003849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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XF0252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-614 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLRLAGVDGPYSVLLSAD------VYTKVSETSD----HGYPIREHLNRLVDGDIIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGRDLRPIAEVQQQLVAAQLAMERDYETQREMETRYRVVLDVSRDP--MVLVSMSTGRIV
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A; Molecule type: DNA
A; Residues: 1-673 < XUA>
A; Cross-reference
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A;Status: preliminary A;Molecule type: DNA A;Residues: 658-673 <XUI>A;Coss-references: UNIPARC:UPI0000175098 A;Cross-references: UNIPARC:UPI0000175098 A;Coss-references: UNIPARC:UPI0000175098 A;Note: sequence extracted from NCBI backbone (NCBIN:123409, NCB C;Superfamily: NADH dehydrogenase (ubiquinone) chain 11 C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P29915; UNIPARC:UPI000016FD3C; GB:M84572; NID:g150599; R;Xu, X.; Matsuno-Yagi, A.; Yagi, T.
Biochemistry 32, 968-981, 1993
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Matches 66
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;Date: 24-Feb-1994 #sequence_revision 12-Apr-1996 #text_change
;Accession: S23948; A45456
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les 66; Conserv
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  507
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                                                                                                                                                                                                                                                     346 RVDG--ARLPAGN---RSAYVGTARIEDIDDAEMIQLIGTNPRDEAPVLNARIRKAWSKG 400
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                                                                                                                                                                                                                                                                                    61 PTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVER----GSKOSDWBPVKBAAKKLAFVED 116
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                                                                                                                                                                                                                                                                                                                                      RENGRIRPASWPEALEAAARAMK----GKKIAGLIGDLVPAEAAFSLKQLVEGLGGKVEC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLQLGTDVAIGYASHDTDTERL 244
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                                         VLTTRGGD-FDLQLGTDVAIGYASHDTDTERLYLQETLTFLCYTABASV 261
                                                                                                                       AGVDGPYSVLLSADVYTKVSETSDHGYPIRE-----HLNRLVDGDIIWAPAIDGAF 213
                                                                                                                                                                                                            RTI-----PEGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRL 162
                                                                                                                                                                                                                                                                                                                                                                               RDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLID-----VKA 60
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                                                                                  ARRDGE-AVLAHA--
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chain 11
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Repering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Superfamily:
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B79982
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A;Experimental source: strain H37Rv
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62; Conserv
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Search completed: April 14, 2006, 17:34:23 Job time : 18.539 secs

RESULT 15

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Total number of hits satisfying chosen parameters:
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Q7U191 MYCBO
Q7Y43F5 MYCPA
Q5YP13 NOCPA
Q7WAG7 BORPA
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Q4LT19 9BURK
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Q4SE9 THEMA
Q7MSM9 WOLSU
Q5LL119 GBOKA
Q7MSM9 TRYCR
Q5L149 GBOKA
Q7MSM9 GIALA
Q4WXE 9BELT
Q67639 GIALA
Q8MUYZ GIALA
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Q9WSAZ AERRE
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DT 01-JUL-1997 (TrEW
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DE 29 kDa antigen.
GN Name=cfp29;
OS Mycobacterium tub
OC Bacteria; Actinob
OC Corynebacterium tub
OC Bacteria; Actinob
OC Corynebacterium tub
OC Mycobacterium tub
OX NCBI_TAXID=1773;
RN NCBI_TAXID=1773;
RN NGDINESOE05159;
RX MEDLINE=98261519;
RA Andersen P.;
Tidentification a
RT Mycobacterium tub
RT effector Cells.";
RL Infect. Immun. 66
DR EMBL; Y12820; CAA
DR InterPro; IDRO075
DR Pfam; PF04454; Li
SQ SEQUENCE 265 AA
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EMBL; Y12820; CAA73350.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_M18.

Pfam; PF04454; Linocin_M18; I.

SEQUENCE 265 AA; 28860 MW; AlC4E96904
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NCBI_TaxID=1773;
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STRAIN=H37Rv;
MEDLINE=98261519; PubMed=9596740;
MEDLINE=98261519; PubMed=9596740;
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Mycobacterium tuberculosis.
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(TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 1.2e-94;
tive 0; Mismatches 0;
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Q7UYQ8 BORPE
Q7UZ68 BORPE
Q7UZ68 BORPE
Q92514 RHIME
Q7UZ39 RHOBA
Q4KN75 BORBR
Q87X3 STRAW
Q7MNY9 BORBR
Q87P88 VIBPA
Q4TQP6 95PHM
Q98BJO RHILO
Q8H6BO MAIZE
Q6DW74 LOTJA
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Q98ej0
Q8h6b0
Q86dw74
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Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 s

Scoring table: Sequence: Title: Perfect score:

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Database

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the nu score greater than and is derived by  $\varepsilon$ 

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RESULT 3
007181 M
1D 007181 M
AC 007181;
DT 01-JUL-1
DT 01-JUL-1
DT 13-SEP-2
DE 29 kDa A
GN Name=cfp
OS Mycobact
OC Bacteria
OC Coryneba
OC Coryneba
OC Wycobact
OX NCBI Tax
RN NCLEOTI
RC STRAINH
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248336; CAD93683.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_M18; I.
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
29 kDa ANTIGEN (TPP?)
                                                                                                                                                                                                                                               O07181_MYCTU PRELIMINARY; PRT; 265 AA.
O07181; Q7D997;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation updat
29 kDa ANTIGEN (CPP29 (Bacteriotin CPP29).
Name=cfp29; OrderedLocusNames=MT0819, Rv0798c;
                                                                                                                                        Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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Q7U190;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
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  MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
                                  STRAIN=H37Rv;
                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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Harris D.E., Gordon S.V., Biglmeier K., Gas S., Barry C.B. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
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J. Bacteriol. 184:5479-5490(2002).

EMBL; BX842574; CAB09572.1; -; Genomic_DNA.

EMBL; BX8000516; AAK45061.1; -; Genomic_DNA.

EMBL; 70520; E70520.

TIGR; MT0819; -.

Thberculist; RV0798c; -.

InterPro; IFR007544; Lincoin_M18.
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STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
MEDLINS=2226494; PubMed=12218036;
MEDLINS=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Pleischmann R.D., Alland D., Bisen J.A., Carpenter L., Whiteleschmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D. Hickey B.K., Kolonay J.F., Melson W.C., Umayam L.A., Brmoll Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Kodill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C. Fraser C.M.;
                             Hypothetical protein.
OrderedLocusMames=MAPG630c;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotte Shikawa T., Hattori M.;
"The complete genomic sequence of Nocardia farcinica IFM 10152.";
Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
EMBL; AP006618; BAD59878.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_M18.
Pfam; PP04454; Linocin_M18; I.
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative bacteriocin family protein.
OrderedLocusNames=nfa50260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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                                                                                                                                                                      Similarity
                                                                           MNNLYRDLAPVTBAAWABIBLBAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKA
                                                                                                                                                                                                                                                                 proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTNGVIAHLRASKFLVRLRVPFTLSRNEIDDVERGSKDSDWEFVKBAAKKLAFVEDRTIF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGYAAASIDGIRSASSNKPLALPADPREIPDVITQAISELRLAGVDGPYSVLLSADVYTK
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PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF
                                               MNNLHRELAPITSEAWAAIEEEAGRTFKRHIAGRRVVDVAGPHGVDFSAVGLGRTTGIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSETTEHGYPILEHIDRLVPGDIIWAPAIDGAFVLTT
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                                                                                                                                                                                                                                            266 AA;
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nocardiaceae; Nocardia.
                                                                                                                                                                                                                                          28763 MW;
                                                                                                                                                                 67.8%;
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                                                                                                                                             Score 914.5;
Pred. No. 1.4e
35; Mismatches
                                                                                                                                                                                                                                          D77C77B24F4F73FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
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                                                                                                                                          1.4e-61;
ches 50;
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                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                          Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kurita H., Hotta K.,
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                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7WAG7;
01-OCT-2003
01-OCT-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=12822 / ATCC BAA-587;

MEDLINB=22827954; PLMP6d=12910271; DOI=10.1038/ng1227;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Peltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007544; Linocin Pfam; PF04454; Linocin M18; T Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative analysis of the genome sequences of Bordetella Bordetella parapertussis and Bordetella bronchiseptica."; Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=12822 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7WAG7_BORPA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BX640427; CAE36712.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=linM18; OrderedLocusNames=BPP1410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BORPA
                                                            181
                                                                                            121
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                                                                                                                                                                                                                                     1 MNNLYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKA
                                                                                                                                                                                                                                                                                                 Similarity
                                                       VSETSDHGYPIREHLMRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD
                                                                                           DGYKAAGIVGIREGSSNSRLELPTDAADYPAAVGRALEQLRLAGVDGPYSVLLGADAYTA
                                                                                                                        EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180
                                                                                                                                                                         PINGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF
                                                                                                                                                                                                                                                                                                                                            proteome.
267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSETSDHGYPIREHLNRLV-DGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180
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                                                                                                                                                         POKGYDAKLREVKALVELTVPFELORDEIDAVERGANDADWQPAKDAATELAYAEDRAIF
                                                                                                                                                                                                                     MNNLYRDLAPISAAAWAQIEEEVARTFKRSVAGRRVVDVKDPGGFGLAAVGTGHLRGIAA
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                                LSEGSDDGYPTIDHIKRIVSGDIIWAPALNGGCVLSTRGGDFELHLGQDLSIGYQSHTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                             28506 MW;
                                                                                                                                                                                                                                                                                              62.3%;
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                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                               Score 840; DB 2;
Pred. No. 6.9e-56;
1; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                             M18.
                                                                                                                                                                                                                                                                                                                                             BED8667BD81DBE25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Genomic_DNA
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Matches 165
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XX MEDLINE-RESO / ATCC BAA-588;
XX MEDLINE-2827954; PubMed=12910271; DOI=10.1038/ng1227;
XX MEDLINE-2827954; PubMed=12910271; DOI=10.1038/ng1227;
XX MEDLINE-2827954; PubMed=12910271; DOI=10.1038/ng1227;
XX MEDLINE-2827954; PubMed=12910271; DOI=10.1038/ng1227;
XX MINISTER S. Sebashia M. R. Thomson N.R., Mungall K.L.,
XX ACHILLING B.R., Marier S., Basham D., Bason N., Cherevach I.,
XX ACHILLING B.R., CTONIN A., Davis P., Doggett J.,
XX ACHILLING B.R., CTONIN A., Davis P., Doggett J.,
XX Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
XX Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
XX ACHILLING B.R., Norberczak H., O'Neil S., Ormond D., Price C.,
XX ACHILLING B.R., Norberczak H., O'Neil S., Ormond D., Price C.,
XX AL, Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
XX AL, Leather S., Moule S., Sanders M., Saunders D., Seeger K.,
XX AL, M. Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M. Marier B.R., Stevens K.,
XX AL, M. Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M. Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M. Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M. Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Sanders M., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Marier B.R., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Marier B.R., Marier B.R., Saunders D., Seeger K.,
XX AL, M., Marier B.R., Marier
                                                                                                                        ULT 8
TI19 9BURK
Q4LT19 9BURK PRELIMINARY;
Q4LT19;
13-SEP-2005 (Trembirel. 31)
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L4_BORBR
Q7WJL4_BORBR
13-SEP-2005
13-SEP-2005
Linocin_M18
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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Matches 160
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EMBL; AAHLO1000017; EAM19345.1

SEQUENCE 271 AA:
                                                                                                                                                  Q45296 BRELN
Q45296;
01-NOV-1996
01-NOV-1996
01-MAR-2004
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
            MEDLINE=97077222; PubMed=8919789; Valdes-Stauber N., Scherer S.; "Nucleotide sequence and taxonomical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia cenocepacia HI2424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                           NCBI_TaxID=1703;
                                                                                                                            Linocin M18.
Name=linM18;
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Larimer F., Land M.;
"Annotation of the draft genome assembly
                                              NUCLEOTIDE
STRAIN=M18;
                                                                                                       Bacteria, Actinobacteria,
                                                                                                                   Brevibacterium linens.
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Pred. No. 1.4e
34; Mismatches
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Last annotation update)
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AC Q9WZPZ;
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Best Local Similarity
Matches 154; Conserv
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MEDLINE-99287316; PubMede-10360571; DOI-10.1038/20601;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,

Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

Byidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=TM0785;
Thermotoga maritima.
Bacteria; Thermotogae; Th
                                                                                                                                                                                                                                                                                                                                      EMBL; AE001747; AAD35867.1; -; PIR; B72333; B72333.
                                                                                                                                                                                                                                                                                                                                                                                    genome sequence of Thermotoga maritima.", Nature 399:323-329 (1999).
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01-JUN-2003
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                                                                                                                                                                                                          Complete proteome. SEQUENCE 262 AA;
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EMBL; X93588; CAA63787.1; -; Genomic_DNA.
InterPro; IPR007544; Linocin_MI8.
InterPro; IPR000169; Pept_cye_AS.
IPfam; PF04454; Linocin_MI8; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; UNKNOWN 1.
SEQUENCE 266 AA; 28597 MW; C33D960AC4C0529E
                                                                                                                                                                                                                                                                                        interPro;
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                                                                                                                                                                                                                                                     PF04454; Linocin_M18;
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                                                                                                 Score 384; DB 2;
Pred. No. 4.2e-21;
8; Mismatches 108
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Pred. No. 2.4e-51;
3; Mismatches 67;
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Bacteria; Proteobacteria; Eps
Helicobacteraceae; Wolinella.
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RESULT 12 Q5L1H9\_GEOKA

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Best Local S
Matches 68
  NUCLEOTIDE SEQUENCE.

STRAIN=2CP-C;

STRAIN=2CP-C;

SUBOR Joint Genome Institute (JGI-PGF);

Copeland A., Lucas S., Lapidus A., Barry K., Del A Hammon N., Israni S., Pitluck S., Richardson P. T "Sequencing of the draft genome assembly of Ana T dehalogenans 2CP-C.";

Submitted (MAY-2005) to the EMBL/GenBank/DDBJ d
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01-FEB-2005
01-FEB-2005
                                                                                                                                                                                                                                                                                                        ORFNames=AdehDRAFT 1692;
Anaeromyxobacter dehalogenans 2CP-C.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales
                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Similar to Uncharacterized protein linocin/CFP29 ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 32:6292-6303(2004).
EMBL; BA000043; BAD75201.1; -; Genomic
InterPro; IPR007544; Linocin_M18.
Pfam; PP04454; Linocin_M18; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15576355; DOI=10.1093/nar/gkh970;
Takami H., Takaki Y., Chee G.-J., Nishi S.,
Matsui S., Uchiyama I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FBB-2005 (TrEMBLrel. 2
Hypothetical conserved pr
OrderedLocusNames=GK0916;
                                                                                                                                                                                                                                                 Cystobacterineae; Myxococcaceae; Anaeromyxobacter. NCBI_TaxID=290397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q4NSX8_9DELT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=HTA426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4NSX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome; Hypothetical protein.
284 AA; 31836 MW; EFCDE94846619166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTDVAIGYASHDTDTERL-YL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVIA----HLRASKPL--VRLRVP----FTLSRNBIDDVERGSKDSDWEPVKEAAKKLA
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(TrEMBLrel. 29, Last sequence up)
(TrEMBLrel. 29, Last annotation
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Pred. No. 9.4e-07;
9; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272
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                                                                                 Anaeromyxobacter
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                                                                                                                                Glavina
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                                    Query Match
Best Local S
Matches 63
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                                                                                    SEQUENCE
                                                                                                                                                                                MEDLINE-98196666; PubMed-9537320; DOI=10.1038/32831; Deckert G., Warren P.V., Gaasterland T., Young W.G., Len Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M. Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Last
01-JUN-2003 (TrEMBLrel. 24, Last
Hypothetical protein aq 1760.
OrderedLocusyames=AQ_1760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CAUTION: The sequence shown here is der EMBL/GenBank/DDBJ whole genome shotgun preliminary data.

EMBL; AAHD01000020; EAL78653.1; -; Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C.";
                                                                                                                                                                                                                                                                                            Aquifex aeolicus.
Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                              067639 AQUAE
067639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SE
STRAIN=2CP-C;
                                                                                                          Pfam; PF04454; Linocin_M18;
                                                                                                                                    PIR; E70451; E70451.
                                                                                                                                                EMBL; AE000754; AAC07600.1; -;
                                                                                                                                                                        aeolicus
                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998
                                                                                                                         InterPro;
                                                                                                                                                           Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                               NCBI_TaxID=63363;
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1 MUNITEDIAPVTEAAWAEIELEAARTFKRHIAGRRVVDVSDPGG----
                                     63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                    proteome.
281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTDVAIGYASHDTDTERLYLQETLTFLCYTAEASVAL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAAAVSPARFYOLFRPFAGTALTPYQQLLPAFEGGIVKAPGLRDGAVVVVRSASGPQAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABDRLLFEGHAGA---GVRGLLEHPGLVEVPAGDWADPGRAGDALLAALTALDDAGRHGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQELTAAYDGREGIFHLVSLAESVTLL-PGAPGSVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSVLLS-ADVYTKVSETSDHGYPIREHLNRLVDGDIIWAPAI-DGAFVLTTRGGDFDLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGEDEPEAGDETHVHVPSVRALPVLHRTFRLGARAVEALERRGEPLTLTEAAEAARRIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDGAPFGQQVWDRIDEAIEAAAABAR--AGRRLLRVIGFLGFEARAGVAD-----DAPA
                                                                                                             IPR007544; Linocin_M18
4454; Linocin_M18; I.
                                                                                                                                                                                                                                                          SEQUENCE.
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                                    10.5%;
ilarity 24.2%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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28470 MW; 477948F0A22C0A49
                                                                                     31847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%;
                                                                                                                                                                                                                                                                                              Aquificales;
                                                                                     MW;
                                     41;
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                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                    Score 142; DB 2;
Pred. No. 0.013;
1; Mismatches 120
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                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                       C0B36F6296801631 CRC64;
                                                                                                                                                Genomic_DNA
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66 IAHLRASGSK 97	13 EAAMAEIELEAARTEKRHIAGRRVVDVSDPGGEVTAAVSTGRLIDVKAPTNGV 65	Query Match 8.3%; Score 112; DB 2; Length 453; Best Local Similarity 25.8%; Pred. No. 4.9; Matches 76; Conservative 41; Mismatches 96; Indels 82; Gaps 18;	PS00076; PYRIDINE RE oprotein; Oxidoreduc 1 1 1 453 453 453 AA; 49416 MW;	EI. TASE. ano reduc;	Pro; IPR001100; Pyr_redox Pro; IPR004099; Pyr_redox Pro; IPR001864; Trypnth_r PP00070; Pyr_redox; 1.	m.	C : B	1-117(19 he class		NUCLEOTIDE SEQUENCE. STRAIN=CAI;	ᇄᆿᇜ	01-NOV-1996 (TEMBLEEL 01, Lest sequence update) 01-NOV-1996 (TEMBLEEL 01, Last sequence update) 11-JUN-2003 (TrEMBLEEL 24, Last annotation update) Trypanochione reductase (Fragment). Trypanogna cruzi:	15 TRYCR Z6970_TRYCR PRELIMINARY; 26970;	ASPANĖDLA	215 LTTRGGDFDLQLGTDVAIGY 234 :: :    :    : :		117 AAAASSLAVAEDKLILPGNQEWGIEGPLTAKGTLREELSDWEKVGNAPQDVV-KGI 171	KEAAKKLAFVEDRTIFEGYSAASIEGIRSASSNPALTLPEDPREIPDVISQAL	61 GVCEVKPGQEYKVCEPVRTGERKHVPVPTLYKDFVISWRDLEHWRQENLPVDTTGV 116		1 MBFLQRDQAPLTABEWEQIDKTAYEVPKSTVVCRKFMPVVGPFGAGHQVVSYDVLYGVEP 60

Search completed: April 14, 2006, 17:32:09 Job time : 101.776 secs

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/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-252-991A-20218
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US-09-252-991A-29565
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Sequence 10, Appl
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Sequence 2, Appl
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Sequence 268, App
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Sequence 7043, Ap	Sequence 6, Appli	Sequence 1, Appli	Sequence 30, Appl	Sequence 16307, A	Sequence 16656, A	Sequence 12020, A	Sequence 4165, Ap	Sequence 12219, A	Sequence 294, App	Sequence 31483, A	Sequence 296, App	Seguence 4, Appli	Sequence 12221, A	Sequence 3623, Ap	Sequence 29606, A	Sequence 40, Appl	Sequence 40, Appl

## ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: ADDEREN, Peter

APPLICANT: NIELSEN, Rikke

APPLICANT: OETTINGER, Thomas

APPLICANT: RASMUSESU, Peter Birk

APPLICANT: ROSENKRANDS, Ida

APPLICANT: WELDINGH, Karin

TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

FILE REFERENCE: 670001-2002.1

CURRENT APPLICATION NUMBER: US/09/050,739

CURRENT FILING DATE: 1998-03-30

EARLIER APPLICATION NUMBER: 0376/97

EARLIER FILING DATE: 1997-04-02

EARLIER APPLICATION NUMBER: 1277/97

EARLIER APPLICATION NUMBER: 10/044,624

EARLIER APPLICATION NUMBER: 60/044,624

EARLIER APPLICATION NUMBER: 60/044,624

EARLIER APPLICATION NUMBER: 60/070,488

EARLIER APPLICATION NUMBER: 60/070,488

EARLIER APPLICATION NUMBER: 60/070,488

EARLIER APPLICATION NUMBER: 1997-04-18

SOFTWARE: PATE: 1998-01-05

NUMBER OF SEQ ID NOS: 173

SOFTWARE: PATE: 1998-01-05

SEQ ID NO 16

LENGTH: 265

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GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity
Matches 60; Conserv
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APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT FILING DATE: 1998-03-30
EARLIER APPLICATION NUMBER: 0376/97
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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APPLICANT: RASMUSSEN, Peter Birk
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24.6%; Pred. No. 1.2e-07;
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RESULT 5
US-09-504-357-10
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US-09-354-129-10
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-23
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EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/070,488
EARLIER APPLICATION NUMBER: 60/070,488
EARLIER FILING DATE: 1998-01-05
NUMBER: OF SEQ ID NOS: 173
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TITLE OF INVENTION: GENES ENCODING DENITRIFICATION
FILE REFERENCE: CL-1255
CURRENT APPLICATION NUMBER: US/09/354,129
CURRENT FILING DATE: 1999-07-15
EARLIER APPLICATION NUMBER: 60/093,181
EARLIER FILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
                                               Sequence 10, Application US/09504357
Patent No. 6429003
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT: YE, RICK W.
TITLE OF INVENTION: GENES ENCODING DENITRIFICATION REACTIONS
FILE REFERENCE: CL-1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 853
TYPE: PRT
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.0%;
Local Similarity 25.1%;
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                                                                                                                                                                           SMDLADIPLVFKPGTDLAILNYIANHIIQTGRVNQEFIDKVTKFMQATTDIGYGL
                                                                                                                                                                                                            GGDF-DLQL----GTDVAI-GY-ASHDTDTERL---YLQETLTFLCYTAEASVAL 263
                                                                                                                                                                                                                                                  DDFEHADAFVLWGSNMAEMHP-
                                                                                                                                                                                                                                                                                   SVILSADVYTKVSETSDHGYPIREHLNRLVDGDIIWAPAIDGAF------VLTT---R
                                                                                                                                                                                                                                                                                                                      GOWTIFEGYAATKLMRAGFRSNNL-----DPNARHCMASAAYGFMRTFGMDBPMGCY
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100.0%; Pr
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; Pred. No. 0.5;
27; Mismatches
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US-09-252-991A-20218
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US-09-252-991A-20218
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Best Local S
Matches 57
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CURRENT FILING DATE: 2000-02-15
EARLIER APPLICATION NUMBER: 60/093,181
EARLIER FILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Microsoft Office 97
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 20218
LENGTH: 269
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Best Local Similarity
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                            l Similarity
57; Conserv
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                                                                                                                                                                                                      7 HHAGAR----PDPRQPVA-----LRSARAPRHASALQLRADRPA-----TLRRQGA
TSDHGYPIR-----FDLQ 225
                                                                                                                             DPMTDMPATAD-EPVRLLLVDDHPMMRKGVAQLLELEDDLSVVGBAGSGBBALRLAA---
                                                                                                                                                                  DDVERGSKDSDWEPV-----KEAAKKLAFVEDRTIFEGYSAASIEGIRSASSNP 138
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                                                       -----ELDPDMILLDLNMKGMNGLDTLRALREAGVDARIVVPTVSDDKGDVVNVLR 155
                                                                                           ALTLPEDPREI-PDVI-----
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Pred. No. 0.096;
28; Mismatches 91;
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Pred. No. 0.5;
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                                                                                         ---SQALSELRLAGVDGPYSVLLSAD---VYTKVSE 183
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US-09-252-991A-20287
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US-09-489-039A-8355
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                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20287
LENGTH: 530
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8355
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                  Matches
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20287,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 TDVTISIDADLQDDVNCIEKMI-DAYSQGYDIVYGVRCNRDSDTFFKRTTANAFYAIMSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 SNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHG-YPIREH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 AGADGYLLKDMEPERLLEHIRQAATGQMTLSPQLTQILAQALRGDDRSKSLDELTERERQ 215
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                                     17 ABIBLE-----AARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 IARNKINNNSYLLFVDDGSRDNTWAQIKDASTAYHYVRGIKLSRNKGHQIALMAGLRSVD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 LSRNBIDD-----VERGSKDSDWEPVKEAAKKLAFVEDRTIF--EGYSAASIEGIRSAS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                      Similarity
ABRDLEVPPVNASQALSGRGIQGEVEGRRL-----ALGNRRLLDEQELKPGAL
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                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09252991A
                                                                             6.7%; Score 90; DB 2
23.5%; Pred. No. 0.72;
tive 32; Mismatches
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                                                                                                                     Length 530;
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RESULT 10
US-09-252-991A-18091
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US-09-252-991A-32791
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Sequence 18091, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLESIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PILING DATE: 1990-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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LENGTH: 268
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING '
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TEAAWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVS---TGRLIDVKAPTNGVIAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RVSKTFSRLRTSITLSEPPLQSGCHVRKGQVQQQVQRGDAEPDLEGGERGGDRLAAALG 123
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29565
LENGTH: 744
TYPE: PRT
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US-09-252-991A-29565
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LENGTH: 755
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                         188 ---GYPI----REHL-NRLVDGDIIWA----PAIDGAFVLTTRG----GDFDLQLG
                                                                                                                    184 ITKRPTDRLRGSMTVFTNIPESSKDGATRRANFSLSGPLTEALSFRAYGSANKTDSDDTD
                                                                                                                                                                                                      131 SSRNSVRYGWRGERDTRGDSNWVPPEE-----VERIEVLRGPAAARYGSGAAGGVVNI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 GAFVLTTRGGDFDLQLGTDVAI --- GYASHDTDTERL
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                                                                                                                                                                                                                                          84 LSRNEIDDVERGSK----DSDWEPVKEAAKKLAFVEDRTIFEGYSAASI-EGIRSASSNP
                                                                                                                                                                                                                                                                                           81 VNDLSEIRTMPGVNLTGNSSSGQRGNNRQIDIRGMGPENTLI--LVDGKPV-----
                                                                                                                                                                                                                                                                                                                                    36 VVDVSD-----PGGPVTAAVSTG-----RLIDVK--APTNGVIAHLRASKPLVRLRVPFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 APTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVER-----
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                                                                                                                                                                                                                                                                                                                                                                          h 6.6%; Score 88.5; D
Similarity 24.8%; Pred. No. 1.9;
64; Conservative 30; Mismatches
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                               INLGHTVNPSRTVAGREGVRNRDLSGMLSWQVTPDQVVDFEAGFSRQGNIYAGDTQNNNG
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                          ----REIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSET-SDH--
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US-09-461-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mycobacterium tuberculosis
US-09-461-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09461774
Patent No. 6887481
GENERAL INFORMATION:
APPLICANT: CHAN, Lily
APPLICANT: CHUNG, Maxey Ching Ming
APPLICANT: LIM, Renee Lay Hong
TITLE OF INVENTION: Bacterial-derived molecules
TITLE OF INVENTION: diagnostic uses therefor
FILE REFERENCE: 1781-0180P
                                                                                                                                                                                                                                                                                                                                             Sequence 268, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gil H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/461,774
CURRENT FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                             TITLE OF INVENTION: Enterococcus faecalis Polynucleotides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
  APPLICATION NUMBER:
                                                                                                                                  COUNTRY: U
                                                                                                                                                                        STATE:
                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 SYGDL----AADGVIDPVKVTR 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 VDGDIIWAPAIDGAF--VLTTR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 DPRBIPDVISQALSE-----LRLAGVDGPYSVLLSADVYTKVSE-TSDHGYPIREHLNRL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 AVIKVGAATDTALKERKESVEDAVAAAKAAVEEGIVPGGGASLIHQARKALTELRASLTG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 DLAVVTGGHVVNPDAGIVLREVGLEVLGSARRVVVSKDDTVIVDGGGTAKAVANRAN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 VKAPTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVBRGSKDSDW--BPVKBAAKKLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 DLAPVTEA-----AWAEIELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLID
                                                                                                                                                                                       T: 9410 Key West Avenue
Rockville
                                                                                                                                                                      Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVLGVDVFSEALAAPLFWIAANAGLDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KSDSDWDREKLGERLAKLAGGV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANTOGLADEGAETNRMY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                               Human Genome Sciences,
                                                                                                                                                                                                                                                                                                             H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----FVBDRT-----IFEGYSAASIEGIRSASSNPALTLPE 144
US/09/071,035
                                                                                        3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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Pred. No. 1.4;
9; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SVVVNKVSELPAGHGL----NVNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99;
                                                                                                                                                                                                                                                                                       and Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6913907
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 268,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 558 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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TOPOLOGY: lir
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                                                  COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOPTWARBE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
PILING DATE: 29-U1-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 TEK----ETLTALTTDTQGNVS 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 LATPTIDSI-TGNSSKGYEITGTÄEPKTTIDVRDADGTIIAATTÄ-----NETGQYTV 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 LSRNEIDDVERGSKDSDWEPVKEAAKKLAF---VEDRTIFEGYSAASIEGIRSASSNPAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 VDVSDPGGPVTAAVSTG-----RLIDVKAPTNGVI-----AHLRASKPLVRLRVPFT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TERLYLQETLTFLCYTAEASVA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEVRDADGTVLGMATTGTDGKYTVTLEPGKASANETITVVAKNATGKESQP-ATATTPVD 197
                                                                                                                                                                                                                                                               STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----REHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLPAGVVTPGETITIISKDGAGNESQPATAVIPADVVLAAPTITKVEGNKANGYTVTGTA 309
                                                                                                                                                                                                                            ZIP: 20850
                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10206576
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24.4%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
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US-09-071-035-258
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; SEQUENCE DESCRIPTION: SEQ ID NO: 268:
US-10-206-576-268
                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6448043

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.4%; Score 86.5; DB 2; Best Local Similarity 24.4%; Pred. No. 1.9; Matches 64; Conservative 28; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/JOCKET NUMBER: PB:
INFORMATION FOR SEQ ID NO: 268:
                                                                                                                                            COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VES
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
ATTORNEY/AGENT INFORMATION:
                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                   APPLICATION NUMBER: FILING DATE:
                                                                                                       FILING DATE:
                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 20850
                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 558 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 LATPTIDSI-TGNSSKGYBITGTABPKTTIDVRDADGTIIAATTA-----NETGQYTV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 VEVRDADGTVLGMATTGTDGKYTVTLEPGKASANETITVVAKNATGKESQP-ATATTPVD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 LSRNEIDDVERGSKDSDWEPVKEAAKKLAF---VEDRTIFEGYSAASIEGIRSASSNPAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 VDVSDPGGPVTAAVSTG-----RLIDVKAPTNGVI-----AHLRASKPLVRLRVPFT
                                                                                                                                                                                                                                                                                                                                       T: 9410 Key West Avenue Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TERLYLOETLIFICYTAEASVA 262
                                                                                                                                                                                                                                                                                                                   Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----REHLNRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPAGVVTPGETITIISKDGAGNESQPATAVIPADVVLAAPTITKVEGNKANGYTVTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09071035
                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                        MSDOS version 6.2
                                                                                                                             US/09/071,035
                                                                                                                                                                                                                                3.50 inch, 1.4Mb storage
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i LENGTH: 1638 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-258
Search completed: April 14, 2006, 17:37:52
Job time : 26.5038 secs
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Best Local Similarity
Matches 64; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: A. Anders Brookes
REGISTATION NUMBER: 36,373
REFERENCIOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                1355 DPNVTVQFYNSSEQL--LASGN------
                                                                                                                                                                                                                                                  1295 TLPAGVVTPGETITIISKDGAGNESQPATAVIPADVVLAAPTITKVEGNKANGYTVTGTA 1354
                                                                                                                                                                                                                                                                                                                                 1243 LATPTIDSI-TGNSSKGYEITGTAEPKTTIDVRDADGTIIAATTA-----NETGQYTV 1294
                                                                                                                                                                                                                                                                                                                                                                                                                   1184 VEVRDADGTVLGMATTGTDGKYTVTLEPGKASANETITVVAKNATGKESQP-ATATTPVD 1242
                                                                                                                                                                                                         192 -----REHLMRLVDGDIIWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHDTD 240
                                                                                                                                                                                                                                                                          141 TLPE---DPREIPDVISQ--ALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPI---- 191
                                                                                                                        241 TERLYLQETLTFLCYTAEASVA 262
                                                                                                                                                                                                                                                                                                                                                                        84 LSRNEIDDVERGSKDSDWEPVKEAAKKLAF---VEDRTIFEGYSAASIEGIRSASSNPAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 VDVSDPGGPVTAAVSTG-----RLIDVKAPTNGVI-----AHLRASKPLVRLRVPFT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 86.5; Dilarity 24.4%; Pred. No. 11; Conservative 28; Mismatches
                                                                               BTLTALTTDTQGNVS
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Gaps

13;

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                              Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                               seq length: 0
seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                               US-10-620-246-16
1348
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                                                                                                                                                                                                                                                                                1867569 seqs, 417829326 residues
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	w	2	<b>.</b>	Result No.
90	90	90	90.5	90.5	91	91	92	92.5		95	96	96	96	96	98	98	100	100	100	101	101	103	108	1348	1348	1348	Score
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US-10-369-493-15662	-10	US-10-282-122A-71439	US-10-450-763-54677	US-10-369-493-18051	US-10-282-122A-52256	US-10-739-930-9412	US-10-425-114-54770	US-10-389-566-1542	US-10-732-923-20546	US-09-980-217-22	US-11-097-143-25428	US-10-369-493-17504	US-10-369-493-9415	US-10-369-493-9172	US-10-732-923-1986	US-10-156-761-14324	US-10-620-246-23	US-09-804-980-23	US-09-791-171-23	US-10-991-347-21	US-10-125-692-21	US-11-097-143-28128	US-10-205-032-16	US-10-620-246-16	US-09-804-980-16	US-09-791-171-16	ID
Sequence 15662, A	Sequence 15296, A		Sequence 54677, A	Sequence 18051, A	52256,	Sequence 9412, Ap	Sequence 54770, A	Sequence 1542, Ap	205	Sequence 22, Appl	254	Sequence 17504, A	9415,	9172,	Sequence 1986, Ap	1432	23,	N	23,	21,	21	2812	Sequence 16, Appl	Sequence 16; Appl	16,	Sequence 16, Appl	Description

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11 8 76 51 1 8 2 5 4 4 4 5 5 4 4 5 5 4 4 4 5 5 4 4 4 5 5 4 4 4 4 5 5 6 5 6	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5		89	89.5	89.5	89.5	90	90	90	•
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3 US-09-815-242-11966 4 US-10-127-022-165 4 US-10-282-1228-6654 4 US-10-437-963-174225 4 US-10-369-493-4737 4 US-10-369-493-660 6 US-10-369-493-12042 7 US-10-369-493-12042 8 US-10-369-493-12042 9 US-10-156-761-10897 1 US-10-494-836-112 1 US-10-156-761-8159 1 US-10-156-761-8159 1 US-10-732-923-7244 9 US-10-732-923-7244 9 US-10-425-114-322796 9 US-10-425-114-34293 9 US-10-425-114-34293	1185	910	767	765	751	498	342	317	299	684	309	416	416	415	792	792	792	
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	US-10-437-963-173561	US-10-425-114-54293	US-10-425-115-322796	US-10-732-923-7244	US-10-156-761-8159	US-09-893-519A-33	US-10-494-836-112	US-10-156-761-10897	US-09-738-626-4484	US-10-369-493-12042	US-10-369-493-660	US-10-369-493-7496	US-10-369-493-4737	US-10-437-963-174225	US-10-282-122A-66574	US-10-127-032-165	US-09-815-242-11966	
	173561,	54293, A	322796,	7244, Ap	8159, Ap	33, Appl	112, App	10897, A	4484, Ap	12042, A	660, App	7496, Ap	4737, Ap	174225,	66574, A	165, App	11966, #	

# ALIGNMENTS

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APPLICANT: WELDINGH, Karin

APPLICANT: PLORIO, Walter

ITITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1

CURRENT FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 03/050,739

PRIOR PILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 0376/97

PRIOR APPLICATION NUMBER: 1277/97

PRIOR PILING DATE: 1997-04-02

PRIOR PILING DATE: 1997-04-18

PRIOR PILING DATE: 1997-04-18

PRIOR PILING DATE: 1997-04-18

PRIOR PILING DATE: 1997-04-18

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR PILING DATE: 1998-01-05

PRIOR PILING DATE: 1998-01-05
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                                                                                                                                                                                                                                                                                                                                                                  ; LENGTH: 265
; TYPB: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OSTTINGER, Thoma
APPLICANT: RASMUSSEN, Peter
APPLICANT: ROSENKRANDS, Ida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-791-171-16
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 265; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09791171
Patent No. US20020094336A1
GENERAL INFORMATION:
121
                   121 EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK 180
                                                                                          5
                                                                                                                  61 PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF
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                                                                                          PTNGVIAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIF
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EGYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTK
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RASMUSSEN, Peter Birk
ROSENKRANDS, Ida
                                                                                                                                                                                                                                                                            100.0%; Score 1348; DB 3; ilarity 100.0%; Pred. No. 1.7e-124; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           Length 265;
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180
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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
ITITE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 265
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thoma
APPLICANT: RASMUSSEN, Peter
APPLICANT: ROSENKRANDS, Ida
                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-620-246-16
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US-09-804-980-16
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                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/10620246 Publication No. US20040115211A1
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Best Local Similarity
APPLICANT: OETTINGÉR, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: 09/050,246
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
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                                                                US-10-205-032-16
                                                                             SOPTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 1574
TYPE: PRT
ORGANISM: micromonospora carbonacea subspecies aurantiaca
                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/10205032 Publication No. US20030113874A1 GENERAL INFORMATION:
Best Local Similarity
                   Query Match
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Best Local (
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                                                                                                                                                                                       APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
FILE REFERENCE: 3016-20S
CURRENT FILING DATE: 2002-07-26
UNMBER OF SEQ ID NOS: 39
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OR FILING DATE: 1997-04-02
OR APPLICATION NUMBER: 1277/97
OR FILING DATE: 1997-11-10
OR APPLICATION NUMBER: 60/044,624
OR FILING DATE: 1997-04-18
OR APPLICATION NUMBER: 60/070,488
OR FILING DATE: 1998-01-05
OR APPLICATION NUMBER: 10/138,473
OR FILING DATE: 1998-01-05
OR APPLICATION NUMBER: 09/791,171
OR FILING DATE: 2001-02-20
OR APPLICATION NUMBER: 09/791,171
OR FILING DATE: 1999-10-08
OR APPLICATION NUMBER: 09/116,673
OR APPLICATION NUMBER: 60/116,673
OR APPLICATION NUMBER: 1281/98
OR APPLICATION NUMBER: 1281/98
OR PILING DATE: 1999-10-08
OR APPLICATION NUMBER: 1281/98
OR PILING DATE: 1999-10-08
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8.0%;
27.7%;
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100.0%; Pred. No. 1.7e-124;
tive 0; Mismatches 0;
Pred. No.
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                      Length 1574;
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RESULT 5
US-11-097-143-28128
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SOFTWARE: PastSEQ for
SEQ ID NO 28128
LENGTH: 8805
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Publication No. US20050208558A1
GENERAL INFORMATION:
                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
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PRIOR APPLICATION NUMBER: 60/160,191
                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                OR FILING DATE: 1999-10-19
OR APPLICATION NUMBER: 60/161,932
OR FILING DATE: 1999-10-28
OR PILING DATE: 1999-11-12
OR PILING DATE: 1999-11-12
OR APPLICATION NUMBER: 60/173,383
OR FILING DATE: 1999-12-28
OR FILING DATE: 1999-12-28
OR APPLICATION NUMBER: 60/175,693
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/191,637
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/184,831
                                      1474
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                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 LTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIREHLNRLV 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 ---VAAPTGRTVFVFPGQGTHWAGMGADLLDQSPVFAESMRRCEQALSAHTDWKLGEVIR 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 DGDIIWAPAIDGAFV-----LTTRGGDFDLQL-----GTDV-----AIGYASHDTDTER 243
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                                      SQIQFNEIRTLKRSQQLGGHSVLDIAGIRDPRTGRVLTIGEAIQLRILDVRTGEMLVGDR 1533
                                                                           ABIBLEAARTFKR--HIAGRRVVDVSDPGGPVTAAVST-----GRLIDVK-----
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                                                                                                                       Conservative
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  ---APTNGVIAHLRASKPLVRLRVPFTLSRNBIDDVERGSKD-SDWEPVKEAAKKLA 112
                                                                                                                                                                                                                                                                                                   for Windows Version
                                                                                                                                                                                                                                                                                                                                                                             2000-02-24
                                                                                                                                                                                                                                                                                                                                        2000-03-23
                                                                                                                                       7.6%; Score 103; Di
23.4%; Pred. No. 45;
                                                                                                                    39; Mismatches 108;
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EXPRESSION OF 10,000 OR MORE
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RESULT 7
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; ORGANISM: E.
US-10-125-692-21
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Publication No. US20030044429A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 101; DB 4; Length 55. Best Local Similarity 22.9%; Pred. No. 1; Matches 67; Conservative 44; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/125,692
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEG ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka
APPLICANT: Smith, Kelly D.
APPLICANT: Underhill, David M.
APPLICANT: Ozinsky, Adrian
TITLE OF INVENTION: 7011-Like Receptor 5 Ligands and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: P-IS 5155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 554
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                                                                                                                                           210 DGAFVLTTRGGDFDLQLGTDVAIGYASHDTDTBRLYLQETLTFLCYTABASV 261
                                                                                                                                                                                                                                                 172 LLSADVYTKVSETSDHGYPIREHLNRLVDG----------DIIWAPA-I 209
                                                                                                                                                                                                                                                                                                                                               116 DRTIFEGYSAASIEGIR--SASSNPALTLPEDPREIPDVISQALSELRLAG--VDGPYSV 171
                                                                                                                                                                                                                                                                                                                                                                                               73 SVAQTTEGALSEINNNLQRIRELTVQATTGTNSDSDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                               57 DVKAPTNGVIAHLRASKPLVR-LRVPFTLSRNBIDDVBRGSKDSDWEPVKEAAKKLAFVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 NNINKNOSALSSSIERLSSGLRINSA---KUDAAGQAIANRFTSNIKGLTQAARNANDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NNLYRD---LAPVTEAAWABIELEAARTFKRHIAGRRVVD--VSDPGGPVTAAVSTGRLI
                                                                                                     DGSKVSTB-----ADVGFGAAAPGTPVEYTYHKDTNT---YTASASV 267
                                                                                                                                                                                                                                                                                              GQTQFNGVNVLSKDGSMKIQVGANDGETITIDLKKIDS-----DTLNLAGFNVNGE---
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Sequence 21, Application US/109
Publication No. US20050147627A:
GENERAL INFORMATION:
APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka

Application US/10991347 No. US20050147627A1

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APPLICANT: RASHOUSER, FEUEL BALA
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: WELDINGH, KARIN
APPLICANT: PLORIO, WALTER
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILL REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
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; ORGANISM: E.
US-10-991-347-21
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ANDERSEN, Rikke
APPLICANT: OETTINGER, Tho
APPLICANT: RASMUSSEN, Pet
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SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 554
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Best Local Similarity
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CURRENT FILING DATE: 2004-11-16
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 10/125,692
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APPLICANT: Underhill, David M.
APPLICANT: Ozinsky, Adriand M.
APPLICANT: Ozinsky, Adriand
TITLE OF INVENTION: TOll-Like Receptor 5 Ligands and Methods
TITLE OF INVENTION: Of Use
FILE REFERENCE: 66661-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 NNINKNOSALSSSIERLSSGLRINSA---KDDAAGQAIANRFTSNIKGLTQAARNANDGI
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SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGSKVSTB-----ADVGFGAAAPGTPVEYTYHKDTNT---YTASASV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGAFVLTTRGGDFDLQLGTDVAIGYASHDTDTERLYLQETLTFLCYTAEASV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVAQTTEGALSEINNNLQRIRELTVQATTGTNSDSDL-----DSIQDEIKSRLDEIDRVS
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RASMUSSEN, Peter Birk
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22.9%;
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Pred. No. 1;
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APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 67001-202.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 19
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-804-980-23
APPLICANT: WELDINGH, KARIN

APPLICANT: WELDINGH, KARIN

APPLICANT: FLORIO, WALTER

FITTLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

FITTLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1A

CURRENT APPLICATION NUMBER: US/10/620,246

CURRENT FILING DATE: 2003-07-15

PRIOR APPLICATION NUMBER: 09/050,739

PRIOR APPLICATION NUMBER: 09/050,739

PRIOR PILING DATE: 1997-04-02

PRIOR PILING DATE: 1997-04-02

PRIOR APPLICATION NUMBER: 1277/97

PRIOR FILING DATE: 1997-04-02

PRIOR APPLICATION NUMBER: 60/044,624

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR APPLICATION NUMBER: 1998-01-05

PRIOR PILING DATE: 1998-01-05

PRIOR PILING DATE: 1998-01-05

PRIOR PRIOR PILING DATE: 1998-01-05

PRIOR PILING DATE: 1998-01-05

PRIOR PILING DATE: 1908-01-05

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; SEQ ID NO 23
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-23
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/10620246 Publication No. US20040115211A1
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APPLICANT:
APPLICANT:
APPLICANT:
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19; Conserv
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RASMUSSEN, Peter Birk
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PRIOR APPLICATION NUMBER: 09/791,171
PRIOR FILING DATE: 2001-02-20
PRIOR PRIOR APPLICATION NUMBER: 09/415,884
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR RILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: 1281/98
PRIOR APPLICATION NUMBER: 1281/98
PRIOR PILING DATE: 1998-10-08
NUMBER OP SEQ ID NOS: 173
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 23
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US-10-156-761-14324
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Best Local Similarity
Matches 57; Conserv
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14324
LENGTH: 410
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Publication No. US20030119018A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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                                           334
                                                                                        170
                                                                                                                                 281
                                                                                                                                                                          130 GIRSASSNPAL-------TLPEDPREIPDVISQALSELRLAGVDGPY 169
                                                                                                                                                                                                                     245 GKSVVRLKGGDPFVFGRG-----
                                                                                                                                                                                                                                                                                                       185 VRGRRLLAEADVVIADRIGPROLLAELPPHVEVIDAAKIPYGRFMAQEAINNALIEHARQ 244
                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                   31 IAGRRV-----VDVSDPGGP------VTAAVSTGRLIDVKAPTNGVIAHLRA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNNLYRDLAPVTEAAWAEI 19
--LQLGTDVAIG 233
                                           VILMGVDKIGKIADTLVAHGKPAGTPVALVQEGTTAAQRRVDATLATVAETVRAQDVKPP 393
                                                                                    SVLLSADVYTKVSET-SDHGYPIREHLNRLVDGDIIWAPAIDGAFVL---TTRGGDFD-- 223
                                                                                                                                                                                                                                                              SKPLVRLR---VPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFEGYSAASIE 129
                                                                                                                                 GISSSISVPGAAGIPVTHRGVAHBPTVVSGHVAPDDERSLVD--WPALAKLR-----GTL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNNLYRDLAPVTEAAWAEI 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                              7.3%;
llarity 22.6%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                              29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 98; DB 4; Length 410; Pred. No. 1.3;
                                                                                                                                                                                                                     -----GIPCTVVP 280
                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                           ; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-369-493-9172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-732-923-1986
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Publication No. US20050108791A1

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (52796) C
FILE REFERENCE: 38-15 (52796) C
CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT PILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: 10/310,154

PRIOR PRILING DATE: 2002-12-04
                                                                                                           CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9172
LENGTH: 565
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9172, Application US/10369493 Publication No. US20030233675A1
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Best Local Similarity
                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 VILMGVDKIGKIADTLVAHGKPAGTPVALVQEGTTAAQRRVDATLATVAETVRAQDVKPP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 GIRSASSNPAL-------TLPEDPREIPDVISQALSELRLAGVDGPY 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
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7.1%;
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  Score 96;
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4.
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Length 565;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9415
LENGTH: 579
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US-10-369-493-9415
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US-10-369-493-9415
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                       y Match 7.1%;
Local Similarity 26.0%;
hes 68; Conservative 3
                                  223
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290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
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                                                                                                                                                      ATMPPQIRRI-----AQTYLQDPIB----VTIATKTTTAANIRQRYWWVSGLHKLDAL 229
                                                                                                                                                                                            GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPY---SVLLSADVY 178
                                                                                                                                                                                                                                                                     NGVIAHL-RASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFE 121
                                                                                                                                                                                                                                                                                                                                                  LAPVTEAAWAEIELEAARTFKRH---IAGRRVVDV--SDPGGPVTAAVSTGRLIDVKAPT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYSAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDGPY---SVLLSADVY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAPTRELA----IQVAEAFQRYAASISGFRVLPVYGGQSYGQQLAALKRGVHVIVGTP-
DILVATDV----AARGLDVERI 307
                                  DLQLGTDVAIGYASHDTDTERL
                                                                           TRILEVETFDAMIIFVRTKAATEELAEKLQARGLTAAAINGDMQQAQRERTIHQLKDGKL 289
                                                                                                               TKVSETSDHGYPI-----REHLNRLVDGDIIWAPAIDGAF-----VLTTRGGDF 222
                                                                                                                                                                                                                                   GRVIDHLERGTLDLSELK---TLVLDEADEMLRMGFIED---VEEVLRKLPASRQVALFS 180
                                                                                                                                                                                                                                                                                                            LAPTRELA----IQVAEAFQRYAASISGFRVLPVYGGQSYGQQLAALKRGVHVIVGTP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRILEVETFDAMIIFVRTKAATEELAEKLQARGLTAAAINGDMQQAQRERTIHQLKDGKL 297
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                                                                                                                                                                                                                                                                                                                                                                                     ; Score 96; DB 4; Length 579; Pred. No. 3.4; 31; Mismatches 111; Indels
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US-10-369-493-17504
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Coloman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17504, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 614
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
306
                                          223 DLQLGTDVAIGYASHDTDTERL 244
                                                                                      246
                                                                                                                                     179
                                                                                                                                                                               197
                                                                                                                                                                                                                                                                     143 GRVIDHLERGTLDLSELK---TLVLDEADEMLRMGFIED---VEEVLRKLPASRQVALFS 196
                                                                                                                                                                                                                                                                                                        63 NGVIAHL-RASKPLVRLRVPFTLSRNBIDDVERGSKDSDWEPVKEAAKKLAFVEDRTIFE
                                                                                                                                                                                                                                                                                                                                                         89 LAPTRELA----IQVAEAFQRYAASISGFRVLPVYGGQSYGQQLAALKRGVHVIVGTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 7.1%; Score 96; DB 4; Length 614; I Similarity 26.0%; Pred. No. 3.8; 68; Conservative 31; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   8 LAPVTEAAWAEIELEAARTFKRH----IAGRRVVDV---SDPGGPVTAAVSTGRLIDVKAPT
DILVATOV----AARGLDVERI 323
                                                                                      TRILEVETFDAMIIFVRTKAATEELAEKLQARGLTAAAINGDMQQAQRERTIHQLKDGKL
                                                                                                                                  TKVSETSDHGYPI-----REHLNRLVDGDIIWAPAIDGAF-----VLTTRGGDF
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Search completed: April 14, 2006, 18:40:29 Job time: 95.095 secs

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Title:
Perfect score:
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1: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

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6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.2	6.3	6.3	6.3	6.4	6.4	6.5	6.6	6.6	6.6	6.6	6.8	Query Match Length
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33997	Sequence 508, App	352,	Sequence 20429, A	Sequence 5491, Ap	5492,	Sequence 808, App	3008,	440	Sequence 1, Appli	Sequence 1132, Ap		Sequence 6012, Ap	8396	Sequence 436, App	Sequence 10907, A	10906	Sequence 238, App	8172,	1639	Sequence 18, Appl	Sequence 18131, A	Sequence 10005, A	Sequence 493, App	Sequence 1169, Ap	Description

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	13412, A	7003, Ap	5701, Ap	922, App	13516, A	5898, Ap	26, Appl	13272, A	1500, Ap	7521, Ap	18, Appl	1477, Ap	200, App	2003, Ap	17834, A	12330, A	17914, A	17915, A	33996, A	1ddv '82

# ALIGNMENTS

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							Query Match Best Local Similarity Matches 67; Conser	; ORGANISM: Meth US-10-506-454-1169	IVI	SEQ ID NO 1169	SOFT	NUMBER OF SEC ID NOS: 1722	PRIC	PRIOR	PRIC	PRIC	CURF	SEC	FILE	TI
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RLVI	BBFH	-BIP	LRIL		AVIL	- <b>V</b> DV	<i>\$6.56</i>	ORGANISM: Methanopyrus kandleri 0-506-454-1169			SOFTWARE: PatentIn version 3.2		-04	60/3	-04	ES.	CURRENT FILING DATE: 2004-08-31	: US		etho
::	DRVI	-DVIS	LAHR		KGPC	SDPG	Scc Pre	j.						APPLICATION NUMBER: 60/361,742		COSU	31	/10/		E E
SETSDHGYPIREHLURLVDGDII	EAWN	-Ö	CKGS	- 33 - 12 - 13	Ğ-	-GPVT	Score 91; Pred. No. ; Mismatc							42		PRIOR APPLICATION NUMBER: PCT/US03/06664		CURRENT APPLICATION NUMBER: US/10/506,454	į	Š
-	ECK.	BLR	GDA	. Pamc	TRRI	PAAV	Score 91; DB Pred. No. 2.1; 40; Mismatches									64		454		ë j
_ <u></u>	3LGK	-Ģ-	VVBA	-VICEA	DEV	STGR	DB 6; 2.1; hes !													TITLE OF INVENTION: and Methods of Use Thereof
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Sequence 10005, Application US/11188298

publication No. US20060075522A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569

SEQ ID NO 10005
                                                                                                                                                                                                                                                                           RESULT 3
US-11-188-298-10005
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US-10-506-454-493
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US-10-506-454-493
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SOFTWARE: Patentin version 3.2
SEQ ID NO 493
LENGTH: 263
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Best Local Similarity
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PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR FILING DATE: 2002-03-04
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CURRENT FILING DATE: 2004-08-31
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TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
TITLE OF INVENTION: and Methods of Use Thereof
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APPLICANT: Mezhevaya, Katja
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Polushin, Nikolai N
Shcherbinina, Olga V
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Malykh, Andrei G
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21.1%; Pred. No. 1.7;
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVI
FILE REFERENCE: 38-21(53452)B
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 18131
LENGTH: 315
TYPE: PRT
ORGANISM: Corynebacterium glutamicum ATCC 13032
US-11-188-298-18131
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US-11-188-298-18131
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LPATKTVPKELL--PVVDT--PGIELIAAEAAELGATRLAIITAPNKAGVLAHFERSSEL
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                                                     DAIDLLIDEGHPVH
                                                                                          LGTDVAI -- GYASH 237
                                                                                                                                       BIEADTKDSDVKKVKGMVEKPAIEDAPSRLAATGRYLLDRKIFDALRRITPGAGGELQLT 242
                                                                                                                                                                                                                  DDDEDVVAVMLPDDLVLPTGVMERMAQVR-ABFGG--SVLCAVE----VSEADVSKYGIF 182
                                                                                                                                                                                                                                                        SASSNPALTLPEDPREIPDVISQALSELRLAGVDGPYSVLLSADVYTKVSETSDHGYPIR 192
                                                                                                                                                                                                                                                                                                                                            VRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAA----KKLAFVEDRTIFEGYSAASIEGIR 132
                                                                                                                                                                                                                                                                                                                                                                                       LPATKTVPKELL--PVVDT--PGIELIAAEAAELGATRLAIITAPNKAGVLAHFERSSEL
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                                                                                                                                                                             EHLNRLVDGDI-----IWAPAID-----GAFVLTTR----
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23.6%; Pred. No. 2.2;
Live 37; Mismatches
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%; Pred. No. 2.1;
37; Mismatches
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RESULT 6
US-10-506-454-1639
; Sequence 1639, Application US/10506454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 870109.408
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 31-DEC-1997
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE TITLE OF INVENTION: HSP60 FAMILY NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mizzen, Lee
APPLICANT: Wisniewski, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
mes 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/1 FILING DATE: 11-AUG-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 701 Fifth Avenue, 6300 Columbia Center CITY: Seattle
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                                                                                                                                     199 VDGDIIWAPAIDGAF--VLTTR 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DLAPVTEA-----AWABIBLEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLID 57
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                                                                                                  SYGDL----AADGVIDPVKVTR
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                                                                                                                                                                                                                                                   AVIKVGAATETALKERKESVEDAVAAAKAAVEEGIVPGGGASLIHQARKALTELRASLTG 434
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                                                                                                                                                                           DEVLGVDVFSEALAAPLFWIAANAGLDG-----SVVVKKVSELPAGHGL----NVNTL 483
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                                                                                                                                                                                                                                                                                         -----FVEDRT------IFEGYSAASIEGIRSASSNPALTLPE 144
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25.2%;
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; Pred. No. 4.8;
20; Mismatches
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RESULT 7
US-11-087-099-8172
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                                                                                                ; ORGANISM: Bradyrhizobium japonicum USDA 110 US-11-087-099-8172
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                                                                                                                                       APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 8172
LENGTH: 581
TYPE: PRT
Query Match
Best Local Similarity
Matches 57; Conserv
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Publication No. US20060041961A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
SOPTWARE: PatentIn version 3.2
SEQ ID NO 1639
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APPLICANT:
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APPLICANT: Kozyavkin, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophil
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
TITLE OF INVENTION: and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Slesarev, Alexi I
APPLICANT: Mezhevaya, Katja
APPLICANT: Polushin, Nikolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/506,454
CURRENT FILING DATE: 2004-08-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 AELTLAGLLELGYEVEVTTLEGKSLPGRRRIELADE----VKGVVTGRYVEELLDSDRV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APVTEAAWAEI--ELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTGRLIDVKAPTNGVI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVSTREPSFTDLVVDLGAAPGGWSSFAAQMAENV--VAVDPA-RLEDRVRELENVHHLRI 196
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Shakhova, Vera V
Malykh, Andrei G
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Polushin, Nikolai N
             Conservative
             6.4%; Score 86.5; ]
28.1%; Pred. No. 8.2
tive 30; Mismatches
                                                    DB 7;
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             77;
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                                                       Length 581;
             Indels
             39;
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CURRENT APPLICATION NUMBER: US/10/506,454
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/US03/06664
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
SOPTWARE: PATENTIN VERSION 3.2
SEQ ID NO 238
LENGTH: 455
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US-10-506-454-238
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US-11-096-568A-10908
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US-10-506-454-238
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Best Local S
Matches 42
Sequence 10908, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 238, Application US/10506454 Publication No. US20060068386A1 GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOZYAVKIN, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: FID001
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                                                                                                                                                                                                                                                 102 EPVKEAAKKLAPVEDRTI--FEGYSAASIEGIRSASSNPALTLPEDPREIPDVIS
                                                                                                                                                                                                                                                                                       295 YYVINYVEFFSATRRFDGRRYGRRIEHVCGKEVLRRIVAGAAISRQEV----RG-----
                                                                                                                                                                                                                                                                                                                                                               248 LVREFLEVSEPEIAEVAKEAARALER-----
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                                                                                                                                                                                                              345 QYYERALRARTWIRRELLEALEGYDALL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 ---HLR-ASKPLVRLRVPFTLSRNEIDDVERGSKOSD--WEPVKEAA--KKLAFVEDRTI 119
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                                                                                                                                                                                                                                                                                                                        63 NGV-----IAHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDW 101
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42; Conserv
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Polushin, Nikolai N
Shcherbinina, Olga V
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Malykh, Andrei G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 86; DB
24.0%; Pred. No. 6.4;
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Monophyly of
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10908
LENGTH: 390
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Ceres Seq. ID no. 1359745
US-11-096-568A-10908
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA F
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT PILING DATE: 2005-04-01
KUMBER OF SEQ ID NOS: 34471
SEQ ID NO 10907
LENGTH: 436
TYPE: PRT
ORGANISM: Triticum aestivum
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US-11-096-568A-10907
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; NAME/KEY: misc feature
; LOCATION: (1)...(436)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-10907
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Best Local S
Matches 59
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                                         113 DIVINHRCAED-----KDGRGIYCIFKGGGPEGLLDWGPGMICSDDTKF-SDGT---GYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 TTRG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 SADVARTYVQNTSPGFVVAEIWNSLSYDGDGKPAVNODGERQELVNWAKAVGGPAMAFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 DTGADFAAAPDIDHLN------PRVQKELSDWLNWLKSDL---GFDGWRLDFAKGY
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                                                                              81 PFTLSRNEIDDVERGSKDS-----
                                                                                                                     55 IAGAGVTHVWLP--PPTHSVSSQGYMPGRLYDLDASKYGTAVELRSLIAAFGAKGIKCVA 112
                                                                                                                                                     31 JAGRRYVDVSDPGGPVTAAVST-----GRLIDVKAPTNGVIAHLRA-----SKPLVRLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 DIVINHRCAED-----KDGRGIYCIFKGGGPEGLLDWGPGMICSDDTKF-SDGT---GYR
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                                                                                                                                                                                            6.3%;
ilarity 24.2%;
Conservative 2
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     SAASIEGIRSASSNPALTLPEDPREIPDVISQALSELRLAGVDG----PYSVLL
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Pred. No. 5.7;
27; Mismatches
                                                                                                                                                                                            Score 85.5; Di
Pred. No. 6.7;
27; Mismatches
                                                                                                                                                                                                                                                                                            ID no.
                                                                                  -----DWEPVKEAAKKLAFVEDRTIFEGY-
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and

79;

Gaps

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163 123 Corresponding Polypeptides

--IIWAPAIDG---AFVL

173 117 123

164

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US-11-024-959-436
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                                                                                                                                                                                                                                                    RESULT 12
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US-11-024-959-436
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                                                                                                                                                                Sequence 8396, Application US/11188298 Publication No. US20060075522A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.3%; Score 85.5; DB 7; Best Local Similarity 21.8%; Pred. No. 9.1; Matches 52; Conservative 38; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KODRŽYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 792
SOFTWARE: Patentin version 3.3
SEQ ID NO 436
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               APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GESAS AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(5345.2)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILLING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILLING DATE: 2004-07-31
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TYPE: PRT
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SEQ ID
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TTKG 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LAFVEDR-----TIFEG---YSAASIEGIRSASSNPALTLPEDPREIPDVIS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGFSRDSFQATNAPDGQMYAESLRNLTENPDMLRTMQSLMKNVDPDSLV--ALSGGKLSP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNLYRDLAPVTEAAWAEIELEAARTFKRHIAGRRVVDV----SDPGGPVTAAVSTGRLI- 56
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                                                                                                                                                                                                                                                                                                                    QNMSPEMMASMSEQFGVKLSPEDAVKAQNAMASLSP--NDLDRLMN----WATRLQTA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVKAPTNGVIAHLRASKPLVRLRVPFTLSR-----NEIDDVBRGSKDSDWBPVKBAAKK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNETT, MARIE B.
EMERSON, SARAH JANE
GRIGOR, MURRAY ROBERT
HIGGINS, COLLEEN M.
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US-11-079-463-6012
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TILL REFERENCE: PATHOO-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 6012
LENGTH: 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6012, Application US/11079463 Publication No. US20060073161A1 GENERAL INFORMATION:
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LENGTH: 538
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                                                                                                                                                                                                                                                                                                                                     ORGANISM: B.fragilis
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372
163 SIASAGQLIVRGLGDRYSTTTLNGLPIASPNPDNKLIPLDLFPASTVKNITVSKVYAAGA
                                                                            108 LDAVTVVARKNLEGEKALLQERQKATLA---IENM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 DPSVAARTPVGTAIIGNVADAIARLSAATSPAPPRAVPDAALPAPNVVGSGTAIEEALLM 371
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                                                                                                                                                       48
                                                                                                                                                                                          31 IAGRRVVDVSDPGGPVTAAVSTG-------RLIDVKAPTNGVI------
                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 IAHL----RASKPLVRLRVPFTLSRNEIDDVERGSKDSDWEPVKEAAKKLAFV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 EAAWAB-IELEAARTFKRHIAGRRVVDVSDPGGPVTAAVSTG-----RLIDVKAPTNGV 65
                                                                                                                                                                                                                                                    h 6.2%; Score 84; DB 7; Length 901; Similarity 23.0%; Pred. No. 26;
                                   B-----DRTIFEGYSAASIEGIRSASSNPALTL-PEDPREIPDVISQALSELRLAGV
                                                                                                                                                       IAGTTTGTVADVDGNYTLTLSNGTYTIEVKYIGYKTLRMNEVKVKANATLNFELEVDAQT 107
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                                                                                                               ----AHLRASKPLVRLRVPFTLSRNEIDDVERGSKDSDWE----PVKEAAKKLAFV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQLATL-RPKGIIISEEAPSTRGPMHDH-FPIR---
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US-10-453-372-1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR APPLICATION NUMBER: 60/185967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
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APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
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APPLICATION NUMBER: 60/199476
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APPLICATION NUMBER: 09/823187
FILING DATE: 2001-03-29
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FILING DATE: 2000-03-10
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                                                                                                                                                                                                               PYSVNVPENLGTLPRTILQTASPC----VRFASASKAYFTTIPEDAPTGTDVLLVNASDA 2218
TDTERLYL 246
                                          TSVLVTVTDVHDNPPRFQHHPYVTHIPSPTLPGSFVFAVTVTDAD--IGPNSELHYSLSG 2336
                                                                                 LNRLVD-GDI----
                                                                                                                              DASKNAVISYRIIGGNSQFTINPSTGQIITSALLDRETKDNYTLVVVCSDAGSPEPLSSS 2278
                                                                                                                                                                    ---SQALSELRLAGVDGPYS-----VLLSA------DVYTKVSETSDHG--YPIREH 194
                                                                                                                                                                                                                                                          KKLAFVED-----RTIFEGYSAASIEGIRSASSNPA--LTLPEDPREIPDVI-----
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                                                                                 IWAPAIDGAFVLTTRGGDFDLQLGTDVAIGYASHD
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US-10-453-372-1132
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 1132
LENGTH: 4961
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PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOE FILE REFERENCE: 21402-589 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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FILING DATE: 2001-03-19
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2385 RNSEKFHI 2392
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                                   239 TDTERLYL 246
                                                                                                                      195 LNRLVD-GDI-----
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Gene vacc	M. tuberc	M. tuberc	M leprae	Antigen 8	M. tuberc	Recombina	Recombina	M. tuberc	M. tuberc	Mycobacte	Gene vacc	Gene vacc	M. tuberc	M. tuberc	M. tuberc	M bovis 8	M tubercu	Mycobacte	Ag85A. 12	Mycobacte

## ALIGNMENTS

RESULT 1
AAW72899
ID AAW7
XX AAW7
AC AAW7
XX Mycc
XX M 02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 01-APR-1998; 08-OCT-1998. WO9844119-A1 Mycobacterium tuberculosis. Mycobacterium tuberculosis antigen MPT51. 21-JAN-1999 AAW72899; AAW72899 standard; protein; 299 AA. infection. Mycobacterium tuberculosis; antigen; vaccine; (first entry) 97DK-00000376. 97US-0044624P. 97DK-00001277. 98US-0070488P. 98WO-DK000132 immunological; immunogen;

(STAT-) STATENS SERUM INST.

Oettinger T, Andersen P, Nielsen , Florio E 70 Rosenkrands I, Weldingh K, Rasmussen PB;

WPI; 1998-542705/46.

N-PSDB; AAV63923.

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis. for

Claim 1; Page 151-152; 163pp; English.

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

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 polypeptide comprising a one fusion partner; (2)
                        protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion
                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                         05-JAN-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CEP7A; CEP3OA; CFP7B; CFP19; CFP27; CFP3OA; RD1-ORF; CFP1OA; CFP16; CFP19; CFP23;
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                                                              The invention
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                                                                                                             immunogenic fragment of Mycobacterium
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                                               describes a substantially pure immunogenic polypeptide from Mycobacterium tuberculosis that is able to evoke a
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98US-0070488P.
98WO-DK000132.
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                                                                                                                                                                                                                                                                                                         CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second CC different amino acid sequence from M. tuberculosis, and/or including a CC sequence which protects the first amino acid sequence from in vivo CC degradation or post-translational processing; (3) a nucleic acid fragment CC that encodes the above polypeptides. The polypeptides and nucleic acid care useful as pharmaceuticals, for diagnosis of and as antigens for CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or CC previous sensitization in an animal with bacteria belonging or CC previous sensitization in an animal with bacteria belonging to the CC tuberculosis complex. The invention also describes the use of CFP7A or CC previous in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for the induction of a strong inmune CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell ceptiope of for diagnosis of TB in a mammal by performing a DTH type skin CC test; use of CFP27, CFP30A, CFP16, CFP19, CFP23, CFP23A, CFP30B, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and CC for the preparation of a subunit vaccine
                                                                                                                                                                                 Matches 299;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                      Sequence 299
                                                                                                                                                                                                      Local
    61
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                                                                                                                  1 MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIFVAFLAGGPH
                                                                                                                                                                                                         Similarity
    AVYLLDAFNAGPDVSNWYTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                              AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                                                                             MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                      Score 1621; DB 2;
Pred. No. 7.2e-121;
                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                    Indels
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ADR12610 standard; protein; 299
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241 181 181 121 121

AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR AMIGQTABAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR GAIAAGMOOFGGVDTNGMWGAPOLGRWKWHDPWVHASLLAONNTRVWVWSPTNPGASDPA GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNYTRVWVWSPTNPGASDPA SABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN

299 299 240

180 180

(first entry)

Gene vaccine protein #34.

RESULT 3
ADR12610
ID ADR12610
ADR12610
AC ADR1
haemostatic; protozoacide; antiinflammatory; neuroprotective; virucide; gene vaccine; ubiquitin; antigen; intracellular parasite; protozoan parasite infection; antlaria; tuberculosis; toxoplasmosis; trypanosomiasis; AIDS; cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis; Ebbla hemorrhagic fever; Trypanosoma; Chagas disease; Japanese encephalitis; influenza; rubeola; dengue virus; poliomyelitis; Herpes virus; severe acute respiratory syndrome. antimalarial; antitubercular; tuberculostatic; anti-HIV; antibacterial;

12-AUG-2004.

30-JAN-2004; 2004WO-JP000975

31-JAN-2003; 2003JP-00023507

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AAW18162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A gene vaccine (I) comprises nucleic acid sequence encoding ubiquitin, and a nucleic acid sequence encoding the antigen protein of an intracellular parasite containing T-cell target sequence. (I) is useful for preventing or treating the disease resulting from intracellular protozoan parasite infection such as malaria, tuberculosis, toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection, achlamydia disease, infections caused by Rickettsia, leishmaniasis, achlamydia disease, infections caused by Rickettsia, leishmaniasis, achlamydia disease, Trypanosoma infections, Chagas disease, Japan encephalitis, Herpes virus (alpha) infections, or severe acute. Poliomyclitis, Herpes virus (alpha) infections, or severe acute.
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                                                                                                                                                                                                                                                                                                       Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW18162
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                                                                                                                                                       Mycobacterium
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                                                                                                                                                                                                               vaccinating agent; protozoan; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
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                                                                                                                                                                                                                                                                                                       tuberculosis extracellular 24KD protein.
                                                                                                                                                       tuberculosis
                                                              Location/Qualifiers 34. .299
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                                                                                                                                                                                                                                            M.tuberculosis; pathogen; bacteria; virus;
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 298
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31-OCT-1995;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccines derived from M.tuberculosis major abundant extracellular proteins - are easy to prepare and less toxic than conventional killed attenuated vaccines, useful for protecting against or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 24; Page 41; 193pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterial infections.
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                      AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
                                                                                         GAIAAGMQQFGGVDTNGMWGAPQIGRWKWHDPWVHASILAQNNTRVWVWSPTNPGASDPA
                                                                                                                                                                 SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                                                                                                                                                                                                                                             MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
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                                                                                                                                          SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                                                                                                                                                                         AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
                                                                      GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
                                                                                                                                                                                                                  AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL
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95US-00545926.
95US-00551149.
95US-00568357.
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                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                              Score 1616; DB 2;
Pred. No. 1.8e-120;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                 Length
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccines against Mycobacterium containing major extracellular proteins used to, e.g. induce protective and therapeutic immune responses, and idetecting an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; vaccination; extracellular product; immunodominant epitope; interleukin-12; MF59; immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Page 45-46; 236pp; English.
                          SAELPDWLAANRGLAPGGHAAVGAAQGGYGAWALAAFHPDRFGFAGSMSGFLYPSNTTTN 180
                                                                                                                                                            MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
                                                                                              AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL 120
                                                                                                                              MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH
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                                                                                                                                                                                                         99.7%;
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                                                                                                                                                                                                           Score 1616; DB 2;
Pred. No. 1.8e-120;
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AVYLLDAENAGEDVSNWYTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEDDGSKQWDTFL
SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN

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06-DEC-1995;
23-MAY-1996;
                                                                                                                                                             The invention relates to a novel nucleic acid encoding an abundant extracellular protein of Mycobacterium tuberculosis useful as vaccines for generating protective or therapeutic immune response against viral, bacterial, fungal and protozoal infections. They are also used as immunotherapeutic agents. The present sequence is M. tuberculosis strainmunotherapeutic agents. The present sequence is M. tuberculosis strainmunotherapeutic agents.
                                                                                                                                                                                                                                                                        A nucleic acid encoding an abundant extracellular protein of Mycobacterium tuberculosis useful as vaccines for generating or therapeutic immune response against viral, bacterial, fun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; antibacterial; fungicide; protozoacide; virucide; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis
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                                                                                                                            Sequence
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                                                                                                                                                                                                                                                              protozoal infections.
                                                                                                                                                                                                                                                                                                                                                             Horwitz MA,
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23-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-NOV-1993;
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                                                                                                                                                     extracellular
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                               MKGRSALLRALWIAALS FGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDI PVAPLAGGPH
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                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                             Harth G;
                                                                                                                                                                                                                                                                                                                                                                                     CALIFORNIA.
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94US-00289667.
95US-00447398.
95US-00551149.
95US-00568357.
96US-00652842.
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99.7%;
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      Best Loc
Matches
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Best Local Similarity
                                                                                                                                                                                                            protozoan parasite infection such as malaria, tuberculosis, toxoplasmosis, trypanosomiasis, AIDS, cytomegalovirus infection, achlamydia disease, infections caused by Ricketteia, leishmaniasis, abola hemorrhagic fever, Trypanosoma infections, Chagas disease, Japencephalitis, influenza, rubeola and dengue viral infections, poliomyelitis, Herpes virus (alpha) infections, or severe acute respiratory, syndrome. This sequence represent a protein used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene vaccine having nucleic acids encoding ubiquitin and antigen protein of intracellular parasite, useful for treating parasite infections such as malaria, tuberculosis, toxoplasmosis.
                                                                                                                                                                                                                                                                                                                                                                                                                        A gene vaccine (I) comprises nucleic acid sequence encoding ubiquitin, and a nucleic acid sequence encoding the antigen protein of an intracellular parasite containing T-cell target sequence. (I) is useful for preventing or treating the disease resulting from intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antimalarial; antitubercular; tuberculostatic; anti-HIV; antibacterial; haemostatic; protozoacide; antiinflammatory; neuroprotective; virucide; gene vaccine; ubiquitin; antigen; intracellular parasite; protozoan parasite infection; malaria; tuberculosis; toxoplasmosis; trypanosomiasis; AIDS; cytomegalovirus infection; achlamydia disease; Rickettsia; leishmaniasis; Ebola hemorrhagic fever; Trypanosoma; Chagas disease; Japanese encephalitis; influenza; rubeola; dengue virus
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2003; 2003JP-00023507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    poliomyelitis; Herpes virus; severe acute respiratory syndrome
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99.7%;
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Score 1616; D
Pred. No. 1.8e
0; Mismatches
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Conservative

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The present invention relates to a vaccinating agent for promoting an immune response in a mammalian host against an infectious Mycobacterium pathogen. The vaccinating agent comprises at least a portion or at least one immunodominant epitope of at least one majorly abundant extracellular product selected from M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 224, 23.5, 23, 16, 14 or 12 XD protein and their analogs, homologs, and subunits, and an II-12 or MF 59 adjuvant. The compositions of the present

New vaccinating agent i Mycobacterium pathogen extracellular products

for promoting an immune response against and HIV infection using majorly abundant from Mycobacterium tuberculosis.

against infectious

Example

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SEQ

ID NO

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109pp;

English.

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31-OCT-1995;
23-MAY-1996;
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-1993;
12-AUG-1994;
23-MAY-1995;
                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                           Horwitz MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                      (LEEB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HORW/)
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Anti-HIV; Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-2005
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LEE B.
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95US-00447398.
95US-00545926.
95US-00551149.
96US-00652842.
96US-00568357.
97US-00786533.
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Best Local S
Matches 298
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The invention relates to a novel method mycobacterial disease or infection in a assaying a biological fluid sample from active tuberculosis for the presence of
                                                                           Early detection of mycobacterial infection in a subject by assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies for early Mycobacterium tuberculosis antigens.
                                                                                                                                                                              YNYU)
                                                                                                                                                                                                                                                                                                                          mycobacterial
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                                                                                                                                                                                                                         21-JUN-2001; 2001WO-US020545
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                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                   2003-721815/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are useful for stimulating a protective immune hosts against intracellular pathogens, such as viruses and fungus, particularly Mycobacterium irus. The present sequence is a M. tuberculosis
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                                                                                                                                                                                                                                                                                           tuberculosis.
                                                                                                                                                                                                                                                                                                                           disease; infection;
                                                                                                                                                                                                                                                                                                                                                 tuberculosis
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99.7%;
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Pred. No. 1.8e-120;
                                                                                                                                                                                                                                                                                                                                                 51
                                                       English
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                                                                                                                                                                                                                                                                                                                             tuberculosis;
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for the early detection of
subject. The method comprises
a subject having symptoms of
early antibodies specific for
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Best Local S
Matches 266
                                                                                                                                                                                                                                                                                                                                                                         or more early Mycobacterium tuberculosis antigens. The invention furelates to: a kit for early detection of M. tuberculosis disease; are antigenic composition for early detection of the M. tuberculosis discor infection. The compositions of the invention have antibacterial activity. The method is useful for early detection of mycobacterial disease or infection in a subject and for preparing a vaccine against tuberculosis infection. This sequence represents a Mycobacterium tuberculosis MPT 51 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                 Sequence
                           274
                                                       181
                                                                                    214
                                                                                                                121
                                                                                                                                            154
                                                                                                                                                                                                                                                                                         266;
                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                             APYENIMVPSPSMGRDIPVAFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGIS
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                  ASGDNGWGSWAPQLGAMSGDIVGAIR
                                                    VHASLLAQNNTRVWVWSPTNPGASDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFP
                                                                        VHASLIAQNNTRVWVWSPTNPGASDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFP
                                                                                                               LAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                                                                                                  LAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                                                                                                                                        VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMA
                                                                                                                                                                                         VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLLAANRGLAPGGHAAVGAAQGGYGAMA
 ASGDNGWGSWAPQLGAMSGDIVGAIR
                                                                                                                                                                                                                                                                                        90.2%;
ilarity 100.0%;
Conservative
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K
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                                                                                                                                                                                                                                                                                      Score 1462; DB 7;
Pred. No. 2.9e-108;
D; Mismatches 0;
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ADZ97846
ID ADZ97
XX ADZ97
AC ADZ97
XX Y28-JU
DT 28-JU
XX Vacci
XX Vacci
XX Vacci
XX AYCOB
XX JP200
PN JP200
PN JP200
PR 31-OC
XX WPI;
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XX WPI;
XX WPI;
XX The i
CC the M
CC the 28-JUL-2005 vaccine; mycobacterium tuberculosis ADZ97846 ADZ97846 standard; protein; (first tuberculosis MPB51 entry) 266 ₹ protein infection; SEQ ij

antibacterial; MPB51

Mycobacterium tuberculosis

JP2005130807-A.

31-OCT-2003; 2003JP-00372782

31-OCT-2003; 2003JP-00372782

(poxu-) GYOSEI NICOH KAGAKU GIJUTSU £

WPI; 2005-369245/38.

Novel el MPT51 peptide having i preparing anti-tubercle immune act e bacillus activity vaccine. with respect ç н cell, useful

Example ۲, Ħ ĕ 4 gpp;

for preparing a vaca sequence represents invention comprises the amino acid sequence of Mycobacterium tuberculosis MPB51 protein. The preparing a vaccine against tuberculosis. The uence represents the Mycobacterium tuberculosis. of a C-terminal region of he MPB51 peptide is useful he present amino acid sis MPB51 protein.

Sequence

one

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RESULT 11
ADP11940
ID ADP11940
IT ADP111
XX ADP11
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Query Match
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Matches 256; Conserv
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Best Local Similarity
Matches 263; Conser
                                                                                                                                                                                   of, or immunising a subject against Mycobacterium tuberculosis disease on infection. The composition of the invention contains a peptide from the M. tuberculosis GICB protein. The antigenic composition of the invention is useful for the early detection of, or immunising a subject against M. tuberculosis disease or infection. The present amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigenic composition, useful for early detection of, or subject against, Mycobacterium tuberculosis disease or in
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic composition; tuberculosis; GlcB; vaccine; MPT45;
secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis secreted protein MPT45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF11940 standard; peptide; 256
                                                                                                                                                                                                                                                                                                                             The invention comprises an antigenic composition for the early detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2001; 2001US-0309185P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2002; 2002WO-US024297
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98.9%;
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Score 1394; D
Pred. No. 7.3e
0; Mismatches
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Pred. No. 6.6e-107;
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7.3e-103;
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                                               Length 256;
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      The sequences given in AAB47555-57 show the protein subunits of the M. tuberculosis antigen 85 complex, Ag85A, Ag85B and Ag85C. Peptides of the invention derived from Ag85 can be recognized by a CD8 T-cell and may be used in the manufacture of agent for vaccinating prophylactically or therapeutically against infection by a mycobacterium by stimulating a CD8 T cell response. These peptides bind very strongly to HLA-B3501. Some of these peptides were able to induce cell mediated cytotoxicity using peptide-pulsed macrophages, and Ag85C(204-212) caused CD8 T cells to kill M. tuberculosis infected macrophages and induced intracellular IFN-gamma in activated CD8 cells. Ag85 derived polypeptides are useful for vaccinating a pre-selected host to stimulate a CD8 T cell response against a Mycobacterial infection. They are also useful for detecting in a population of T cells the presence or absence of CD8 T cells that
                                                                                                                                                                                                                                                                        Use of a polypeptide comprising CD8 T-cell groups derived from Mycobacterium tuberculosis antigen 85 in manufacture of a medicament vaccinating prophylactically or therapeutically against mycobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ag85C.
                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                              Disclosure; Page 50-51; 56pp;
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611506/70.
                                                                                                                                                                                                                                                                                                                                                                                       Klein
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Matches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 340 AA;
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                                WPI; 2002-164602/21
                                                                                    Orme IM,
                                                                                                                                                                                                   10-JUL-2000; 2000US-0217646P
                                                                                                                                                                                                                                                          10-JUL-2001; 2001WO-US021717
                                                                                                                                                                                                                                                                                                                                                                         WO200204018-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM50731 standard; protein; 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPYWNEQLVAMKADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWYYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPFNGTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWVW----SPTNPGASD-PAAMI-GOTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
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                                                                                       Belisle JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ag85C; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                              COLORADO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis immunodominant Mtb protein FbpC2 Ag85C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Signal_peptide
/note= "SEC-dependent signal secretion
47...340
                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                              STATE
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                                                                                                                                              RES
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Pred. No. 1.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mycobacteria; immunisation; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                 FOUND
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Query Match

Local

Similarity

34.8%;

Pred. Score

564.5; DB 5 No. 1.3e-36;

DB 5;

Length

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Vaccine for boosting immunity to mycobacteria when administered in midlife in a subject who has been vaccinated in childhood with Bacillus Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis
                                                                                                                                                                   tuberculogia
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Claim 8; Page 17; 61pp; English

strain H37Rv gene Rv0129c product, designated FbpC2 Ag85C. This is one of 31 immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see AAM50729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom protective immunity has waned. The vaccine compositions comprise 1 or more of the 31 purified immunogenic proteins. When used as immunogens, the secreted Mtb proteins lack the secreted signal sequence. A preferred protein is Ag85A (see AAM50759), the secreted product of the Rv3084v gene Sequence 340 present sequence Š is that of the Mycobacterium tuberculosis (Mtb)

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Matches
                                                                                                                                               191 ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                    166
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                                                                                                                                                                                                                                                                                                                                                                                                        4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
                                      WGSWAPQLGAMSGDI
                                                                        IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS
                                                                                                       VWVW----SPINPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                                        GSMSGFLYPSNTTTNGALAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                                                                                                                                                                                                                      QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
                                                                                                                                                                                                                                                     SK-----QWDTFLSABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA
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WPYWNEQLVAMKADI
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85-C.
                                                                                  25-MAR-2003
02-FEB-1993
            Protein
                                            Mycobacterium
                                                                                                                   AAR26167
                       Peptide
                                                         Immunise; antibody; vaccine;
                                                                                                                  standard; protein;
                                                                                   (first
                                                                                         (revised)
                              Location/Qualifiers
      /label= Mature_peptide
                  /label= Signal_peptide
                                                                                   entry)
                                                                                                                    340 AA.
                                                         PCR; antisera; amplify.
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RBSULT 15
AAY14857
ID AAY14
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Best Local :
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Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; can respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis
                                                                                                                                                                                                  AAY14857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSMSGFLYPSNTTTNGALAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSA---LLRALWIAA----LSFGL----GGVAVAABPTAKAAPYENLMVPSPSMGRDIPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSAATTLPRRVAIAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVBYLQVPSASMGRDIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : peptide(s)
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                                                                                         protein
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                                                                                                                             entry)
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                                                                                           tuberculosis
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Pred. No. 2.3e-36;
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                                       cancer;
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11-JUN-1998;
17-SEP-1998;
04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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dermatitis; eczema; alopecia areata; skin squamous cell carcinoma; melanoma.
                                              1999-430163/36
                                                                                          GENESIS RES
                        immune response
  Page 160;
                                                                                                                                                                                                                                                            tuberculosis.
                                                                                                              97US-00997362.
98US-00095855.
98US-00156181.
98US-00205426.
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97US-00997080
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                        antigen
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sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, elematitis, estantial carcinoma, squamous ce allopecia areata, and skin cancers such as basal carcinoma, squamous ce M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, carcinoma and melanoma invention provides heat-killed Mycobacterium vaccae, Š 34.6%; Score 561.5; DB 2 Pred. No. 2.3e-36; Length or recombinant cell are

39;

Mismatches

119;

Indels

27;

Gaps

8

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WGSWAPQLGAMSGDI
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                                                                                    IWVYCGNGTPSDLGGDNIPAKFLEGLT
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Search completed: April 14, 2006, 17:18:37 Job time : 117.851 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

summaries

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	v	4	w	N	_	No.	Result	
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hypothetical glyci hypothetical prote	probable integral outer membrane pro	tributyrin esteras tributyrin esteras	probable PPE prote		hypothetical glyci	hypothetical glyci	probable pntAA pro	hypothetical prote	fibroin - Chinese	probable secreted	hypothetical glyci

## ALIGNMENTS

fbpCl protein precursor - Mycobacterium tuberculosis

N;Alternate names: major antigen MPT51

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Cacession: G70867; A60274

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A.Accession: G70887

G70887

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-299 <COL> A; Accession:

A;Cross-references: UNIPROT:Q48923; UNIPARC:UPI000012F437; GB:AL022076; GB:AL123456; NI A;Experimental source: strain H37Rv

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M. Infect. Immun. 59, 372-382, 1991 A;Title: Isolation and partial characterization of major protein antigens in the cultur A;Reference number: A60274; MUID:91099989; PMID:1898899 A; Accession: A60274

A;Status: preliminary A;Molecule type: protein A;Residues: 34-40,'Y',42-49;'K',51-58;59-76;77-78 <NAG> A;Cross-references: UNIPARC:UPI0000175922; UNIPARC:UPI00001794FC; UNIPARC:UPI00001794FD Genetics:

A;Gene: fbpC1

C;Superfamily: Mycobacterium avium alpha-antigen F;34-299/Product: fbpCl protein #status experimental <MAT>

Query Match 99.7**%**; 99.7**%**; Score 1616; DB 2; Pred. No. 2.4e-111; Length 299;

Local

5 문 밁 S 밁 8 Matches 181 GAIAAGMQQFGGVDTNGMWGAPQLGRWXWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA 121 121 SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 180 61 AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDTFL 120 Similarity 99. 98; Conservative SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAFAGGAYSMYTNWEQDGSKQWDTFL 120 MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH MKGRSALLRALWIAALSFGLGGYAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH 0 Mismatches 1; Indels 0, Gaps 180 60 240 0

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Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; !
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B86921
A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-301 <STO>
A;Residuse: 1-301 <STO>
C;Genetics:
C;Genetics:
A;Genetics:
A;Ge
                     MPT51 protein - Mycobacterium leprae (fragment)
(;Species: Mycobacterium leprae
(;Species: Mycobacterium leprae
(;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
(;Accession: S3211
(;Accession: S3211)
R;Rinke de Wit, T.F.; Bekelie, S.; Osland, A.; Wieles, B.; Janson, A.A.M.; Thole, submitted to the EMBL Data Library, March 1993
A;Description: The M.leprae antigen 85 complex gene family: identification of the A;Reference number: S32107
A;Reference number: S32107
A;Accession: S32111
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 cRIN>
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     A; Cross-references:
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Species: Mycobacterium leprae
Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change
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     UNIPROT: Q05868; UNIPARC: UPI000016FB12;
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Pred. No. 1.4e-84;
3; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feltwell, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
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Fraser, 1
  EMBL: Z21949; NID: g287923;
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Holroyd,
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                                                                                                                                                                                                               J.E.R
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A;Start codon:
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P31953; UNIPARC:UPI0000042501; GB:Z92770; GB:AL123456; NI A,Experimental source: strain H37Rv R;Content, J.; de la Cuvellerie, A.; De Wit, L.; Vincent-Levy-Frebault, V.; Ooms, J.; Infect. Immun. 59, 3205-3212, 1991
A;Title: The genes coding for the antigen 85 complexes of Mycobacterium tuberculosis n of the gene coding for antigen 85-C of Mycobacterium tuberculosis. A;Reference number: A43603; MUID:91348869; PMID:1715324
A;Recession: A43603; MUID:91348869; PMID:1715324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen fbpC2 - Mycobacterium tuberculosis (strain H37RV)

N;Alternate names: antigen 85-C

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: D70615; A43603; S15504

C;Accession: D70615; A43603; S15504

C;Accession: R; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devinin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Stature 393, S37-544, 1998
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D70615
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A;Residues: 1-20,'V',22-340 <CON>
A;Cross-references: UNIPARC:UPI000002DC31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A;Title: Deciphering the biology of Mycobacterium tuberculosis fi A;Reference number: A70500; MUID:98295987; PMID:9634230
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-QMDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA
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Pred. No. 1e-
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1.3e-34;
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RESULT 5

$32114

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C;Species: Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: $32114

R;Rinke de Wit, T.F.; Bekelie, S.; Osland, A.; Wieles, B.; Janson, A.A.M.; Thole, J.E.

submitted to the EMBL Data Library, March 1993

A;Description: The M.leprae antigen 85 complex gene family: identification of the gene
A;Reference number: $32107

A;Accession: $32114

A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-333 <RIN>
A;Cross-references: UNIPROT:Q05862; UNIPARC:UPI0000125061; EMBL:Z21951; NID:g287921; P
C;Superfamily: Mycobacterium avium alpha-antigen
RESULT 6
$10326
$10326
alpha-antigen A, extracellular - Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Accession: $10326; B41499
R;de Wit, L; de la Cuvellarie, A.; Coms, J.; Content, J.
Nucleic Acids Res. 18, 3995, 1990
A;Title: Nucleotide sequence of the 32 kDa-protein gene (antigen A;Accession: $10326
A;Accession: $10326
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                             WPTMIGLAMNDSGGYNANSMWGPSTDPAWKRNDPMVQIPRLVANNTRIWVYCGNGAPNEL
                                                                                                                                                                                                                                                                                                                                    GGDNI PAKFL -- ESLTLSTNE I FONTYAASGGRNGVFNF PRIGTHSWPYWNOOLVAMKPD
                                                                                                                                                                                                                                                                                                                                                                     GASD-PAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                               TNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLTQEMPSWLQANKNVLPTGNAAVGLSMSGSSALILASYYPQQFPYAASLSGFLNPSEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLSABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGLRAQEDYNGWDINTPAFEEYYHSGLSVIMPVGGQSSFYSNWYQPSQGNGQHYTYKWET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQ--DGSKQ-----WDT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVIGTALLAGIVGVVGDTAIAVAFSKPGLPVBYLQVPSPSMGHDIKIQFQGGGQHAVYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPHAVYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPYWNEQLVAMKADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGSWAPQLGAMSGDI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWVW----SPTNPGASD-PAAMI-GQTABAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTPRDTYAADGGRNGVFNPPPNGTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
                                                                                                                                                                                                                                                                                                    294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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Pred. No. 5.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 333;
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                                                         (antigen
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                                                         Mycobacterium
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A;Molecule type: DNA
A;Residues: 1-338 <WIT>
A;Residues: 1-338 <WIT>
A;Residues: NIPROT:P17944; UNIPARC:UPI000002CE66;
A;Cross-references: UNIPROT:P17944; UNIPARC:UPI000002CE66;
R;Wiker; H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990
A;Tile: Bridence for three separate genes encoding the pro
A;Reference number: A41499; MUID:90093478; PMID:2403534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 44-82 < WIK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: B41499
A;Status: preliminary
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Matches
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324
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AL 325
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                                                                                                                                                                                                                                                          TSELPGWLQANRHYKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
                                                                                                                                                                                                                                                                                                     SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN 180
                                                                                                                                                                                                                                                                                                                                                  LRAQDDFSGWDINTPAFEWYDQSGLSVVMPVGGQSSFYSDWYQPACGKAGCQTYKWETFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AALSFGL----GGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDA
                                                                                    NNLPAKFLEGFVRTSNIK-FQDAYNAGGGHNGVFDFPDSGTHSWEYWGAQLNAMKPDLQR
                                                                                                                                                                        TLÍGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG
                                                                                                                                                                                                                 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGA
                                                                                                                                                                                                                                                                                                                                                                                           FNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----SKQWDTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                    AALVSGLVGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGANSPALYLLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                           298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%; Score 532; DB 2
40.1%; Pred. No. 8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126;
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32K antigen fbpA precursor - Mycobacterium tuberculosis (strain H37RV)
N;Alternate names: 30K native antigen; major protein antigen MPT45
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Accession: H70887; A37024; C60274; A54318
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;

D.; Holroyd,

S

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230 A; Reference number: A70500; A; Accession: H70887 complete genome

A;Status: nucleic acid sequence not shown; translation not

A;Experimental source: strain H37Rv
R;Borremans, M; De Wit, L; Volckaert, G;
R;Borremans, M,; De Wit, 198
Infect. Immun. 57, 3123-3130, 1989
A;Title: Cloning, sequence determination, a
A;Reference number: A37024; MUID:89379378; A; Molecule type: DNA
A; Residues: 1-338 <CVL>
A; Cross-references: UNIPROT: P17944; UNIPARC: UP1000002CE66; GB: AL022076; GB: AL123456;
A; Cross-references: UNIPROT: P17944; UNIPARC: UP1000002CE66; GB: AL022076; GB: AL123456; G.; Ooms, J.; De Bruyn, ٠ : Huygen, ۲. . Van

A; Accession: A37024 and expression of ; PMID:2506131 a 32-kilodalton-protein <BOR

gen

Z

A;Molecule type: DNA
A;Residues: 1-23,25,'R',27-130,'R',132-291,'R',293-323,'HWVPRPTP'
A;Residues: UNIPARC:UPI00001794FB; GB:M27016; GB:X53898
A;Cross-references: UNIPARC:UPI00001794FB; GB:M27016; GB:X53898
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991 ,332-333,335-338

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A;Accession: A54318
A;Status: preliminary
A;Molecule type: protein
A;Residues: 44-63 <SAL>
A;Cross-references: UNIPARC:UPI0000B9FC4
A;Experimental source: H37Ra
A;Note: sequence extracted from NCBI backbone (NCBIP:68909)
C;Genetics:
A;Gene: fbpA
C;Superfamily: Mycobacterium avium alpha-antigen
F;1-43)Domain: sigmal sequence #status predicted <SIG>
F;44-338/Product: 32K antigen fbpA #status experimental <MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Isolation and partial characterization of major protein antigens A;Reference number: A60274; MUID:9109989; PMID:1898899 A;Accession: C60274
A;Molecule type: DNA
A;Residues: 1-330 <STO>
A;Cross-references: UNIPROT:Q05861; UNIPARC:UPI0000125057; GB:AL450380; NID:g13092479;
C;Genetics:
A;Gene: fbpA
                                                                                                                     eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: A86921
                                                                                                                                                                                                                                     antigen 85A, mycolytransferase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: A86921 C;Accession: A86921 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheel R; Davies, R.M.; Deviin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, R.; Davies, R.M.; Deviin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.;
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R;Salata, R.A.; Sanson, A.J.; Malhotra, I.J.; Wiker, H.G.; Harboe,
J. Lab. Clin. Med. 118, 589-598, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A54318; MUID:92078747; PMID:1720803
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Best Local Simi
Matches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNLPAKFLEGFVRTSNIK-FODAYNAGGGHNGVFDFPDSGTHSWEYWGAQLNAMKPDLQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLIGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----SKQWDTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>AALVSGLVGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDIKVQPQSGGANSPALYLLDG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from NCBI backbone (NCBIP: 68909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 532; DB 2
Pred. No. 8e-32;
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A; Residues: 1-325 <WIT>
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A; Residues: 1-325 < COL>
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Matches
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                          TAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----
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Query Match Best Local Similarity 173 YPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW---136 TYKWETFLTSELPQYLQSNKQIKPTGSAAVGLSMAGLSALTLAIYHPDQFIYVGSMSGLL 113 SKOWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFL 61 -AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----4 RSALLRALWIAALS--FGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH-DPSNAMGPSLIGLAMGDAGGYKAADMWGPSTDPAWKRNDPTVNVGTLIANNTRIWMYCGN PALYLLDGLRAQDDFSGWDINTTAFEWYYQSGISVVMPVGGQSSFYSDWYSPACGKAGCQ RRLVVEÁMGVÁLLSALIGVVGSÁPÁEAFSRPGLPVEYLQVPSPSMGRDIKVQPQNGGANS Conservative 32.1%; 39; Score 521; DB 2 Pred. No. 5e-31; Mismatches DB 2; 132; Length 330 Indels 16; Gaps 135 255 229 195 172 75

288

A;Cross-references: UNIPROT: D31952; A;Experimental source: strain H37Rv R;de Wit, L.; Palou, M.; Content. J. R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genon A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70516 probable fbpB protein - Mycobacterium tuberculosis (strain H37RV)
N;Alternate names: antigen 85-B precursor
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Accession: C70516; S29664 A; Reference number: S29663 A; Accession: S29664 R;de Wit, L.; Palou, M.; Content, J submitted to the EMBL Data Library, A; Status: preliminary; nucleic acid sequence not shown; translation Similarity GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDAFNAGPDVSNWV ĠĠĄĄTĄGĄFSRPGLĖVĖYLQVPSPSMĠRDIKVQFQSĠĠNNSPĄVYLLDGLRĄQDDYNGWD Mycobacterium avium alpha-antigen 32.0%; Score 519; DB 2; ilarity 38.7%; Pred. No. 6.9e-31; Conservative 39; Mismatches 124; UNIPARC: UPI0000042500; EMBL: X62398; NID: g44563; PIDN: CAA44269.1; December 1991 UNIPARC: UPI0000042500; Length Indels GB: Z97193; GB: AL123456; 325 16; not shown Gaps 92 78 ū Gordon,

NID:

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genome

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-SKQWDTFLSABLPDWLAAN

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RBSULT 11

A32348

alpha-antigen B precursor, extracellular - Mycobacterium bovis alpha-antigen B precursor, extracellular - Mycobacterium bovis N;Alternate names: 32k antigen
C;Species: Mycobacterium bovis
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_changeriaterion: A32348; A41499; A60278
R;Matsuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Yamada, J. Bacteriol. 170, 3847-3854, 1988
A;Title: Cloning and expression of the Mycobacterium bovis BCG A;Reference number: A32348; MUID:88314872; PMID:2842287
A;Accession: A32348
A;Molecule type: DNA
A;Residues: 1-323 <MAl>
A;Cross-references: UNIPROT:P12942; UNIPARC:UPI000012505B; GB:1 R;Wiker; H.G.; S:Stetten, K.; Nagai, S.; Harboe, M.
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C;Species: Mycobacterium bovis
C;Date: 06-Jan-1995 #sequence_revision 06
C;Accession: $29663
R;de Wil, L.; Palou, M.; Content, J.
submitted to the EMBL Data Library, Decem
A;Reference number: $29663
A;Accession: $29663
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A; Residues: 1-325 <WIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRS--SNLKFQDAYNAAGGHNAVFNFPPNGTHSWEYWGAQLNAMKGDLQSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVDTNGMWGAPQLGRWXWHDPWVHASLLAQNNTRVWVW----SPTN-PGASDPAAMIGQT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAVKPTGSAAIGLSMAGSSAMILAAYHPQQFIYAGSLSALLDPSQGMGPSLIGLAMGDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----SKQWDTFLSAELPDWLAAN 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTPAFEWYYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWETLLTSELPQWLSAN
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Pred. No. 1.9e-30;
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                                                   GB:M21839; NID:g149935;
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--SKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSG 170

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R;Matsuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Terasaka, K.; Yamada, T. Infect. Immun. 58, 550-556, 1990
A;Title: Cloning and expression of the gene for the cross-reactive alpha antigen A;Reference number: A37185; MUID:90129315; PMID:2404875
A;Accession: A37185
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A;Molecule type: DNA
A;Residues: 1-325 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-antigen precursor - Mycobacterium kansasii
C;Species: Mycobacterium kansasii
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992
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R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Title: Purification and characterization of major antigens from a Mycobacterium
A;Reference number: A60278; MUID:91147217; PMID:1900061
닭
                                                                                         문
                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P21160; UNIPARC:UPIO:C;Superfamily: Mycobacterium avium alpha-antigen
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C;Superfamily: Mycobacterium avvum alpha-antigen
F;1-40/Domain: signal sequence #status predicted
F;41-323/Product: alpha antigen, extracellular #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Evidence for three separate genes encoding the proteins of A;Reference number: A41499; MUID:90093478; PMID:2403534 A;Accession: A41499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 41-59 < FIF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A60278
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                                                                                                                                                                               Matches
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                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.6%;
Similarity 38.7%;
                                              H--AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRS--SNLKFQDAYKPAGGHNAVFNFPPNGTHSWEYWGAQLNAMKGDLQSSL
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  NSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSVIMPVGGQSSFYSDWYSPACGKAG 131
                                                                                           GRRLLVGAAAAAALPGLVGLAGGAATAGAFSRPGLPVEYLQVPSAAMGRSIKVQFQSGGD
                                                                                                                                   GRSALLRALWIAALS--FGL-GGVAVAARPTAKAAPYENLMVPSPSMGRDIPVAFLAGGP 59
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                                                                                                                                                                             31.1%; Score 504.5; DB 2; 36.7%; Pred. No. 7.9e-30; 47. Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium kansasii
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Pred. No. 2.2e-30;
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                                                                                                                                                                                                                            Length 325;
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R;Kitaura, H.; Ohara, N.; Matsuo, T.; Tasaka, H.; Kobayashi, K.; Yamada, T Biochem. Biophys. Res. Commun. 196, 1466-1473, 1993
A;Title: Cloning, sequencing and expression of the gene for alpha antigen A;Reference number: JN0897; MUID:94071912; PMID:8250904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-antigen precursor - Mycobacterium intracellulare
N;Alternate names: Ag85B
C;Species: Mycobacterium intracellulare
C;Species: Mycobacterium intracellulare
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change |
C;Accession: JN0897
C;Accession: JN0897
R;Kitaura, H.; Ohara, N.; Matsuo, T.; Tasaka, H.; Kobayashi, K.;
RESULT 14
$32773
alpha-antigen - Mycobacterium avium
c;Species: Mycobacterium avium
C;Sate: 06-Jan-1995 #sequence_revision
C;Aate: 06-Jan-1995 #sequence_revision
C;Accession: $32773
R;Ohara, N.; Matsuo, K.; Yamaguchi, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: This protein is one of antigen 85.
C;Comment: This protein is an important stimulant of cellular C;Superfamily: Mycobacterium avium alpha-antigen E;1-40/Domain: signal sequence #status predicted <SIG>
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A; Residues: 1-330 < KIT>
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Matches 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.3%; Score 490.5;
37.6%; Pred. No. 8.6
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   R.; Yamazaki,
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                                   06-Jan-1995 #text_change 31-Dec-2004
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   A.;
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     H.; Yamada,
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                                                                     61 AVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG-----S
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     KQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLY
                                                                                                           GAAATLPSLISLA----
                                                                                                                                           GRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAG--GPH
                                       AVYLLDGLRAQDDYNGWDINTSAFEWYYQSGLSVVMPVGGQSSFYSDWYSPACGKAGCTT
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Conservative

40;

Mismatches

133;

Indels

21;

Gaps

9

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GGAATASAFSRPGLPVEYLQVPSEAMGRSIKVQFQNGGNGSP

72 60

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antigen 85A, mycolyltransferase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87162
                                                                                                                                                                                                                                                            eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonde, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: Si
A;Accession: S32773
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-327 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, December 1991
A;Description: Nucleotide sequence of the alpha-antigen gene of Mycobacterium
A;Reference number: S32773
                                                                                                                                                                                                                                                                                                                                                                             R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-330 <OHA>
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                                                                                                                                                                                                                                        A; Accession: G87162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 FLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQD-----
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                                                                     Mycobacterium avium alpha-antigen
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29.5%; Score 478.5; DB 2; 36.6%; Pred. No. 6.4e-28;
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Pred. No. 8.6e-29;
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Feltwell, T.;
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                                                                                                                                               GB:AL450380; NID:g13093650;
                                                                                                                                                                                                                                                                                                               Skelton,
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Holroyd,
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	Search completed: April 14, 2006, 17:34:30	Search con
	311 AMKPDL 316	Db
	289 AMSGDI 294	Ş
310	253 TPSELGGTNVPAEFLENFVHGSNLKFQDAYNGAGGHNAVFNLNADGTHSWEYWGAQLN 310	B
288	230 SPTNPGASD-PAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQIG 288	Ą
252	193 SSQGIEPQLIGLAMGDAGGYKAADMWGPPNDPAWQRNDPILQAGKLVANNTHLWVYCGNG 252	망
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext 0.5
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1621
1 MKGRSALLRALWIAALSFGL.....WGSWADQLGAMSGDIVGAIR 299
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(without alignments)
1912.171 Million cell updates/sec
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   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration
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MPTS1_MYCBO
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A85C_MYCCBA
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A85C_MYCTU
Q731037 MYCBA
A85C_MYCTU
A85C_MYCTU
A85A_MYCBO
A85A_MYCBO
A85A_MYCTU
Q84706_MYCBO
A85A_MYCTU
A85B_MYCTU
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A85B_MYCTO
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TANDARD;  O48923;  40, Created)  40, Last sequences  40, Last sequences  41, Last sequences  yois  Dacteria; Actinces  bacteria; Actinces  antionalist complex  antigens of Mycobacteriac  fing 185 complex.  Antigens of Mycofile (Actinomy)  pubMed=1278897  pubMed=1278897  pl. 41:433-442(19  pl. Sci. Content  i. Sci. Grondin S.,  rs., Gorondin S.,  rs., Grondin S.,  rs., G	304 304 344 3324 3324 3338 349 349
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update) n update n upda	E87_MYCPA 3G6 NOCPA 3G6 NOCPA 3G7_NOCPA JB0 CORGL LR1_CORGL 1R1_CORGL 2G8 NOCPA 2G5_NOCPA 2G5_NOCPA 2G7_CORDI 2G7_CO
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Best Loc
Matches
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CDC 1531 / Oshkosh;

STRAIN=22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O. Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva | Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
                                                                                                                                             Nature 393: [3]
NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                    [2]
NUCLEOTIDE SEQ
STRAÎN=H37RV;
                                                                                                                                                                         MEDLINE-88295987; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
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MYCTU
STANDARD; PRT; 299 AA.
PDA4VG; O33176; Q48923;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
MPT51/MFB51 antigen precursor.
Name=mpt51; Synonyms=fbpD, mpb51; OrderedLocusNames=Ry3803c,
ORFNames=MTV026.08c;
                                                                                                                                                                                                                                                                                                                                                                                                                    Oettinger T., Andersen P.;
"Bridence for the secreted protein MPT51 from tuberculosis is a T-cell antigen.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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nilarity 99.7%;
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RESULT 3
Q74512 MYCPA
ID Q74512 MYCPA 1
AC Q74512;
DT Q5-JUL-2004 (1)
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CONFLICT
SEQUENCE
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  EMBL;
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PubMed=14672660; DOI=10.1016/j.jmb.2003.11.001;

Wilson R.A., Maughan W.N., Kremer L., Besra G.S., Fuettere:

"The structure of Mycobacterium tuberculosis MPTS1 (PbpC1)

new family of non-catalytic alpha/beta hydrolases.";

J. Mol. Biol. 335:519-530(2004).
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SIMILARITY: Belongs to the mycobacterial A85 antigen
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BX842584;
AE000516;
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Pred. No. 5.5e
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MPT51/MPB51 antigen.
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Actinobacteridae; Actinomycetales; cteriaceae; Mycobacterium;

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RESULT 4

MPTS1 MYC
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DT 10-0
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OS MYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li L., Bannantine J., Zhang Q., Amonsin A., Al Submitted (SEP-2003) to the EMBL/GenBank/DDBJ EMBL; AB017227; AAS02534.1; -; Genomic_DNA. SMR; Q745L2; 35-300.

InterPro; IPR0001801; Esterase put. InterPro; IPR0001801; Esterase put. InterPro; IPR001412; tRNA-synt_I. Pfam; PP00756; Esterase; 1. CASSE_I; UNKNOWN_1. COMPOSTE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
                                                                                                             submitted (MAY-1995) to [2]
                                                                                                                                                                                                                     Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
 Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B. Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Haml Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moul
                                                      STRAIN=TN;
MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomso
                                                                                                                                                                                                                                                                MPT51 antigen precursor.
Name=mpt51; OrderedLocusNames=ML0098;
                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN=Tha153;
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NCBI_TaxID=1769;
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EMBL/GenBank/DDBJ databases
-; Genomic_DNA.
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Best Local S
Matches 234
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EMBL; AL583917; CAC79947.1; -; EMBL; Z21949; CAA79947.1; -; PIR; B86921; B86921
PIR; S32111; S32111
HSSP; P31953; 1DQZ.
SMR; Q05868; 36-301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acyltransferase;
SIGNAL 1
CHAIN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93366419; Rinke de Wit T.F., Thole J.B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000801; Esterase put.
Pfam; PF00756; Esterase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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IR
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                                                                                                        DPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGA
                                                                                                                                                                     TFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDREGFAGSMSGFLYPSNT
                                                                                                                                                                                                                                                                                                                                                    GPHAVYLLDAFNAALDVSNWVTAGNAMTTLGGRGISVVAPAGGAYSMYTNWENDGSKQWD
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                                                                                    DIDAMIGQAVASMGSSREFYQQYRSVGGHNGHFDFSGGGDNGWGAWAPQLAAMSGDIVGA
                                                                                                                                                                                                                                                            TFLSSELPDWLATKRGLAPDGHAAVGASQGGYAALALAAFHPDRFGFAGSLSGFVYPSST
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366419; PubMed=8359887;
it T.F., Bekelie S., Osland
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77.5%;
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Pred. No. 1e-7
23; Mismatches
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Potential.
MPT51 antigen.
S -> F (in Ref. 1).
S -> F (in Ref. 1).
APQLAAMSGDIVGAIR -> GAAVGCYVGRYRRHSLGRNQ
WHGRCCGDEPVSCMGRARMVSGEHRHRTPYVHRNLPRDLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLAGDPEWSRKCHVSATESSPGRLPCRWRPSWRWPLWLW (in Ref. 1).
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85A, 85C, and
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related
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Best Local Simi
Matches 131;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)
transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriae; Mycobacterium; Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                               Acyltransferase; Antigen; SIGNAL 1 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 15769;
MEDLINE=97427949; PubMed=9284137;
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000801; Esterase_put.
Pfam; PP00756; Esterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium avium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of the genes encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium avium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ect. Immun. 65:3680-3685(1997).

PUNCTION: Proteins of the antigen 85 complex are responsible for the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure neces for mainteaining cell wall integrity (By similarity).

SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR EDONGS to the mycobacterial A85 antigen family.
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                       190
                                            165
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                                                                                                                                                                                                               Similarity
                                                                 VAFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQD
 RVWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDN
                                            AGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNT
                                                                                                              VQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEBFYQSGLSVIMPVGGQSSFYSNWYQP
                                                                                                                                                          LRGAAATMPRRLATAAVGASLLSGVAVAAGGSPVAGAPSKPGLPVEYLEVPSPSMGRNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohara-Wada
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102
170
274
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352
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352
112
170
274
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37756
                        LNPSEGWWPTLIGLAMNDSGGYNANSMWGPSTDPAWKRNDPMVQIPRLVANNT
                                                                                                                                                                                                                                                                                                                                                                                                                content is in no
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                                                                                                                                                                                                                                                                                                                           Signal; Transferase.
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Fibronectin-binding.

Acyl-ester intermediate (By 8:
By similarity.

By similarity.

A29277CB650D60A4 CRC64;
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Pred. No. 1.1
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RESULT 7
Q8KY58 MYCPA
ID Q8KY58 M
AC Q8KY58 7
DT 01-QCT-2
DT 01-QCT-2
DT 01-UN-2
DB Antigen
OS Mycobact
OC Bacteria
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Best Local 9
          OBKY58 MYCPA PRELIMINARY; PR
OBKY58;
O1-OCT-2002 (TrEMBLrel. 22, Last
O1-OCT-2003 (TrEMBLrel. 24, Last
O1-JUN-2003 (TrEMBLrel. 24, Last
Antigen 85C complex.
Mycobacterium paratuberculosis.
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Q73U37;
05-JUL-2004 (
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1770;
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  Actinobacteria;
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AB017239; AAS06081.1; -; Genomic_DNA.
SMR; Q73U37; 49-326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000801; Esterase_put.
Pfam; PF00756; Esterase; 1.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                   GS-----KOWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGF
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[2]
NUCLEOTIDE SEQUENCE.
Chang Y.-F., Shin K.-S.;
Submitted (JUN-2000) to the ENEMBL; AP280068; AAM73518.1; -:
HSSP; P31953; 1DQY.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)
Arransferase 85C) (RC 2.3.1.-) (Fibronectin-binding protein Name=EbpC; Synonyms=mpt45; OrderedLocusNames=Mb0134C;
Mycobacterium bovis.
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MEDLINB-22481140; PubMed=12592709; DOI=10.1080/1042517021000019269;

MEDLINB-2248140; PubMed=12592709; DOI=10.1080/1042517021000019269;

Dheenadhayalan V., Shin K.S., Chang C.F., Chang C.D., Wang S.J.,

McDonough S., McDonough P., Stehman S., Shin S., Torres A.,

McDonough S., McDonough P., Stehman S., Shin S., Torres A.,

Chang Y.F.;

"Cloning and characterization of the genes coding for antigen 85A, and 85C of Mycobacterium avium subsp. paratuberculosis.";

DNA Seq. 13:287-294(2002).
        MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon
                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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InterPro; IPR000801; Bsterase put
Pfam; PP00756; Bsterase; 1.
SEQUENCE 352 AA; 37754 MW; 391
                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE STRAIN=AF2122/97;
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NCBI_TaxID=1770;
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-; Genomic_DNA.
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ORFNames=MTCI5.03c; Mycobacterium tuber

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MT0137;

tuberculosis

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STANDARD;
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POA4V4; P31953; P96806;
01-UUL-1993 (Rel. 26, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)
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-- FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure nece for maintaining cell wall integrity (By similarity).

-- SUNCELLULAR LOCATION: Secreted (By similarity).

-- I. SIMILARITY: Belongs to the mycobacterial A85 antigen family.
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P0A4V5; 49-328.
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                                                                                                                                        VWVW----SPINPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
                                                                                                                                                                                                         ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
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WPYWNEQLVAMKADI
                                                 WGSWAPQLGAMSGDI
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Fibronectin-binding.
Acyl-ester intermediate (
By similarity.
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STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Hatt D.H., Hitchey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M.D. Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Fraser C.M.;

Fraser C.M.;
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Nature 39
[3]
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                                                                                                                                                                                                                                                                                                                                                    potential targets for mycobacterial drugs and vaccines.";
Nat. Struct. Biol. 7:141-146 (2000).
-I- FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure nece for maintaining cell wall integrity.
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: Belongs to the mycobacterial A85 antigen family.
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Infect.
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MEDLINE=20122630; PubMed=10655617; DOI=10.1038/72413;
Ronning D.R., Klabunde T., Besra G.S., Vissa V.D., Be
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Mycobacterium tuberculosis complex.
MCBI_TaxID=1773;
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MEDLINE=91348869; PubMed=1715324;
~----- la Cuvellerie A., de
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Bacteriol. 184:5479-5490(2002).
BI; X57229; CAA40506.1; -; G
BI; BX842572; CAE55244.1; -;
BI; AE000516; PAK44361.1; AI;
R; D70615; D70615.
B; 1DQY; X-ray; A=47-328.
B; 1DQY; X-ray; A/B=49-328.
R; P0A4V4; 49-328.
R; P0A4V4; 49-328.
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Immun. 59:3205-3212(1991)
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Pfam; PF00756; Estera
                                                                                                                                                                                                                                                                                                                                       3D-structure; Acyltransferase; Antigen; Complete proteome; Signal;
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166 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
                            71
                                                          4
                                                                         Similarity
         AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG
                                               RSAATTLERRLAIAAMGAVLVYGLVGTFGGPATAGAFSREGLEVEYLQVESASMGRDIKV
                                                         RSA----LLRALWIAA----LSFGL-----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
                            QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS
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                                                                                                 34.8%;
                                                                                       36771 MW;
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                                                                         Score 564.5;
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B; Mismatches
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RESULT
A85C_MY
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                                                                                                                                                                                                                                                                              MEDLINE-21128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B., Wheeler P.R., Basham D., Brown D., Chillingworth T., Connor R., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Hallin N., Holroyd S., Hornisby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYCLE
                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011 (2001).

-i-FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure nece for maintaining cell wall integrity (By similarity).

-i-SUNCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C)
transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein (Name=fbpC; Synonyms=fbpC2; OrderedLocusNames=ML2655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE-93366419; PubMed=8359887;
MINE de Wit T.F., Bekelie S., Osland A.,
Thole J.E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A85C
                                                                                                                                                                                                                                                                         Squares S., S. Barrell B.G.;
                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.
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                                                                                            ween the Swiss Institute of Bioinfo
European Bioinformatics Institute.
as long as its content is in no way
          S32114; S32114.
; P31953; 1DQY.
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                                 Z21951; CAA79949.1; -; Genomic DNA. M90649; AAA91865.1; -; Genomic DNA. AL583926; CAC32187.1; -; Genomic DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                      :a-Lima L.;
(MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                 Genomic_DNA
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the 85A, 85C, and
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RESULT 11
A85A_MYCBO
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  A85A MYCBO STANDARD; PRT; 338 AA.
PDA4V3; P17944; P17996;
01-NOV-1990 (Rel. 16, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A)
transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A
Name=fbpA; Synonyms=mpt44; OrderedLocusNames=MD3834c;
Harris B., Al
Parkhill J.,
"The complete
                                                                                                                                                                       NUCLEOTIDE SEQUENCE.

STRAIN-BCG / Paris 1173 P2;

MEDLINE-90326531; PubMed=2197602;

de Wit L., de la Cuvellerie A., Ooms J., Content
"Nucleotide sequence of the 32 kDa-protein gene
Mycobacterium boyis BCG.";
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CHAIN
REGION
ACT SITE
ACT SITE
ACT SITE
                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
             Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.
                                                                                                         STRAIN=AF2122/97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leproma; ML2655; -. InterPro; IPR000801; Esterase put. Pfam; PF00756; Esterase; 1.
                                                                                        MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis.
                                                                                                                                                             Nucleic
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGLRAQEDYNGWDINTPAFEEYYHSGLSVIMPVGGQSSFYSNWYQPSQGNGQHYTYKWET
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                                                                                                                            SEQUENCE
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112
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 sequence of Mycobacterium bovis.
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Fibronectin-binding.

Acyl-ester intermediate (

By similarity.

By similarity.
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RESULT 12
A85A MYCTU STANDARD; PRT; 338 AA.
ID A85A MYCTU STANDARD; PRT; 338 AA.

AC POAAVZ; P17944; P17996;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A)
DE transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A
UNAME-ÉDAA; Synonyms-mpt44; OrderedLocusNames=Rv3804c, MT3911
GN ORFNames=MTV026.09c;
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HSSP; P31952; 1FON.
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FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure neces for maintaining cell wall integrity.
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PTM: Contains one disulfide bridge.
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X53034; CAA37206.1; -; Genomic DNA.
BX248347; CAD96020.1; -; Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121;
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Ribronectin-binding.
Acyl-ester intermediate (
By similarity.
By similarity.
By similarity.
CRC64;
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Gill J.,
Fraser C.
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STRAIN-CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.194.19.5479-5490.2002;

Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Ermolaeva M.D., Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg N.L., Bishai W., Jacobs W.R. Jr., Venter J.C.,
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Horneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R. Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Erdmann;
MEDLINB=9633337; PubMed=8757831;
Harth G., Lee B.Y., Wang J., Clemens D.L., Horwin
"Novel insights into the genetics, biochemistry,
immunocytochemistry of the 30-kilodalton major e.
of Mycobacterium tuberculosis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete
                                                  removed
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                                                                                                                                                                                                                                                                                              laboratory strains."
                                                                                                                                                                                                                                                                             Bacteriol. 184:5479-5490(2002)
                                                                                                                                          FUNCTION: Proteins of the antigen 85 complex are responsible the high affinity of mycobacteria to fibronectin. Possesses mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure nector maintaining cell wall integrity.

SUBCELLULAR LOCATION: Secreted.
PTM: Contains one disulfide bridge.

SIMILARITY: Belongs to the mycobacterial A85 antigen family.
                                                                                                                Swiss-Prot
 M27016;
U47335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            te genome sequence.";
393:537-544(1998).
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                                                                                Swiss Institute of Bioinfo
Bioinformatics Institute.
 AAA50288.1;
AAC44295.1;
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                                                                                              entry is copyright. It is produise Institute of Bioinformatics
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M., Verhofstadt R., Content J.
expression of a 32-kilodalton-
                                                                   modified
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Best Local :
NUCLEOTIDE SEQUENCE.

Lee C.F., Chang S.Y., Yu D.S.;

Submitted (DEC-2002) to the EMBL/Ge.

EMBL; AY207395; AA062004.1; -; Geno.

HSSP; P31952; 1F0N.

SMR; Q847N5; 43-330.

InterPro; IPR000801; Esterase_put.

Pfam; PF00756; Esterase; 1.
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01-JUN-2003
01-OCT-2003
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EMBL; AE000516; AAK48;
PIR; H70887; H70887.
HSSP; P31952; LPON.
SMR; P0A4V2; 43-330.
TIGR; MT3911;
                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteridae;
Corynebacterineae; Mycobacteridae;
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NCBI_TaxID=1773;
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Jiang X., Li Z.,
Submitted (MAR-2004) to the EMBL/Gen
EMBL, AX577803; AAS89650.1; -; Genom
SMR; Q6PUJ6; 43-330.
InterPro; IPR000801; Esterase put.
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                                      LRAQDDFSGWDINTPAFEWYDQSGLSVVMPVGGQSSFYSDWYQPACGKAGCQTYKWETFL
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44
338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence up
(TrEMBLrel. 27, Last annotation
:igen 85A precursor.
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                        AA;
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338
35686 N
                                                                                                                                               -GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH--AVYLLDA
                                                                                                                                                                                                                            32.8%;
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40.1%;
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                                                                                                                                                                                                                                                                                        MW;
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                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Mismatches
                                                                                                                                                                                                   Score 532; DB
Pred. No. 6.5e.
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
-; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 532; DB 2;
Pred. No. 6.5e-29;
                                                                                                                                                                                                                                                                                    Potential.
secreted antigen 8:
57B1CF95D07D52C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                            DB 2;
.5e-29;
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                                                                               --SKQWDTFL
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994
01-NOV-1997
10-MAY-2005
                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 143-330.
MEDLINE-93366419; PubMed-8359887;
Rinke de Wit T.F., Bekelie S., Osland
Thole J.B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NAY-2005 (Rel. 47, Last annotation update)
Antigen 85-A precursor (85A) (Antigen 85 complex A)
transferase 85A) (EC 2.3.1.-) (Fibronectin-binding I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kansenshogaku
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium leprae.
Bacteria; Actinobacteria;
                                                                                                                                                                                                           proteins.
                                                                                                                                                                                                                                   "The Mycobacterium identification of t
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Massive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leprae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yin Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95130993; PubMed=7829901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=fbpA; OrderedLocusNames=ML0097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A85A_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendonca-Lima
  FUNCTION: Proteins of the antigen 85 complex are responsible for the high affinity of mycobacteria to fibromectin. Possesses a mycolyltransferase activity required for the biogenesis of trehalose dimycolate (cord factor), a dominant structure necessor maintaining cell wall integrity (By similarity). SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.

PTM: Contains one disulfide bridge (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
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                                                                                                                                                                                                                                                                                                                                                                                                               re gene decay in the 409:1007-1011(2001).
                                                                                                                                                                                 Immun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSELPGWLQANRHYKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning of alpha antigen like protein gene of Mycobacterium
its over production in Escherichia coli.";
aku Zasshi 68:1330-1337(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                 61:3642-3647 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cteria; Actinobacteridae;
Mycobacteriaceae; Mycobac
                                                                                                                                                                                                                                 leprae antigen 85
the genes for the 8
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                                                                                                                                                                                                                                 85A, 85C, and
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                                                                                                                                                                                                                                                                                                             Α.,
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VFDFPDSGTHSWEYWGAQLNAMKPDLQR
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                                                                                                                                                                                                                                                                                                             В.,
                                                                                                                                                                                                                                   family:
related
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                                                                                                                                                                                                                                                                                                                Janson
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                                                                                  песеввату
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Matches 119
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PIR; S32107; S32107.
HSSP; P31952; 1FON.
SMR; Q05861; 42-328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Leproma; ML0097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 removed
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                                                                                                                                                    113
315
                   289
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M90648; AAA91864.1; -; Genomic_DNA.
AL583917; CAC29605.1; -; Genomic_DNA.
ZZ1950; CAA79948.1; -; Genomic_DNA.
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                                         GKPTELGGNNLPAKLLEGLVRTSNIK-
                                                                                                  YPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----
                                                                                                                                 TYKWETFLTSELFQYLQSNKQIKPTGSAAVGLSMAGLSALTLAIYHPDQFIYVGSMSGLL
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                                                               -SPTNPGASDPAAMIGOTAEAMGNSRMFYNOYRSVGGHNGHFDFPASGDNGWGSWAPQLG
                                                                                       DPSNAMGPSLIGLAMGDAGGYKAADMWGPSTDPAWKRNDPTVNVGTLIANNTRIWMYCGN
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Fibronectin-binding.
Acyl-ester intermediate ()
By similarity.
By similarity.
By similarity.
O - E (in Ref. 1).
O - E (In Ref. 1).
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Pred. No. 3.7e
99; Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgm2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgm2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgm2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgm2_6/ptodata/1/iaa/AB_COMB.pep:*
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1 MKGRSALLRALWIA
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                      US-09-050-739-42
US-08-107-676-3
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US-08-107-676-3
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US-08-997-305-37
US-09-995-825-37
US-09-205-426-37
US-09-205-426-37
US-09-205-426-37
US-09-205-820-3
US-09-295-820-3
US-09-295-820-3
US-09-295-820-3
US-08-997-080-36
US-08-997-080-36
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894.107 Million cell update
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Sequence 42, Appl
Sequence 3, Appl
Sequence 37, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
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APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUMBER: US/09/050,739
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: 1277/97
EARLIER FILING DATE: 1997-04-02
EARLIER FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/044,624
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US-09-050-739-42
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; SOFTWARE: PatentIn 1
; SEQ ID NO 42
; LENGTH: 299
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Best Local Simi
Matches 299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/070,488
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
                                               121
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        181 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
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                                                                      SABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTTTN
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US-08-873-970-34

US-08-873-970-34

US-09-095-855-32

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US-08-705-347A-32

US-08-705-347A-34

US-09-324-542-32

US-09-205-426-32

US-09-205-426-32

US-09-205-426-32

US-09-205-43-34

US-09-205-643-34

US-09-342-673-39

US-09-395-820-28

US-09-295-820-28

US-09-295-820-28

US-09-295-820-28
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Pred. No. 2.7e-136;
; Mismatches 0;
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DB seq length: DB seq length:

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US-08-107-676-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 91400388.4
FILING DATE: 14-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAMB: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.89USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/107,676
FILING DATE: 04-OCT-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/EP92/00268 FILING DATE: 07-FEB-1992 PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Mycobacteri
TITLE OF INVENTION: Acids Encoc
TITLE OF INVENTION: Tuberculosi
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                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                              y Match 34.6%; Score 561.5; DB 1;
Local Similarity 41.3%; Pred. No. 6.4e-42;
hes 130; Conservative 39; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3100 No. CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Merchant & Gould STREET: 3100 No. 5955356west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GAIAAGMQQFGGVDTNGMMGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA 240
131 QSNGQNYTYKWETPLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA 190

    Application US/08107676
    5955356

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                    SK-----QMDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                              AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
                                                                                                                                                                                                                     RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIGQTARAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
                                                                                       QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS
                                                                                                                                                                            RSAATTLPRRVALAAMGAVLVYGLVGTFGGPATAGAFSRPGLPVEYLQVPSASMGRDIKV 70
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DeWit, Lucas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
SOPTMARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,676
FILING DATB: 04-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00268
FILING DATE: 07-FEB-1992
PRIOR APPLICATION NUMBER: EP 91400388.4
FILING DATE: 107-FEB-1991
AFTORNEY/AGENT INFORMATION:
NAME: KOWALCHYK, Katherine M.
REGISTRATION NUMBER: 56.848
REFERENCE/DOCKET NUMBER: 8076.89USWO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                   Query Match 34.6%; Score 561.5; DB 1; Best Local Similarity 41.3%; Pred. No. 6.4e-42; Matches 130; Conservative 39; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Appl
Patent No. 595535
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acid
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TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control
TITLE OF INVENTION: Tuberculosis
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5955356west Center
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        CLONE: Protein sequence from antigen 85C from M. CLONE: tuberculosis
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
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                                                                                                                                                                                                                                                                                                                                                                                  340 amino acids
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                                                                                                                                                                                                                                                                                                                                    linear
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                                                                           Indels
                                                                                                                      Length 340;
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; Sequence.
; Patent No. 596032.
; Patent No. 596032.
; PapelicanT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                               ; LENGTH: 340 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-080-37
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                                          Query Match
Best Local Similarity
                              Matches 130;
                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: PASTSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                  TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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 4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
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                                Conservative
                                              34.6%;
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                              Score 561.5; DB 1;
Pred. No. 6.4e-42;
9; Mismatches 119;
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                                                             Length 340;
                              Indels
                              27;
                              Gaps
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US-08-997-362-37
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                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98121
COMPUTER READABLE FORM:
COMPUTER: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tan, P.
                                                                                                                                REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                 TYPE: amino STRANDEDNESS:
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TOPOLOGY:
                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2601 Elliott Avenue, Suite
                                                                                                                206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott, Linda
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 linear
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               single
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APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970 FILLING DATE: June 12, 1997 APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347 FILING DATE: August 29, 1996 ATTORNEY/AGENT INFORMATION: NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS 307
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RESULT 6
US-08-873-970-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Applicat Patent No. 6001361 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/705,347
PILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: 7502th TORCAT
                                                                                                                                                                                                                                                                                                                 ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W.
STREET: 2601 Elliott Avenue, Suit
                               TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                       Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPYWNEQLVAMKADI 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prestidge, Ross
VENTION: COMPOUNDS
VENTION: TREATMENT
                                                                                                                                                                                                                                                                                                                                                                        USA
                206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scott,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skinner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hiyama, Jun
Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tan,
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                                                                    11000.1002C1
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Pred. No. 6.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHODS FOR DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Speckman
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US-09-095-855-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tan, Pa
APPLICANT: Visser,
APPLICANT: Skinner
APPLICANT: Prestid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 130;
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Best Local Similarity
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                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                           OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                             ALUK AFFELLATION NUMBER: 08/70 FILING DATE: 29-AUG-1996 APPLICATION NUMBER: 08/87 FILING DATE: 12-UN-1997
                                                                                                                                                                                                                                                                                                                        STATE:
                FILING DATE: 12-JU
APPLICATION NUMBER:
                                                                                                                                         FILING DATE:
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 98121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 SK------QWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37, Application US/09095855
o. 6160093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
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DATE:
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                                                                                                                                                                                                                                                                                                                                                       2601 Elliott Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tan, Paul
Visser, Elizabeth
Skinner, Margot
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                                                   08/873,970
                                                                                    08/705,347
                  08/997,362
                                                                                                                                                            US/09/095,855
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Pred. No. 6.4e-42;
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                                                                                                                                                                                                                                                                                                                                                       Suite
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US-08-705-347A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/08705347A Patent No. 6284255
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Best Local Similarity 41.3%;
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                        APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 55
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Su
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hiyama, Jun
APPLICANT: Visser, Blizabeth
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER:
                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sleath, Janet REGISTRATION NUMBER:
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 340 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                        Tan, Paul
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US/08/705,347A
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Pred. No. 6.4e-42;
                                                                                                                                                                                                                                                                            AND METHODS FOR TREATMENT AND OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                      Suite 4185
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APPLICANT: WATSON, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: MOTHOD COMPOUNDS
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER FILING DATE: 1997-12-23
NUMBER OF EGG ID NOS: 194
SOPTWARE: FastSEQ for Windows Version 3.0
SSPINARE: FastSEQ for Windows Version 3.0
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US-09-324-542-37
; Sequence 37, A
                                                                                                                US-09-324-542-37
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Query Match 34.6
Best Local Similarity 41.3
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 632897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
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TELEPAX: 206.269.0563
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                             ENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS 307
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34.6%; Score 561.5; DB 2
41.3%; Pred. No. 6.4e-42;
tive 39; Mismatches 119
                                                      DB 2;
                                                   Length 340;
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Indels

27;

Gaps

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TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION UNUMBER: US/09/205,426

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-11

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER FILING DATE: 1997-12-23

EARLIER FILING DATE: 1997-16-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-12

EARLIER APPLICATION NUMBER: 08/705,347

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 37

LENGTH: 340
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Best Local S
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Patent No. 6406704
                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis -09-205-426-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J.
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                Local Similarity
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                                                              QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA 190
                                                                                                                                              AFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDG 112
                                                                                                                                                                                            RSAATTLERRVAIAAMGAVLVYGLVGTEGGPATAGAFSREGLEVEYLQVESASMGRDIKV 70
                                                                                                                                                                                                                             RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV
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                                                                                                                               QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVINPVGGQSSFYTDWYQPS 130
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ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
                                                                                               SK-----QWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA 165
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                                                                                                                                                                                                                                                             39; Mismatches 119;
                                                                                                                                                                                                                                                                            Score 561.5; DB 2
Pred. No. 6.4e-42;
                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                            340;
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RESULT 12
US-09-295-820-3
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US-09-200-643-37
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 37
LENGTH: 340
TYPE: PRT
                                                                                                                                      Sequence 3, Application Patent No. 6638511 GENERAL INFORMATION:
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Best Local (
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APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
TILE REFERENCE: 11000.1002CON
CURRENT APPLICATION NUMBER: US/09/200,643
CURRENT FILING DATE: 1996-11-05
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6410720
  NUMBER
                                                            TITLE
                                                                                                                 APPLICANT: Content,
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                DeBruyn, Jacqueline
INVENTION: Mycobacterium Polypeptides and Nucleic
Acids Encoding Them for Diagnosis and o
Tuberculosis
SEQUENCES:
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41.3%;
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Pred. No. 6.4e-42;
9; Mismatches 119
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Control

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TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID
US-09-295-820-3
                                                                                                       RESULT 13
US-09-295-820-31
                   Sequence 31, Application US/09295820
Patent No. 6638511
GENERAL INFORMATION:
APPLICANT: Content, Jean
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,820
FILING DATE: 21-App-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6638511west
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APPLICATION NUMBER: 08/107,676
FILING DATE: <Unknown>
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                      WPYWNEQLVAMKADI 322
                                                                                                                                                                                                                                                                     IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS 307
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REFERENCE/DOCKET NUMBER: 8076.89USWO
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  DeWit, Lucas
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Pred. No. 6.4
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NAME: Kowalchyk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.89USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612.332-5300
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APPLICATION NUMBER: US/09/295,820
FILING DATE: 21-Apr-1999
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLONE: Protein sequence from antigen
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LENGTH: 340 amino acids
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ADDRESSE: Merchant & Gould
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TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
Acids Encoding Them for Diagnosis and (
Tuberculosis
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280 WGSWAPQLGAMSGDI
                                                                                                       226 VWVW----SPTNPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG 279
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                                                                251 IWVYCGNGTPSDLGGDNIPAKFLEGLT---LRTNQTFRDTYAADGGRNGVFNFPPNGTHS
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FILING DATE: «Unknown»
APPLICATION NUMBER: EP 91400388.4
FILING DATE: 14-PEB-1991
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Pred. No. 6.4e-42;
9; Mismatches 119
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Best Local S
Matches 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 393-5350 INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE: ORGANISM: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: System for Protein Expression and TITLE OF INVENTION: Secretion Especially in Corynebacteria NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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nes 123; Conserv
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               EMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYAASLSGFLNPSEGWWPTL 185
                                                                                                                                 AQDDYNGWDINTPAFEBYYQSGLSVIMPVGGQSSFYTDWYQPSQSNGQNYTYKWETFLTR 125
                                                                                                                                                                                                   AVLVYGLVGTFGGPATAGAFSRPGLPVEYLQVPSASMGRDIKVQFQGGGPHAVYLLDGLR 65
IGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTRIWVYCGNGTPSDLGGDN
                                                                                                                                                                AGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSK-----QWDTFLSA 122
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400 Seventh St. N.W.
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Pred. No. 6.3e-42;
B; Mismatches 117;
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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TOPOLOGY: lin
MOLECULE TYPE:
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APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: PASTSEQ for Windows
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                    204 WPTMIGLAMNDSGGYNANSMWGPSTDPAWKRNDPMVQIPRLVANNTRIWVYCGNGAPNEL
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                                                                                                                                                                                                                                                       24 AVIGTALLAGIVGVVGDTAIAVAFSKPGLPVEYLQVPSPSMGHDIKIQFQGGGQHAVYLL
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                                                                                 TNGA I AAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW-----SPTNP
                                                                                                                    FLTQEMPSWLQANKNVLPTGNAAVGLSMSGSSALILASYYPQQPPYAASLSGFLNPSEGW
                                                                                                                                                   FLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSNTT 178
                                                                                                                                                                                      DGLRAQEDYNGWDINTPAFEEYYHSGLSVIMPVGGQSSFYSNWYQPSQGNGQHYTYKWET
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2601 Elliott Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 amino acids
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Search completed: April 14, 2006, 17:37:57 Job time : 28.6477 secs	322 I 322	294   294	264 GGDNIPAKFLESLTLSTNEIFQNTYAASGGRNGVFNFPFNGTHSWFYWNQQLVAMKFD 321

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seq length: 2000000000
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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US-10-332-512A-3
US-09-880-505-37
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TITLE OF INVENTION: DERIVED FRAGMENTS AND POLYPEPTIDE FRAGMENTS
FILE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION UNMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR PRILING DATE: 1997-04-02
PRIOR PILLING DATE: 1997-04-02
PRIOR PILLING DATE: 1997-04-04
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 109/138,473
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 1998-01-05
PRIOR PILLING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILLING DATE: 2001-02-20
PRIOR PILLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 00/416 004
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LENGTH: 299
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PRIOR FILING DATE: 1998-10-08
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RASMUSSEN, Peter Birk
ROSENKRANDS, Ida
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.2e-130;
D; Mismatches 0;
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TITLE OF INVENTION: ABUNDANT EXTRACELLULAR PRODUCTS AND METHODS FOR THEIR PRODUCTION
FILE OF INVENTION: AND USE
FILE REFERENCE: 51326-00004
CURRENT APPLICATION NUMBER: US/10/695,155
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: 08/652,842
PRIOR APPLICATION NUMBER: 08/652,842
PRIOR FILING DATE: 1996-03-23
PRIOR APPLICATION NUMBER: 08/568,357
PRIOR APPLICATION NUMBER: 08/51,149
PRIOR APPLICATION NUMBER: 08/55,149
PRIOR FILING DATE: 1995-10-31
PRIOR APPLICATION NUMBER: 08/447,398
PRIOR APPLICATION NUMBER: 08/447,398
PRIOR APPLICATION NUMBER: 08/289,667
PRIOR FILING DATE: 1995-05-23
PRIOR APPLICATION NUMBER: 08/289,667
PRIOR APPLICATION NUMBER: 08/289,667
PRIOR FILING DATE: 1994-08-12
PRIOR APPLICATION NUMBER: 08/56,358
PRIOR APPLICATION NUMBER: 08/55,358
PRIOR APPLICATION NUMBER: 08/545,926
PRIOR FILING DATE: 1995-10-20
PRIOR FILING DATE: 1995-10-20
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US-10-695-155-166
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 166
LENGTH: 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                       241 AMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
                                                                                181
                                                                                                      181 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNBGASDPA
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                                                                                                                                                             AMIGQAARAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
                                                                                GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVWSPTNPGASDPA
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o. US20040228873A1
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99.7%;
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Pred. No. 5.9e-130;
0; Mismatches 1;
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RESULT 4
US-09-804-980-42
; Sequence 42, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:

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; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 298
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US-10-481-563A-14
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US-10-481-563A-14
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                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 252
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Best Local Similarity
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TITLE OF INVENTION: MYCOBACTERIAL PROTEINS AS
FILE REFERENCE: 32004-173355
CURRENT APPLICATION NUMBER: US/10/481,563A
CURRENT FILLING DATE: 2003-12-22
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/212,048 PRIOR FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                                                        TYPE: PRT
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252; Conserv
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                LAAFHPDRFGFAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                              VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLAANR-----
                                                                                 VVAPAGGAYSMYTNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIGQTARAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVGAIR 299
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- AAFHPDRFGFAGSMSGFLYPSNTTINGALAAGMQQFGGVDTNGMWGAPQLGRWKWHDPW
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                      82.4%;
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99.7%;
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Pred. No. 5.7e-129;
0; Mismatches 0;
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                                                                                                                                                                                       Score 1335; DB 5;
Pred. No. 5.4e-106;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLY ANTIGENS
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 FILE REFERENCE: 11000.1007c2
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CURRENT APPLICATION NUMBER: US/10/332,512A
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: PUS01/21717
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/217,646
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
US-09-880-505-37

Sequence 37, Application US/09880505

Publication No. US20030007976A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Tractidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-332-512A-3
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US-10-332-512A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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APPLICANT: BELISLE, John T.
TITLE OP INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMM
FILE REFERENCE: 38861-186292
                                                                                                                                                                                                                                                                                                                                                                                                                         280 WGSWAPQLGAMSGDI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 VWVW----SPINEGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 GSMSGPLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 QSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASLSGFLNPSEGWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSA---LIRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
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41.6%; Pred. No. 6.9e-40;
vative 38; Mismatches 119;
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CURRENT APPLICATION NUMBER: US/09/880,505; CURRENT FILING DATE: 2001-06-13; PRIOR APPLICATION NUMBER: US 09/324,542; PRIOR FILING DATE: 1999-06-02; PRIOR PILING DATE: 1999-06-02; PRIOR FILING DATE: 1997-12-23; NUMBER OF SEQ ID NOS: 194; SOPTWARE: FASESEQ for Windows Version 3.0; SEQ ID NO 37; LENGTH: 340
                                                                                                                                                                                             APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: System using Mycobacterium Vaccae FILE REFERENCE: 11000.1008c2

CURRENT APPLICATION NUMBER: US/10/051,643

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US09/156,181

PRIOR APPLICATION NUMBER: US09/156,181

PRIOR APPLICATION NUMBER: US09/56,624

PRIOR APPLICATION NUMBER: US08/996,624

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208
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US-10-051-643-37
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                                                                                                ; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 37; LENGTH: 340; TYPE: PRT; ORGANISM: Mycobacterium tuberculosis US-10-051-643-37
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Publication No. US20000100000
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
                                  Matches 130;
                                                  Query Match
Best Local Similarity
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 4 RSA---LLRALWIAA----LSFGL----GGVAVAAEPTAKAAPYENLMVPSPSMGRDIPV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWVW----SPINPGASD-PAAMI-GQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNG
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41.3%;
                               ; Score 561.5; DB 4; ; Pred. No. 1.2e-39; 39; Mismatches 119;
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Pred. No. 1.2e-39;
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US-09-880-505-36
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LENGTH: 333
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Sequence 36, Application US/09880505

Publication No. US2003007976A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
FIIIE OF INVENTION: of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c2

CURRENT APPLICATION NUMBER: US/09/880,505

CURRENT APPLICATION NUMBER: US 09/324,542

PRIOR APPLICATION NUMBER: US 09/324,542

PRIOR APPLICATION NUMBER: US 09/324,542

PRIOR APPLICATION NUMBER: US 09/37,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mycobacterium leprae US-09-880-505-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSEQ for Windows Version 3.0
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GGDNIPAKFL--ESLTLSTNEIFQNTYAASGGRNGVFNFPPNGTHSWPYWNQQLVAMKPD
                                                GASD-PAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGD
                                                                                                            WPTMIGLAMNDSGGYNANSMWGPSTDPAWKRNDPMVQIPRLVANNTRIWVYCGNGAPNEL
                                                                                                                                                                                                                             FLTQEMPSWLQANKNVLPTGNAAVGLSMSGSSALTLASYYPQQFPYAASLSGFLNPSEGW
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Sequence 36, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Diseases of the TITLE OF INVENTION: System using Mycobacterium Vaccae FILE REFERENCE: 11000.1008C2

CURRENT APPLICATION NUMBER: US/10/051,643

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US/9156,181

PRIOR APPLICATION NUMBER: US/996,624

PRIOR APPLICATION NUMBER: US 08/996,624

PRIOR APPLICATION NUMBER: US 08/996,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-051-643-36
                                                                                                                                                                                                                           RESULT 11
US-10-282-122A-64050
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US-10-051-643-36
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                                                   APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlo APPLICANT: Malone, Cheryl APPLICANT: Haselbeck, Rok APPLICANT: Ohlsen, Kari APPLICANT: Zyskind, Judit
                                                                                                                                                                  Sequence 64050, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Best Local S
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               APPLICANT:
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                               Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVIGTALLAGIVGVVGDTAIAVAFSKPGLPVBYLQVPSPSMGHDIKIQFQGGGQHAVYLL 83
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               Wall, Daniel
Trawick, John
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
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Matches
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential
FILE REFERENCE: ELITRA.034A
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33.8%; Score 548; DB 4;
Local Similarity 39.2%; Pred. No. 1.7e-38;
hes 118; Conservative 41; Mismatches 128
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OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application data removed -
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RESULT 12
US-09-880-505-32
; Sequence 32, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:

APPLICANT: Watson, James D APPLICANT: Tan, Paul L.J. APPLICANT: Prestidge, Ros

James D.

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RESULT 13
US-09-880-505-34
US-09-880-505-34
; Sequence 34, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 32
                                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 34
LENGTH: 338
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Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 08/997,080
PRIOR PILING DATE: 1997-12-23
NUMBER OF SEO ID NOS: 194
SOPTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 11000.1007c2
CURRENT APPLICATION NUMBER: US/09/880,505
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/324,542
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 08/997,080
PRIOR APPLICATION NUMBER: US 08/997,080
PRIOR PILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin DisorFILE REFERENCE: 11000.1007c2
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Watson, James D. APPLICANT: Tan, Paul L.J. APPLICANT: Prestidge, Ross
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                                                                     TYPE: PRT
ORGANISM: Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW----SPTNPGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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32.8%;
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Pred. No. 4.1e-37;
Score 532; DB 3; Pred. No. 4.1e-37;
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                      Length 338;
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CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PastSEQ for Windows Version 3.0
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LENGTH: 338
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                             Matches 121; Conservative
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APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008c2
                                                                                                                                                                                                                                                                                                                                                                                                   Match 32.8%;
Local Similarity 40.1%;
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                                                                         181 GAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW-----SPTNPGA
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SDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFDFPASGDNGWGSWAPQLGAMSGDIVG
                                         TLIGLAMGDAGGYKASDMWGPKEDPAWQRNDPLLNVGKLIANNTRVWVYCGNGKPSDLGG
                                                                                                                             TSELPGWLQANRHVKPTGSAVVGLSMAASSALTLAIYHPQQFVYAGAMSGLLDPSQAMGP
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; Pred. No. 4.1e-37;
37; Mismatches 126
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APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REPERENCE: 11000 1008C2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 338
TYPE: PRT
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US-10-051-643-34
; Sequence 34, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
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Published Applications AA New:*

1: /SIDS5/ptcdata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDS5/ptcdata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDS5/ptcdata/2/pubpaa/USO7_NEW_PUB.pep:*

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5: /SIDS5/ptcdata/2/pubpaa/USO3_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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US-11-169-041-138 US-10-517-939-318 US-11-052-554A-144	US-11-052-554A-133 US-11-087-099-12200 US-11-087-099-4274 US-11-052-554A-154	US-11-052-554A-150 US-11-087-099-4262 US-11-188-298-13202 US-11-052-554A-166 US-11-052-554A-160	US-11-052-554A-172 US-11-052-554A-162 US-11-172-740-542 US-11-188-298-17488 US-11-188-298-8448	US-11-188-298-11967 US-11-188-298-19912 US-11-188-298-19912 US-11-052-554A-163 US-11-052-554A-151 US-11-188-298-11858	
Sequence 138, App Sequence 318, App Sequence 144, App	` 4 6 '		Sequence 172, App Sequence 162, App Sequence 542, App Sequence 17488, A Sequence 8448, Ap	11967 11967 19912 163, 151,	on 9174, 68, 1

RESULT 2
US-11-082-389-68
; Sequence 68, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:

97.5 6.0 1436 7 US-11-052-554A-140 97.6 6.0 837 7 US-11-052-554A-140 96.5 6.0 330 7 US-11-188-298-2825 96.5 6.0 330 7 US-11-188-298-21964 96.5 6.0 330 7 US-11-188-298-21964 96.5 6.0 330 7 US-11-188-298-4142 95.5 5.9 273 7 US-11-188-298-4416 95 5.9 433 7 US-11-188-298-4416 95 5.9 3716 7 US-11-052-554A-145 94.5 5.8 639 7 US-11-052-554A-146 94.5 5.8 1538 7 US-11-052-554A-146 94.5 5.8 373 7 US-11-052-554A-146 94.5 5.8 1538 7 US-11-052-554A-12718 93.5 5.8 373 7 US-11-096-568A-12717 93.5 5.8 1901 7 US-11-096-568A-12717 93.5 7 388 7 US-11-188-298-9414 93.5 7 749 7 US-11-188-298-9414	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	
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	14874, A	148, App	9414, Ap	1, Appli	135, App	12717, A	12718, A	2, Appli	146, App	165, App	141, App	152, App	8416, Ap	539, App	142, App	21964, A	2825, Ap		140, App	•

#### ALIGNMENTS

RESULT 1 US-11-079-463-9174

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US-11-079-463-9174
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PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 9174
LENGTH: 331
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Publication No. US20060073161A1
GENERAL INFORMATION:
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Best Local Similarity 30.2%;
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOD-03DIV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                           169
                                                                                          164 NPAYRYETFVSSELVNYIDRNYKTIADRKGRAITGLSMGGHGAMWLGIRHKDVFGAAGST 223
                                                                                                                       111 DGSKQWDTFLSABLPDWLAAN-RGLAP-GGHAAVGAAQGGYGAMALAAFHPDRFGFAGSM 168
                                                                                                                                                                                 107 LGKNAAACPVLYLLHGY--GGHAKTWIQIKPNLPEIADEKGIIFVCP-DGKDSWYWDSPK 163
224
                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                               57 GGPHA-----VYLLDAFNAGPDVSNWVTAGNAMNTLAG-KGISVVAPAGGAYSMYTNWEQ 110
                                                                                                                                                                                                                                                                                                                          1 MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAF----LA 56
                                                                                                                                                                                                                                                                                                                                                                        64; Conservative
                                         SGFL----YPSNTTTNGAIAAGMQQFGGVDTN 196
                                                                                                                                                                                                                                                                              MKRRNLFLACILLFVLPL------SAARVDTLMVKSPSMNKEVQVLVVTPDVA 106
SGGVDIRPFPKNWSMN-----KQLGELASN 248
                                                                                                                                                                                                                                                                                                                                                                   ; Score 176.5; DB 7;
; Pred. No. 2.8e-07;
35; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 331;
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RESULT 3

US-11-052-554A-157

¡ Sequence 157, Application US/11052554A

¡ Publication No. US20050288866A1

¡ PITTLE OF INVENTION: COMPUTATIONAL METHOD FOR IDE

¡ TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDE

¡ TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POT

¡ FILE REFERENCE: 30853/40359A

¡ CURRENT APPLICATION NUMBER: US/11/052,554A

¡ CURRENT FILING DATE: 2005-02-07

¡ PRIOR APPLICATION NUMBER: IN 173/DEL/2004

¡ PRIOR APPLICATION NUMBER: IN 173/DEL/2004

¡ PRIOR APPLICATION NUMBER: IN 173/DEL/2004

¡ PRIOR FILING DATE: 2004-02-06
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CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT APPLICATION NUMBER: US 09/603024
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR PILING DATE: 2000-06-23
PRIOR PPLICATION NUMBER: US 60/141031
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR PILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR APPLICATION NUMBER: DE 19930489.0
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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Corynebacterium glutamicum
-11-082-389-68
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SOFTWARE: PatentIn version 3.3
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
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                      NUMBER OF SEQ ID NOS: 763
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Local Similarity 32.4%; Pred. No. 3.5e-06;
nes 55; Conservative 25; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE 19931550.7
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19932134.5
FILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19931549.3
FILING DATE: 1999-07-08
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LENGTH: 783
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SEQ ID NO 11967
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
    AERIKĖGEFVVĖALILTAĖIY
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; TYPE: PRT; ORGANISM: Synechococcus US-11-188-298-11967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11967, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLF
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 GGLLGAGGHGGAGGLGAVTGGV---GG--TGGAGG---
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                                                                                            104 MY-----TNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GSKQWDTFLSAEL-----PDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFA
                                                                                                                                           77 -LWLLVATILVIFMNAG---FAMVEAGMCRQKNAVNILA-KNLFVFALAVTAYWFVGYSF
                                                                                                                                                                      61 AVYLLDA-----FNAGPDVSNWVTAG-----NAMNTLAGKGISVVAPAGGAY-----S
                                                                                                                                                                                                                                        31 IRGFSSNRAMTWLACAPLALMGLGIFT-LSAKA---EEL------PDLNAAFLANN--
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                                                                                                                                                                                                                                                                                    1 MKGRSALLRALWIAALSFGLGGVAVAABPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH 60
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PDR--FG----FAGSMSGFLYPSNTTTNGALAAGMQQFGGVDTNGMWGAPQLGRWKWHDP 212
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                                                MYGDAAIDGWLYFGGLFFDPTVTAE----TISDAGLVPTVDFLFQAAFAGTAATIVSGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp. WH
                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                  Score 108.5; DE
Pred. No. 0.14;
41; Mismatches 1
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RESULT 6
US-11-052-554A-163
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US-11-188-298-19912
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US-11-188-298-19912
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                                                                                                                                                                                                Sequence 163, Application US/11052554A
Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 19912
LENGTH: 490
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                                                                                  TITLE OF INVENTION: COMPUTATIONAL METHOD FOR TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FILE REFERENCE: 30853/40359A CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILING DATE: 2005-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GERES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 MY----TIWEQDGSKQWDTFLSABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 VGGHN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AERIKFGEFVVFALILTAFIY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYGDAAIDGWLYFGGLFFDPTVTAB----TISDAGLVPTVDFLFQAAFAGTAATIVSGLV 188
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                                                                                                                                                                             IDENTIFYING ADHESIN AND
                                                                                                                                                      POTENTIAL
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PRIOR FILING DATE: 2004-07-20
PRIOR PRIOR PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin variation
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 163
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPUTATIONAL TITLE OF INVENTION: PROTEINS OF THE REFERENCE: 30853/40359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sachdeva, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1053
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis H37Rv
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Local Similarity 23.0%;
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                                                196 GIPALAGGPTAINLGIANVGGGNV-----GNANNGLANIG--
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                                                                                      51 PVAFLAGGPHAVYLLDAFNAGPDVSNWVTAGNAMVTLAGKGISVVAPAGGAYSMYTNWEQ 110
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    DGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGGYGAMALAAFHPDRFGFAGSMS- 169
                                                                                                                                                                             ALLRALWIAALS-----FGLGGVAVAARPTAKAAPYENLM------VPSPSMGRDI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAPQLGRWKWHDPWVHASLLAQNNTRVWVW 229
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                                                                                                                                    ATYEQMWAADVSAMSAYHAGASAIASALSPFSK--PLQNLAGLPAWLASGAPAAAMTAAA 195
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                                                                                                                                                                                                                           Conservative
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Pred. No. 0.5
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Pred. No. 0.
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Sequence 11858, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: US/572,978

PRIOR APPLICATION NUMBER: 007-92,978

PRIOR FILING DATE: 2004-07-31

NUMBER OF SEQ ID NOS: 22569
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RESULT 9
US-11-052-554A-172
; Sequence 172, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
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US-11-188-298-11858
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Best Local (
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                                                                                                                                                                         GKFVGGKAQAIPGHNMSIATLGALILWIGWYGFNPGSQLAMDQWVPYVAVTTTLAAAGGA 320
                                                                                                                                                                                                                                                                                                   TAATIVSGLVABRVKFGEFVVFSLVLTGFIYP-----IA-
                                                                                                                                                                                                                                                                                                                                                                SSYWFIGYSLMYGDPVSAGWLYFNGLFFDPAVTPE----LISEAGLVPSVDFLFQAAFAG 178
                                                                                                                                                                                                                                                                                                                                                                                              GAY----SMY----TNWEQDGSKQWDTFLSAELPDWLAANRGLAPGGHAAVGAAQGG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GFLYPSNTTTNGAIAAGMQQFGGVDTN-----GMWGAPQLGRWKWHDPWVHASLLAQ 221
                                                                                                                                                                                                                                                                    QLGRWKWHDPWVHASL-----LAQNNT--RVWVWSPTNPGASDPAAMIGQTAEAMGN 252
                                                                                                                                                                                                                                                                                                                                  YGAMALAAFHPDR--FG---FAGSMSGFLYPSNTTTNGAIAAGMQQFGGVDTNGMWGAP 202
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21.2%;
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Pred. No. 0.28;
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR ID;
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC PO'
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: 703/DEL/2004
PRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOPTWARE: Patentin version 3.3
SOPTWARE: Patentin version 3.3
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US-11-052-554A-162
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; ORGANISM: Rickettsia
US-11-052-554A-172
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                                     S
                                                                                                                                                                      US-11-052-554A-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 162, Application US/11052554A publication No. US20050288866A1 GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.3 SEQ ID NO 172
                                                                                   Matches
                                                                                                                          Query Match
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NUMBER OF SEQ ID NOS: 763
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                                                                                                                                                                                                              LENGTH: 543
TYPE: PRT
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                                         16 LSFGLGGVAVAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPHAVYLLDAFNAGPDVS 75
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  LFLGLGGDGGAGG----
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                                                                                                       Score 106; DB 7;
Pred. No. 0.34;
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Pred. No. 1.1;
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    TSNNNGGDGGAGGTAGG-----RLFSLGGDGG
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                                                                                     Gaps
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CURRENT APPLICATION NUMBER: US/11/172,740
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,621
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR PILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 2523
SEQ ID NO 542
LENGTH: 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2750-1602PUS2
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                                                                                                                                                                                                                                                 LOCATION:
OTHER INFORMATION: Utility:
                                                                                                                                                                                                                                                                                                                      LOCATION:
OTHER INFORMATION: Utility:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1). (292)
OTHER INFORMATION: Public GI no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)..(292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Triticum aestivum
                        LOCATION:
OTHER INFORMATION: Utility:
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OTHER INFORMATION: Utility:
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                                                                    NAME/KEY: misc_feature
                                                                                                          OTHER INFORMATION: Utility:
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US-11-188-298-17488
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                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 17488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17488, Application US/11188298 Publication No. US20060075522A1
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FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
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246
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                                                                                                                                                                                                              58 GPHAVYLLDA-----FNAGPDVSNWVTAG----NAMNTLAGKGISVVAPAGGAY----
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                           -----APQLGRWKWHDPWV---HASLLAQNNTRV-WV-WSPTNPGA 236
                                                           GLVAERVKFGEFVVFAIVLTAFIYFIAGSWKWNGGWLDSLGFVDFAGSSIVHSVGAWAGL
                                                                                        AFHPDR--FG----FAGSMSGFLYP--SNTTTNGA--IAAGMQQFGG---VDTNGMWG--
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VGAMLLGPRIGKYSDGKPQAMPGHNMAIATLGALILWIGWYGFNPGS
                                                                                                                                                  ----SMYTNWEQDGSKQWDTFLSABLPDWLAANRGLAPGGHAAVGAAQGGYGAMALA 155
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Pred. No. 0.33;
39; Mismatches
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Pred. No. 0.18;
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US-11-052-554A-150
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-36
NUMBER OF SEQ ID NOS: 763
SOPTWARE: Patentin version 3.3
SOPTWARE: Patentin version 3.3
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SEQ ID NO 8448
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                                                                                                     Query Match
Best Local Similarity
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Best Local (
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TITLE OF INVENTION: GENES AND USES FOR PLJ
FILE REFERENCE: 38-21(53452)B
FURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR PILING DATE: 2004-07-31
                                                                                                                                                                                 TYPE: PRT ORGANISM: Mycobacterium tuberculosis H37Rv
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                                                                                                                                                                                                                                LENGTH: 618
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Local Similarity 25.1%;
nes 72; Conservative 3
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                                  MKGRSALLRALWIAALSFGLGGVAVAAEPTAKAAPYE--NLMVPSPSMGRDIPVAFLAGG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPHAVYLLDA----FNAGPDVSNWVTAG----NAMNTLAGKGISVVAPAGGAY----
  LSAQAAMFHEQFVRALAAGGNSYAVAEAATAQSVQQDLLNLI-----NAPTQALLGR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----APQLGRWKWHDPWV---HASLLAQNNTRV-WV-WSPTNPGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/11052554A
                                                                                    Conservative
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                                                                                                   22.24;
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Pred. No. 0.34;
39; Mismatches
                                                                               Score 105; DB Pred. No. 0.48; Mismatches
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                                                                                                                        DB 7;
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                                                                                                                           Length 618;
                                                                                    Indels 100;
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Imp
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 4262
LENGTH: 319
TYPE: PRT
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US-11-087-099-4262
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Search completed: April 14, Job time: 13.8124 secs
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US-11-087-099-4262
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   SPPERNSNKDATAATTTTAAASATQSSGGGGA---TTDSSSSSSRKFECHYCCRNFP---
                                                                                                                                                                                                                                                                                                                                                                                                   AGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDT-FLSAELPDWL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFGLGGVA----VAAEPTAKAAPYENLMVPSPSMGRDIPVAFLAGGPH----AVYLLDAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTVQGVGGFGGQGGN-GGQSGLLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPASGDNGWGSWAPQLGAMSGDIVG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWVHASLLAQNNTRVWVWSPTNPGASDPAAMIGQTAEAMGNSRMFYNQYRSVGGHNGHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHAVYLLDAFNAGPDVSNWVTAGNAMNTLAGKGISVVAPAGGAYSMYTNWEQDGSKQWDT 118
                                                                                                                                              PPPAAGHGNASL---
                                                                                                                                                                                                                      GPTVATLYPSWPTMRPPAPAGAGAGAVAIGGPQFYSGIGSIAQPINGSPLLTAAGLWRGP 234
                                                                                                                                                                                                                                                        GSMSGFLYPSNTTTN-----GAIAAGMQQF-GGVDT--NGMWGAPQL---GRWKWH 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAGGNGGPAPLVGGVGTTGGAGGNGGGAGLFYGFGGAGGNGGMGGVAPSTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GVNQAGGNGGNAGLWGNGGSGGAGGNATTAGRNGFNGGAGGSGGLLWGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLSAELPDWLAANRGLAPGGHAAV--GAAQGGYGAMALAAFHPDRFGFAGSMSGFLYPSN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                         286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 103; DB 7;
24.0%; Pred. No. 0.33;
tive 29; Mismatches 108
                    2006, 18:42:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TTTNGAIAAG-----MQQFGGVDTNGMWG--APQLGRWKWHD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LIGNGANGLPGTGQN----GGDGGILYGNGGNGGSG----
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                                                                                                                                                  PSSPGGERRRPVALSSSSPVFRGDDPRASTSLLAAA
                                                                                                                                                                                                                                                                                                                                 ----AAVGAAQGGYGAMALAAFHPDRFGFA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108; Indels
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                                                                                                                                                                                    -ASDPAAMIGQTAEA 249
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Minimum
Maximum
                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run
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                                                                                                                                                                                                        Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                       DB 80
                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
A Geneseq_21:*
1: geneseqp1980
2: geneseqp2000
3: geneseqp2001
4: geneseqp2001
5: geneseqp2002
6: geneseqp2003
7: geneseqp2003
8: geneseqp2003
8: geneseqp2003
                                                                                                                                                                                                                                                                                                                                                   Gapop
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-620-246-66
1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                            April 14, 2006, 17:03:40 ; Search time 88.341 Seconds (without alignments) 1133.996 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                    2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                   1 MAIEVSVLRVFTDSDGNFGN......PEGWVRVAGRVVSDGVAQLD
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Listing first 45 s
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
geneseqp2004s:*
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                                                                                           geneseqp1980s:*
geneseqp2000s:*
                                                                                                                                                                                                                                                                                                                                                   10.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                                                                                            summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	s	4.	w	2	<b>-</b>	Result No.
100.5	100.5	100.5	110	110	110	110.5	112.5	115	118	125	127.5	129	143	143.5	145.5	145.5	145.5	145.5	151.5	153.5	159.5	1192	1192	Score
8.4		8.4	9.2	9.2	9.2	9.3	9.4	9.6	9.9	10.5	10.7	10.8	12.0	12.0		12.2	12.2	12.2	12.7	12.9	13.4	100.0	100.0	Query Match Length
485	313	255	375	288	288	106	274	295	335	270	293	331	302	211	278	278	278	278	278	292	280	228	228	
4.	7	9	4	8	4	σ	0	7	7	7	o	7	w	4	w	N	N	N	œ	σ	4	N	N	B
AAU54108	ABO71801	AEA04518	ABG22460	ADQ30600	AAM78698	ABP04085	АВJ37463	ADF06706	AB078267	AB072188	ABM67317	ABO73240	AAY95035	AAB79143	AAB18558	AAW69403	AAW31306	AAR87535	ADS15066	ADA33271	AAG92764	AAY21926	AAW72909	B
-	•	Human	Abg22460 Novel hum	Adq30600 Pancreas	Aam78698 Human pro	Abp04085 Human ORF	Abj37463 Benzodiaz	Adf06706 Bacterial	Abo78267 Pseudomon	Abo72188 Pseudomon	Abm67317 Photorhab	Abo73240 Pseudomon	Aay95035 Candida a	Aab79143 Corynebac	Aab18558 Protein p	Aaw69403 Phenazine	Aaw31306 Pseudomon	Aar87535 Pseudomon	Ads15066 Pseudomon		Aag92764 C glutami	Aay21926 Amino aci	Aaw72909 Mycobacte	Description

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosi of or vaccination against tuberculosis caused by M. tuberculosis, M.

diagnosis is, M.

africanum or M.

povis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 177-178; 163pp; English.

WPI; 1998-542705/46. N-PSDB; AAV63933.

Andersen P, Oettinger T,

Nielsen , Florio

**₹**,79

Rosenkrands I,

Weldingh K,

Rasmussen

PB ;

(STAT-) STATENS SERUM INST.

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44.5	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25
92	3	92	92	92	92	92	92	92.5	92.5	92.5	93	94	94.5	95	96.5	96.5	97.5	99	99	100.5
7.7	7 7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.9	7.9	8.0	8.1	8.1	8.2	8 3	8.3	8.4
1517	1504	1488	1482	327	315	315	281	6043	5674	3808	326	279	271	1107	518	513	282	284	217	485
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AAY84726	AAV84728	AAY84725	AAY84727	ADS23140	ADX78415	ADX74285	ADS44582	ADU47673	ADU47676	ADK16029	AB073278	ADS22855	ADF04061	ABU31207	ADF06351	ABU41093	ABB48896	ADS44848	ABG22462	ABM50627
Amino	Amino	Aay84725 Amino aci	Aay84727 Amino aci	Ads23140 Bacterial	Adx78415 Plant ful	Adx74285 Plant ful	Ads44582 Bacterial	Adu47673 S. cyaneo	Adu47676 S. cyaneo	Adk16029 Streptomy	Abo73278 Pseudomon	Ads22855 Bacterial	Adf04061 Bacterial	Abu31207 Protein e	Adf06351 Bacterial	Abu41093 Protein e	Abb48896 Listeria	Ads44848 Bacterial	Abg22462 Novel hum	Abm50627 Propionib

## ALIGNMENTS

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RESULT 1
AAW72909
ID AAW7
02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                            01-APR-1998;
                                                                                                                                                                       08-OCT-1998.
                                                                                                                                                                                               Mycobacterium
                                                                                                                                                                                                               Mycobacterium tuberculosis; antigen; vaccine;
                                                                                                                                                                                                                          Mycobacterium tuberculosis antigen CFP25A.
                                                                                                                                                                                                                                                   AAW72909;
                                                                                                                                                                                                                                                              AAW72909 standard; protein;
                                                                                                                                                                                   WO9844119-A1
                                                                                                                                                                                                         infection.
                                                                                                                                                                                                                                       21-JAN-1999
                                                                                                                                                                                                                                      (first entry)
                                                                                                                             97DK-00000376.
97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                                                                                               tuberculosis.
                                                                                                                                                            98WO-DK000132
                                                                                                                                                                                                                                                              228 AA.
                                                                                                                                                                                                               immunological; immunogen;
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RESULT 2
AAY21926
ID AAY2
XX AAX
AC AAX2
XX Inmm
KW tubb
KW CPP;
XX Mycc
XX
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Best Local Simi
Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1997;
05-JAN-1998;
01-APR-1998;
The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP73, CFP30A; CFP7B; CFP19; CFP30A; CPP10A; CFP19; CFP30A; CFP30A; CFP19; CFP30A; CFP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Page 196-197; 265pp;
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98WO-DK000132.
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Pred. No. 8.8e-114;
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFPTA or CFP30A or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFPTB, CFP19 or MPTS-SARTG or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RD1-CRF2, RD1-CRF3, RD1-CRF3, RD1-CRF3, RD1-CRF3, CFP30B, CFP10A, CFP16, CFP16, CFP23, CFP23B, CFP30B or a T-cell epitope of for the preparation of an immunological composition; and for the preparation of a subunit vaccine
                                                                                          Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino organic acid synthesis.
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DB; AAH67983.
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                                                                                          Mizoguchi
Senoh A,
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2000JP-00159162.
2000JP-00280988.
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                                                                                          S, Hayashi
Ozaki A;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene

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RESULT 4
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Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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                                                                                                                                                                                                                                                                     04-JUN-1999;
                                                                                                                                                                                                                                                                                                                         13-MAY-2003.
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Pred. No. 1.4e-07;
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Identifying a modulator of quorum sensing signaling for treating a biofilm-associated disorder, comprise

ignaling in bacteria, comprises contacting

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11-MAR-2004; 2004WO-US007467

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133
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Pred. No. 6.2e-07;
8; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       controlled protein,
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                                                           (CIBA ) CIBA GEIGY AG.
                                                                                                                    08-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -HWRSRMFSPAYGVVEDAATGSAAGPLAIHLARHRQIPYGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSLRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALGLKGSTFPIEVYRNGPRHVFVGLESVAALSALHPDHRALCDFP-DLAVNCFAGAGR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLGTAIALGAETDKDRLFLETRMGTVPFALERQDGKVVACSMQQPIPTWEHFSRPAELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVGASWWL-RERGTPINTLQVPAGIVQVSYH---GDLTAISARS---EW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNPVAVFFDCDDLSGERMQRMAREMNLSESTFVLRPQQDG-DARIRIFTPVNELPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNPLGY-INASKVEHRDROGLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
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  Schupp T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               chlororaphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aureofaciens phenazine gene cluster ORF3 protein phz3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                    94US-00258261
                                                                                                                                                                            95WO-IB000414
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                   /note= "unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%;
  Beck JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 151.5; DB 8
Pred. No. 9.3e-07;
     H111
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  DS,
  Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
  Gaffney
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     TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192
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Matches
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                         20-AUG-1990;
02-JUL-1992;
31-AUG-1992;
01-JUL-1993;
                                                                                                                                                                                                                     Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene cluster may be expressed in a transgenic poetr-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                 17-OCT-2003
12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New genes for biosynthesis of anti-pathogenic substances - pref
pyrrolnitrin and soraphen, useful for disease control in plants
              08-JUN-1994
                                                                                         01-JUN-1995
                                                                                                                  02-SEP-1997
                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                   phytopathogen;
                                                                                                                                                                                                                                                                                              Phenazine; biosynthesis; antibiotic; antipathogenic; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                       AAW31306;
                                                                                                                                                                                                                                                                                                                                                                                                               AAW31306 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 163-169; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-040226/04.
                                                                                                                                                                                                                                                                                                                       Pseudomonas aureofaciens phenazine phz3 protein
                                                                                                                                          US5662898-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 KALGISD-STFPIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFAGAGRR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 DALAAADPADFPDDIAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 LIGTDIALGAR-TUNHRLFLETQMGTIAFELERQNGSVIAASMDQPIPTWTALGRDAELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEFAI-HDLDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hammer PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                         chlororaphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ž
                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                         90US-00570184.
92US-00908284.
92US-00937648.
93US-00087636.
                                                                                                                                                                                                                                                                                   resistance
              94US-00258261
                                                                                         95US-00457342
                                                                                                                                                                                                                     Location/Qualifiers
1. .278
                                                                                                                                                                   /label= unknown
                                                                                                                                                                                           /product= "phz3"
                                                                                                                                                                                                         label= ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phz3 encoded by the phenazine gene cluster ORF3. expressed recombinantly to produce phenazine, or sgenic plant for disease- resistance. (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uknes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SJ.
                                                                                                                                                                                                                                                                                                                                                                                                                 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 145.5; DB 2
Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278;
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160 134 131 75

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RRESULT 8
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ID AAM6
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DT 07-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins AAW31304-W31307 represent the open reading frames (ORF's) 1-4 encoded by the gene cluster phz1, phz2, phz3 and phz4 involved in phenazine biosynthesis. Phenazines remarked trirogen-containing heterocyclic compounds with a common planar aromatic tricyclic structure. It has beer proposed that phenazine antibiotic function arises from the formation of intercalative complexes with DNA interfering with DNA metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic plants containing such antipathogenic genes should have enhanced resistance to attack by phytopathogens. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protecting plants against pathogens with genetically transformed biological control agent - which expresses all polypeptide(s) involved in pyrrolnitrin biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2003
07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW69403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-447901/41.
N-PSDB; AAT89957.
                                09-OCT-1996;
                                                                                      06-OCT-1998.
                                                                                                                                               US5817502-A
                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrrolnitrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phenazine gene cluster protein phz3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW69403 standard; protein; 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 18; Col 149-150; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CIBA ) CIBA GEIGY
                                                                                                                                                                                                                                                                                                                                                                  yrrolnitrin; biosynthetic pathway; pathogen protection; phenazine;
lant antipathogenic substance production; anti-fungal antibiotic;
angal respiratory electron transport inhibitor; lipoprotein damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KALGISD-STFFIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFÄGAGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DALAAADPADFPDDIAH-----AGS--- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLGTDIALGAR-TONHRLFLETQMGTIAFELERQNGSVIAASMDQPIPTWTALGRDAELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEFAI-HDLDSL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNPVAVFFDADDLSAEQMORIAREMNLSETTFV-LKPRNCGDALIRIFTPVNELPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hill DS,
                                                                                                                                                                                                                                                                                                                   chlororaphis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ß,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                96US-00729214
                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                    /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 145.5; DB 2;
Pred. No. 3.9e-06;
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RESULT 9

AAB18558 standard; protein;

278 B

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Protein phz3 12-SEP-2003 15-JAN-2001 AAB18558;

encoded by a phenazine gene region

(revised) (first entry)

Pyrrolnitrin; PrnA; PrnB; PrnC; PrnD; antibiotic; biocontrol; fungal respiratory electron transport inhibitor; transgenic pla antipathogenic substance; biosynthetic gene; fungal resistance;

plant;

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                                                                                                                                                                                                                                                                                                                                                                       cc enzyme required in the biosynthetic pathway of pyrrolnitrin. The DNA and Cc host cells transformed with it are useful for the production of transgenic plants with protection against phytopathogens. The enzymes are cc transgenic plants with protection against phytopathogens. The enzymes are part of a biosynthetic pathway producing plant antipathogenic substances (Aps). The compound ultimately produced by the pathway, pyrrolnitrin, is celectron transport and causes general lipoprotein damage. The transformed cells can additionally be used in compositions to be applied to plants to provide resistance, as can purified Aps produced by them. Transgene cc dependent resistance eliminates the need to spray crops with chemical based pesticides and antibiotics, which is expensive and time consuming, and in addition, especially in the case of antibiotics, their over use cleads to resistance. In addition, transgenic production of these enzymes covercomes problems of applying micro-organisms which can be slow growing and isolated in their growth areas. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is encoded by the phenazine gene cluster, isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes encoding enzymes of the biosynthetic pathway of pyrrolnitrin useful for producing transgenic plants which can produce pyrrolnitr
                                                                                                                                                                                                                                                                                                                                                                     Sequence 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aureofaciens. This sequence was used to isolate the pyrrolnitrin gene region of the invention, that encodes at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1994;
30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 18; Col 161-162; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-pathogenic
                                    161
                                                                                                                                               76
                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                              62; Conservative
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                                                                                                                                                                                                                                                                                                               Similarity
                                  LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
                                                                      KALGISD-STFFIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFAGAGRR
                                                                                                            DALAAADPADFPDDIAH-----AGS---
                                                                                                                                                                                 TVGASWWLRERGTPINTLQVPAGIVQVSY----HGDLTAISARSEWAPEFAI-HDLDSL 131
                                                                                                                                                                                                                                                          GNPLGY-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP 77
WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ
                                                                                                                                             LLGTDIALGAR-TDNHRLFLETOMGTIAFELERQNGSVIAASMDOPIPTWTALGRDAELL
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95WO-IB000414.
                                                                                                                                                                                                                                                                                                              12.2%; Score 145.5;
28.3%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                33;
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                                                                                                                                                                                                                                                                                            5; DB 2;
3.9e-06;
1es 83;
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                                                                                                                                                                                                                                                                                                                                   278;
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                                                                                                                                                                                                                                                                                                41;
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                                                                                                                                                                                                                                                                                                Gaps
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Query Match
Best Local S
Matches 62
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30-MAY-1995;
09-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prnD enzyme catalyses the conversion of aminopyrrolnitrin to pyrrolnitrin. Pyrrolnitrin has antibiotic activity, and inhibits a broad range of fungi. It is a fungal respiratory electron transport inhibitor. The genes are useful for developing a host as a biocontrol agent, for protecting plants against a pathogen and for producing large, uniform amounts of pyrrolnitrin. The genes are also useful for producing transgenic plants that express antipathogenic substance (APS) biosynthetic genes. The genes and enzymes are useful for increasing the resistance of host plants to disease caused by phytopathogens, e.g. fungi, bacteria or nematodes. The microbial hosts are useful for controlling or inhibiting the growth of a phytopathogen. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligon
Hill r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -chlorotryptophan. The PrnB enzyme catalyses the conversion of 7-chlorotryptophan to monodechloroaminopyrrolnitrin. PrnC enzyme cataly the conversion of monodechloroaminopyrrolnitrin to aminopyrrolnitrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene region. The specification describes pyrrolnitrin gene regions. This region encodes enzymes required in the biosynthetic pathway of pyrrolnitrin. The PrnA enzyme catalyses the conversion of tryptophan to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrrolnitrin biosynthesis genes and enzymes, useful for producing pyrrolnitrin for increasing plant resistance to phytopathogens, efungi or nematodes, and for developing microbial hosts useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biocontrol agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB18556-59 are encoded by a Pseudomonas aureofaciens phenazine ion. The specification describes pyrrolnitrin gene regions. This
                                  LRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK
                                                                                                                                            DALAAADPADFPDDIAH
                                                                                                                                                                                                  LLGTDIALGAR-TDNHRLFLETQMGTIAFELERQNGSVIAASMDQPIPTWTALGRDAELL
                                                                                                                                                                                                                                                     TVGASWWLRERGTPINTLQVPAGIVQVSY-----HGDLTAISARSEWAPEFAI-HDLDSL
                                                                                                                                                                                                                                                                                                            GNPVAVFFDADDLSAEQMQRIAREMNLSETTFV-LKPRNCGDALIRIFTPVNELPFAGHP
                                                                                                                                                                                                                                                                                                                                                                  GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
                                                                                        KALGISD-STFFIEIYHNGPRHVFVGLPSIAALSALHPDHRALYSFHDMAINCFÄGAGRR
     Col 165-168; 124pp;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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95WO-IB000414.
96US-00729214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 145.5; DB:
Pred. No. 3.9e-06
3; Mismatches 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                        83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278;
                                                                                                                                                                                                                                                                                                                                                                                                                        41;
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  RESULT 10
AB79143
ID 7AB79
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum hom and adaptation (HA) proteins given in AAB79023 to AAB79242. Th glutamicum HA genes (I) can be used in vectors for expression cells and production of fine chemicals, such as, an organic ac
                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins
                                                                                                                                            Claim
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DB; AAF71258.
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8 밁 S 밁 5

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Kroeger

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Haberhauer

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464-465; 712pp; English

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194 WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ
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14-JUL-1999;
14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                        25-JUN-1999;
08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering;
                                                                     14-JUL-1999,
14-JUL-1999,
                                                                                                                                                                                 14-JUL-1999;
14-JUL-1999;
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                                                                                                                                              14-JUL-1999;
14-JUL-1999;
                                                                                                                                                                       14-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum; fine chemical production; or
                                                                                                                                   14-JUL-1999;
                                                                                                                                                                                                                                                                                                                     23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                   Brevibacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum HA protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein;
                                                                                                                                                                                                                                                                                                                     2000WO-IB000911
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 glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                   environmental
3-01041390.
3-01041391.
3-01042088.
                                                                                  3-01032935.
3-01032973.
3-01033002.
3-01033003.
                                   -01041378.
-01041379.
                                                           3-01033005.
3-01033006.
                                                                                                                                                                       -01032924
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP982401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans.
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   Claim 3; Page 19-20; 133pp; English
                                                             immunocompromized subjects,
                                                                                         Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially
                                                                                                                                                                                   WPI; 2000-258614/23
                                                                                                                                                                                                                                           Contreras RH,
Logghe MG;
                                                                                                                                                                                                                                                                                                                                  (JANC ) JANSSEN
                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY95035 standard; protein; 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDAACEALGISPDFIRAH----QWVDNGPGWAVVELPSAQHVLDLEPDFSAHPTLKLGVIG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVGASWWLR----ERGTPINTLQVPAGIVQV-SYHGDLTAISARSEWAPBFAIHDLDSLD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTBIPFAGHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNPLAVIADADDLSAEQMARIARWINLSETTFLLKPTQEGADYRVRIFTPTGELPFAGHP
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                                                                                                                                                                                                                                                                       Nelissen B,
                                                                                                                                                                                                                                                                                                                                                                                             98GB-00017796
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98EP-00310694.
                                                                                                                                                                                                                                                                                                                                  PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; growth; survival; medicament; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
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Pred. No. 4.3e-06;
"""matches 79;
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                                                                                                                                                                                                                                                                       Backer MD,
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                                                          patients
                                                                                                                                                                                                                                                                       Luyten WHML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 302
                                                                                                                                         Rubenfield MJ,
                                                                                                                                                                                                                                                   18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                   18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                         22-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa polypeptide #5415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004
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                                                                                                                                                                                               (GENO-) GENOME
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                                                         2003-615309/58.
DB; ABD06811.
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98US-0094190P.
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Pred. No. 7.8e-06;
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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therefore therefore the sequences are useful in diagnosis and the therefore the sequences are useful in diagnosis and the therefore the sequence are useful in diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html
                                                                                                                                                                                                                                                                                 Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful as molecular targets for diagnostics, prophylaxis and treatment pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                              Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM67317;
                                                                          07-FEB-2001; 2001FR-00001659
                                                                                                               07-FEB-2002; 2002WO-IB003040
                                                                                                                                                                                         WO200294867-A2
                                                                                                                                                                                                                                                                                                                                                           Photorhabdus luminescens protein sequence #414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM67317 standard; protein; 293
                                                                                                                                                                                                                                                                 whooping cough.
                   (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GNPLG-VINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGAAAIRITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRRIESGLGLSPGQVRGS-----QWVDNGPGWVAVRL-----ATRDE---VLAIR-PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLGSCQVWLNQGGGNAADEIVQECLAGLIRIRRKGALLSFA----APPLLRGGAVEDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVGA-SWWLRERG---TPINTLQVPAGIVQVSYHGDLTAISARSEWAPEF----AIHD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNAVAVVIGADRLSSROMLEFAAWTQLSETTFLLRPTVAEADYRVRIFTPLRELPFAGHP
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                     CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Pred. No. 0.00024;
4; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 331;
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                                                                                                                                                                                                                                                                                                                                       and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapsutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopseticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                     Sequence 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. lumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-148459/14.
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  134
                                           128 LDS-----
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                                                                                                                                                                                                           19 GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAH-ATIHTPRTEIPFAGH
                                                                                                                                                                                                                                                                          Similarity
LSSEQIDRLESILDCPLDRALTPALIDVGARWIVAHTTGAEAVLATKP-DYARLLEHDTQ
                                                                                     PTIGTAHALLEAG----LIQAREGRIVQECGAGLITLNVTERDEGQKLITFELPEPTITP
                                                                                                                            PTVGASWWLRERGTPINTLQVPAG-IVQVSYHGDLTA-ISARSEW-----APEFAIHD
                                                                                                                                                                 GNPVAVVMDAQELSSIQMQGIANWTNLSETTFI-LPAENPLADYRVRIFTPGSELPFAGH
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22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glaser P,
                                                                                                                                                                                                                                                  39;
                                           ----LDALAAADPADFPDDIAH---
                                                                                                                                                                                                                                                                          Score 127.5; DB 6
Pred. No. 0.00029;
                                                                                                                                                                                                                                                      Mismatches
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                                             148
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# RESULT 14 ABO72188

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193

202 LIHTT-----W--SPEGWVRVAGRVVS 221

MNITGVCLYGAYHEGAEADIEVRSFAPSCGVNEDPVCGSGNGSVAAFM-RHHKVAMIDDK 251 ----YLWTWTDRSAGSLRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGKGS

201

IVHSSQGKKLGRQGSVWLSHSDGKIFVGGSAVT 284

ABO72188 standard; protein; 270

AB072188;

(first entry)

Pseudomonas aeruginosa polypeptide #4363.

Bacterial infection; Pseudomonas aeruginosa infection; antibacterial

Pseudomonas aeruginosa

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RESULT 15
AB078267
ID AB078
XX
AC AB078
XX
DT 29-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid useful as molecular targets pathological conditions resu
 29-JUL-2004
                               AB078267;
                                                               ABO78267 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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27-JUL-1998;
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                                                                                                                                             246
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                                                                                                                                                                                                                                                                                                                                                       HATIHTPRTEIPFAGHPTVGASWWLRER---GTPINTLQVPAGIVQVSYHGDLTAISARS 117
                                                                                                                                                                                                                                                                         K-RPBPCATPDGLLEALGIABAEVLKTD--DYLVVVDDEKTIAALAPDFARLKGLPCRGV
                                                                                                                                                                                                                                                                                                       EWAPEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDR--
                                                                                                                                                                                                                                                                                                                                                                                                    MELTIFQVDAFADSPFQGNPAAVCPLDAWLDDERLQATAEENNLSETAFV-VGRDGD--Y
                                                                                                                                                                                                                                                                                                                                                                                                                                    IEVSVLRVFTDSDGNF-GNPLGVINASK-VEHRDRQQLAAQSGYSETIFVDLPSPGSTTA
                                                                                                                                                                           IHTTWSPEGWVRVAGRVVSDGVAQL 227
                                                                                                                                                                                                          AVTARSQRFDFVSRWFGPNVGVNEDPVTGSAHTSLAPYWAQRLGKTRLSAEQGGARKGRL
                                                                                                                                                                                                                                        --SAGSLR----ARMFAANLGVTEDBATGAAAIRITDYLSRDLTIT----QG---KGSL
                                                                                                                                                                                                                                                                                                                                       RLRWFTPQVEVDLCGHATLATAWVLIHKLDDASPVLRFATRSGELSVRREGDSLAMDFPA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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 (first entry)
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98US-0094190P
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                                                             protein; 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid encoding Pseudomonas aeruginosa polypeptide, gets for diagnostics, prophylaxis and treatment of resulting from bacterial infection.
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Pred. No. 0.00047;
33; Mismatches 108;
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The invention relates to Pseudomonas aeruginosa polypeptides and the copymucleotides encoding them. The sequences are useful in diagnosis and control of the relations as molecular targets for diagnosis and comply of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a compound, such as a polypeptide, of the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-NB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 27013; 455pp; English.
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                                                                                                                 MFAA-----
                                                                                                                                                                      GTCRWFAEAFSL----SANDLSGHPPRVVSTGLPYLLLPVTAEALGRARQVNDLQEALDK
                                                                                                                                                                                                                             ARSEW-APEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRA------R 164
                                                                                                                                                                                                                                                                                    LLGAAALLHHLRGGDNEQHWTLHLASKSVALRSVRAG---SGFYAEMDQGRAEFGATPDA 184
                                                          LGAAFVYLLDVDGREGRTWDSLGLVEDVATGSAAGPVAAYLVEYGLAARGEPFVLHQGRF
                                                                                                                                                                                                                                                                                                                                      TVGAS----
                                                                                                                                                                                                                                                                                                                                                                                                   GNGLAVFDDASTLDDAAMQAWTRELRQFESIFL-LPGDDPRAFRARIFTLEEELPFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
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98US-0094190P
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  -TTWSPEGWVRVAGRV
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Pred. No. 0.0033;
4; Mismatches 98
219
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10

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301

LERPSRLDVQVATDGSVRVGGHV

Search completed: April 14, 2006, 17:18:29 Job time : 91.341 secs

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Minimum
Maximum
                                                              Database
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                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1192
1 MAIEVSVLRVPTDS
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Listing first
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45 gt
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Regult No.	Score	Query	Length	DB	Ħ	Description
1	1192	100.0	228	N	G70532	hypothetical prote
N	407	34.1	214	N	T50577	. prot
w	205.5	17.2	314	N	S75237	
4.	184.5	15.5	305	N	AB2742	•
رب ر	180.5	15.1	333	N	A97523	•
6	161.5	13.5	276	N	AE3481	m
7	156	13.1	290	N	AF3234	Phenazine biosynth
<b>&amp;</b>	154.5		294	N	S46781	hypothetical prote
9	151.5		278	N	B83119	probable phenazine
10	148.5	12.5	308	N	AH3330	phenazine biosynth
1	145	12.2	301	N	H84192	hypothetical prote
12	144.5	12.1	281	N	AI3080	phenazine biosynth
13	144.5	12.1	290	N	H98205	hypothetical prote
14	•	11.0	290	N	G95273	conserved hypothet
15	131.5	11.0	295	N	F83893	hypothetical prote
16	130.5	10.9	293	N	C69800	conserved hypothet
17	126	10.6	296	N	S44972	
18	125	10.5	259	N	A83301	hypothetical prote
19	124	10.4	278	N	D83474	
20	123		284	N	F83056	thetical
21	112.5	9.4	297	N	C64899	
22	112.5	9.4	297	N	C90887	hypothetical prote
23	112.5	9.4	297	N	F85730	hypothetical prote
24	112	9.4	302	N	E97323	-
25	104.5	8.8	404	N	A75285	cinA protein - Dei
26	104		279	N	F82463	conserved hypothet
27	104		282	N	AF1530	conserved hypothet
28	103		286	N	D86163	F15K9.19 protein -
)				,		himothet call prote

181

AAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVSDGVAQLD

228

45	44	43	42	41	40	39	38	37	36	ω 5	ω 4	ω ω	32	31	30
88.5	89	90.5	91	91	91	91.5	94.5	95	95	95	95.5	96.5	97.5	99	100.5
7.4	7.5	7.6	7.6	7.6	7.6	7.7	7.9	8.0	8.0	8.0	8.0	8.1	8.2	8 .3	8.4
572	3413	2591	15281	1145	728	297	321	294	273	261	776	275	282	284	308
2	N	N	N	N	N	ผ	N	N	N	N	N	N	ผ	N	N
JC7833	T17467	T30288	841309	S37136	AF3299	AF0671	T24410	D85036	AB2049	<b>B</b> 83199	T29064	C87648	AB1173	F70024	E75409
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recur	yketi	І ву	ynthe	lypro	8e (E	othet	prote	prote	prote	othet	yase	biosynth	othet	te ep	bioti

### ALIGNMENTS

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70532 A;Molecule type: DNA A;Residues: 1-228 <COL> A;Cross-references: UNIPROT:007215; UNIPARC:UPI000013BF5B; GB:Z96072; GB:AL123456; NID: A;Experimental source: strain H37Rv A;Experimental source: strain H37Rv B;Patki, A.H.; Dale, J.W. submitted to the EMBL Data Library, April 1991 A;Reference number: S21832 밁 S 밁 δ 밁 A;MOLECULE type: DNA
A;REBIQUES: 'MSAGGVTKDVNIVFRLASLPMGSBAMALLR','LPLVLPAVQIAGRIVGQGHRYHQLGARPAQ','CAAHFGRP,
RCASPGWRR','TTVTGADTRVAVLMAIGSNERSATLITTG','SVRALPQVVQSGHG',3-228 <PAT>
A;Cross-references: UNIPARC:UPI000016FBC6; EMBL:X59273; NID:944681; PIDN:CAA41963.1; PI ঠ A; Gene: Rv2716 A; Accession: S21832 A; Status: nucleic acid sequence not shown; translation not shown Query Match 100.0%; Score 1192; DB 2; Best Local Similarity 100.0%; Pred. No. 2.1e-97; Matches 228; Conservative 0; Mismatches 0; 181 AAIRITDYLSRDLTITQCKGSLIHTTWSPEGWVRVAGRVVVSDGVAQLD 121 PEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGA 121 PEFAIHDLDSLDALAAADFADFFDDIAHYLWTWTDRSAGSLRARWFAANLGVTEDEATGA 180 61 61 HATIHTPRTEIPPAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA 120 \_ HATIHTPRTBIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA MAIEVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA MAIEVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA 60 Indels Length 228; 228 0 Gaps 60 180 0

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$75237
$75237
hypothetical protein - Synechocystis sp. (strain PCC 6803)
hypothetical protein - Synechocystis sp.
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: $75237
C;Accession: $75237
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mio, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOI. Microbiol. 21, 77-96, 1996

A,Title: A set of ordered cosmids and a detailed genetic and physical map for the A,Reference number: Z20556; MUID:97000351; PMID:8843436

A,Recession: T50577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SCC75A.14c [imported] - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accession: T50577 R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinamol, Mcrobiol. 21, 77-96, 1996
                                                                                                                                                                                                                                                  A;Note: the nucleotide C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75237
A;Status: nucleic acid sequence not shown; translation
                                                                                                                   S
                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI0000164C3D; EMBL:D90904; GB:AB001339; NID:g1652225; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-314 < KAN>
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A; Residues: 1-214 < RED>
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                       PRTEIPFAGHPTVGASW--WLRERGTPINT----LQVPAGIVQVSYH---GDL------
                                                                                                                        LRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHT
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  PKRELDFAGHPTIGTTYLLGLLQPPSPLVTTTWQLEEPVGLVPVTLHYKQGQLVQTELTV
                                                                                 LDVFTDQLFG-GNPLAVFPDAEGLTDGQMQKIAAEINYSETVFVLPPVTETGNFRLRIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRTLRQYAAVAEVDDLAVPPKGEWV-----YAWAWEDEAAGRVRARAFPGRDDGIDEDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFAIHD --- LDSLDALAAADPADPPDDIAHYLWTWTDRSAGSLRARMF - AANLGVTEDEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATIHTERTEIPFAGHPTVGASWWLRERGTPINTLQVFAGIVQVSYHGDLTAISARSEWAP
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                                                                                                                                                              17.2%; Score 205.5; DB 2 29.9%; Pred. No. 1.6e-10; tive 37; Mismatches 93
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Pred. No. 2e-28;
7; Mismatches
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Yamada, M.; Yasuda
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C; Accession: AB2742
C; Accession: AB2742
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, R; Wood, D.W.; Select, D.; Kutyavin, T.; Leerage, G.; Gillet, W.; Grant, S.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
A.Anthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: product A;A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Cross-references: UNIPROT:Q8UFQ1; UNIPARC:UPI00001645D4; A;Cross-references: UNIPROT:Q8UFQ1; UNIPARC:UPI00001645D4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AB2742 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Atu1346 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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AB2742
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A; Map position: circular chromosome
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                                                                                                                         134
                                                                                                                                                                   120 AVSFA-EFDLPRKSSRVELPLNHAALADALGVSEGHLGFENHVPSIWTAGVPFLLVPMHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                         LAAADPADFPDDIAHYLWTWTD----
PATGSAAAALSGAIHHFDGLTDGHYPLL
                                         EATGAAAIRITDYLSRDLTITQGKGSLI
                                                                                IAAVRDMDFDAN----LWLRTAPLVEGLLAAAYIYCRGGVNHAAKFHARMFSPEMGIAED
                                                                                                                                                                                                                                                   ASLRIFTPSGELPFAGHPTVGAAVAIAERNRGEGDDDIDMVCVLEEKVGPVRCAVKWRAG
                                                                                                                                                                                                                                                                                             AHATIHTPRTEIPFAGHPTVGASWWLRERGT----
                                                                                                                                                                                                                                                                                                                                    MALNYDIYDVFTEAK-MAGNPLAVNYDADDLSQDTMQAIAREMNLSETVFINRSTNPSHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLDDRLDTPGSHHWQIEQGKALGRPSQLQLTVVKDGQGIRAVKVAGRSVLVSEGFMNL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSVWQNLLAGQWADCVYCLAPGDPSLGLSDNKLIHGRMPAPGLGIAEDPATGSGVAALGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          15.5%;
26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 184.5; DB 2
Pred. No. 1.1e-08;
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262
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I.; Levy, R.; Li,
                                                                                                                                                                                                                                                                                             PIN-TLQVPAG
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hypothetical protein AGR\_C\_2485 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep\_2001 #sequence\_revision 30-Sep\_2001 #text\_change 09-Jul-C;Accession: A97523 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 2323-2328, 2001

Genome

Sequence

of.

Plant

Pathogen and

Biotechnology

Agent

Agrobacterium

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Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;

B.; Goldm Markelz,

Goldman,

09-Jul-2004

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C58,

Cere

A97523

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A;Molecule type: DNA
A;Residues: 1-276 < KUR>
A;Cross-references: UNIDS
A;Experimental source: st
C;Genetics:
A;Gene: BMEI1835
A;Map position: I
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A;Accession: A97523
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <KUR>
A;Cross-references: UNIPROT:Q:C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6

AB3481

N-methyl-D-aspartate receptor [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Species: Brucella melitensis

C;Accession: AE3481

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of facultative intracellular pathogen Brucella melitens
A,Reference number: AD3252; PMID:11756688
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A;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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Matches
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;Experimental source: strain 16M
                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                              Similarity
                                                                                                    RYPAPEMEVPFCGHATIALGAALAMRE-GDGRPALFLNHDEISVEGRKEGELFAASLQSP 116
                                                                                                                                                                                                        VSVLRVFTDSDGN-FGNPLGVINASKV-EHRDRQQLAAQSGYSETIFVDLPSPGSTTAHA 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VALNYDIYDVPTEAK-MAGNPLAVMYDADDLSQDTMQAIAREMNLSETVPINRSTNPSHA
                                                                   WAPEFAIHDLDSLDALAAADPADFPDDIAH-----YLWTWTDRSAGSLRARMFAANL--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAAADPADFPDDIAHYLWTWTD----
                                   RTRNRAATEAEIGQALALFNYE--PDDLAHGISPALIHAGADHIVLPLRSREKLASMHYD
                                                                                                                                    TIHTPRTBIPPAGHPTV--GASWWLRERGTPINTLQVPAGIVQVS--YHGDLTAISARSE 118
                                                                                                                                                                        MDVLRTAAFSQGDKGGNPAGVMTADRLPSPQDMQKTAKDVGFSETAFA---APDGESWRV
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                                                                                                                                                                                                                                        13.5%; Score 161.5; DB
27.1%; Pred. No. 1e-06;
:ive 35; Mismatches
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Pred. No. 2.8e-08;
5; Mismatches 92;
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                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                          96;
 GVTEDEATGAAAIRITDYLSRD--
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 192
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                                                                                                                                                                                                                                          RESULT
S46781
                                              A; Molecule type: DNA
A; Residues: 1-294 < DUZ>
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                                ;Cross-references: UNIPROT:P38765; UNIPARC:UPI000013B267; EMBL:U10399; NID:g500689;
                                                                                                                                                                      Accession: S46781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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 MIPS:YHR029c
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A;Authors: Yoo, H.; Tao, Y.; Biddle, F.; umster, E.W.
A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; MUID:21608550;
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.;
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin,
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Description: The sequence of A; Reference number: S46773 A; Accession: S46781
                                                        submitted to the EMBL Data Library, June A;Description: The sequence of S. cerevis
                                                                                                                                                               hypothetical protein YHR029c - yeast (Saccharomyces C;Species: Saccharomyces cerevisiae C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q8U679; UNIPARC:UPI0000D2765; GB:AE008690; PIDN:AAL46292.1
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-290 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 QAPLRLSDALSDVAPLADALGLGLGDILSEPAPRPADTGAAHLMVRVRNAGTVDEARPDA 185
                                                                                                                                                                                                                                                                                                                                                                           246 NLRNNELVIEQGTKMGRRSILHIRLKPEPELSGTGIVVLRGVIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VLRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%;
Similarity 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WAP---BEAIHDLDSL-DALA-----AADPADEPDD--IAH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGAEVFGAGHNALGAWLWLGEHGNLGSLTTARTLQQEIGQDVLPIBLBLIAGRVHGRML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPRTEIPFAGHPTVGASWWLRERG-----TPINTLQVPAGIVQVSYHGDLTA--ISARSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 156; DB 2;
Pred. No. 3.3e-06;
                                                           cerevisiae cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Dupont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Engineer Agrobacterium tumefaciens PMID:11743193
                                                                                                                                                                     #text_change 09-Jul-2004
                                                           8082.
                                                                                                                                                                                                                                   cerevisiae)
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                                                                                                                                                                                                                                                                                                                                                                           290
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A;Gene: PA4215; PA1904
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A;Residues: 1-278 <ST2>
A;Cross-references: UNIPARC:UPI0000131A7B; GB:AE004616; GB:AE004091; NID:g9947890; PIDN
A;Experimental source: strain PAO1
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A;Cross-references: UNIPROT:069754;
A;Experimental source: strain PAO1
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Best Local
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                                          136
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                                                                                                                                                                                    19 GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
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                                                                                                                          TVGASWWL-RERGTPINTLQVPAGIVQVSYH---GDLTAISARS---EW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTITOG
GSLRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQGK 199
                                         ALGLKGSTFPIBVYRNGPRHVFVGLESVAÄLSÄLHPDHRALCDFP-DLAVNCFAGAGR--
                                                                                                 LLGTAIALGAETDKDRLFLETRMGTVPFALERQDGKVVACSMQQPIPTWEHPSRPAELLA
                                                                                                                                                        GNPVAVFFDCDDLSGERMQRMAREMNLSESTFVLRPQQDG-DARIRIFTPVNELPFAGHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDIAHYLWTWTDRSA----GSLRARMFAANLGVTEDBATGAAAIRITDYL-----SRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTPRSELPFAGHPTIGSCKAPLEFTKNTTATSLVQECKIGAVPITINEGLISFKAPMADY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTPRTEIPFAGHPTVGASWWLRB---RGTPINTL--QVPAGIVQVSYHGDLTAISA-----
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28.1%;
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                                                                     APEFAIHDLDSLDALAAADP----ADFPDDIAHYLWTWTDRSA 158
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                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 154.5; DB 2;
Pred. No. 4.6e-06;
                                                                                                                                                                                                                             Score 151.5; DB 2
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                    UNIPARC: UPI0000131A7B; GB: AE004838;
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                                                                                                                                                                                                                                            DB 2;
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RESULT 11
H84192
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letest Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitent A;Reference number: AD3252; PMID:11756688

A;Accession: AH3330
                                                                                                                                                          R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddock Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennie, P.P.; Omer, A.D.; Ebhardt, H.; A;Title: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: H84192
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                                                                  A; Molecule type: DNA
A; Residues: 1-301 <S
                                                                                                                                       A; Reference number: A84160; A; Accession: H84192
                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Vng0332c [imported] - Halobacterium sp. C;Species: Halobacterium sp. NRC-1
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A;Experimental source: strain 16M
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A; Residues: 1-308 < KUR>
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                                         A; Cross-references:
                                                                                                                   A;Status: preliminary
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VNG0332C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 TPRTEIPFAGHPTVGASWWLRERGTP-----INTLQVPAGIVQVS-YHGDLTAIS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VFDVFADK-ALAGNFLAIVHDCEGLTDACMQAIAREFNLSETVFIHAFANFAHEASVRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VLRVFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIH
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                                         UNIPROT:Q9HS99; UNIPARC:UPI00000635E1; GB:AE004437; NID:g10579960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148.5; DB 2
Pred. No. 1.6e-05;
1; Mismatches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SSQWWI
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                                                                                                                                                                                                                   Ebhardt, H.; Lowe, T.M.;
                                                                                                                                                                                                                                                                                     D.W.; Maddocks,
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G:
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G., Jable
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Best Local Matches 7

Similarity

12.2%; Score 145; Di 26.8%; Pred. No. 3.2; :ive 32; Mismatches

DB 2; 1 .2e-05; les 96;

Length 301;

Indels

82;

Gaps

17;

Query Match

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RESULT 12
AIJO80
AIJO80
AIJO80
phenazine biosynthesis protein [imported] - Agrobacterium tumefaciens (strain co., phenazine biosynthesis protein [imported] - Agrobacterium tumefaciens (strain co., phenazine biosynthesis protein 11-Jan-2002 #text_change 09-Jul-2004 C; Accession: AIJO80
C; Accession: AIJO80
R; Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; l; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Reference number: AB257
A, Accession: AI3080
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-281 KUR>
RESULT
H98205
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A;Residues: 1-281 <KUR>
A;Cross-references: UNIFROT:Q8U830; UNIPARC:UFI00001648FC; GB:AE008689; FIDN:AAL45063.1
A;Experimental source: strain C58 (Dupont)
C;Genetics:
C;Genetics:
A;Gene: phzC
A;Map position: linear chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                        ASLAQWLFATGMVAADYVA 242
                                                                                                                                                                                                                                                                    RRAQGRUSFA---APPLIRSGAPTPAELEEALQUIGIEAHDVVDAAWIDNGPGWLGVRLA
                                                                                                                                                                                                                                                                                                              ARSEWAPEFAIHDLDSLDALAAADPADFPDDI-----AHYL--WTWTDRSAGSLRARMF 166
                                                                                                                                                                                                                                                                                                                                                             YRVRIFSLDREMPFAGHPTLGSCHAWLSADGSPKNETAIIQECGAGLVPV------
                                                                                                                                                                                                                                                                                                                                                                                                    AHATIHTPRTEIPPAGHPTVGASW-WLRERGTPINTLQV----PAGIVQVSYHGDLTAIS
                                                                                                                                  WSPEGWVRVAGRVVSDGVA
                                                                                                                                                                              SAEKVLSIDPVRSWPGRIDVGVVGPHAEGGEAAFEVRAFFSDHLGAIAEDPVTGSL----N
                                                                                                                                                                                                                          AA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DLTITQGKGSLIHTTWSPEGWVRVAGRVVSD-----GVAQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDIAH ---YLWTW--TDRSAGSLRARMFAANLGVTEDEATGAAAIRITDYLSR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYERVAEATGTEAAALRGASDDIPLAVADTGLPPLIVPITYLSDLGDADP-DPDAVEALA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYH------GDLTAISARSEWAP-----EFAIHDLDSLDALAAADPADF-----P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVDLCGHATIASHAHLYDDGALAAGEHTLETNVGVLDIEVAEDGTVWMAQNPPTVREVEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIPFAGHPTVGASWWLRERGTPI---NTLQVPAGI----
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                                                                                                                                                                                                                        -NLGVTEDBATGA-AAIRITDYLSRDL-TITQG--KGSLIHTT
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Pred. No. 3.3e-05;
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A;Cross references: UNIPROT:0930U9; UNIPARC:UPI00000CAF97; GB:AB006469; PIDN:AAK64753.1 A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                          R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.I.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the er A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
G95273
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R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein SMa0180 [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: G95273
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                               A; Contents: annotation
                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-290 < KUR>
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: AGR_L_1187
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A; Residues: 1-290 < KUR>
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Genetics:
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Similarity 27.4%;
71; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAEKVLSIDPVRSWPGRIDVGVVGPHAEGGEAAFEVRAFFSDHLGAIAEDPVTGSL---N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRVRIFSLDREMPFAGHPTLGSCHAWLSADGSPKNETAIIQECGAGLVPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AHATIHTERIEIPFAGHETVGASW-WLRERGTPINTLOV----PAGIVOVSYHGDLTAIS
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Pred. No. 3.4e-05;
2; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
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                                                                                                                                                                                                                                                                                                                                                                                                      functions of the entire Sinorhizobium PMID:11481432
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ki, R.; Wells, D.H.;
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A;Gene: SMa0180

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hypothetical protein BH1950 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Pate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Pate: 01-Dec-3000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Paccession: F83893 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the A;Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: F83893
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F83893
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A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1950
Search completed: April 14, 2006, Job time : 14.3694 Becs
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Matches 55; Conserv
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tuberculosis clinical and  DBJ databases. in two aspects; its sequence its (including one that fuses otein) and it was wrongly produced through a collaboration	Gas S., Barry C.B. III, D., Chillingworth T., well T., Gentles S., Hamlin N., h A., McLean J., Moule S., il M.A., Rajandream M.A., n S., Squares S., Squares R., Barrell B.G., um tuberculosis from the  C DNA].  C DNA].  C DNA].  C DNA].  C DNA].  C DNA].	.37; ycetal	Q8nil3 schizosacch Q4nmas arthrobacte Q89339 brucella su Q8yep3 brucella me Q7wap5 bordetella Q7wju9 bordetella Q7wju9 bordetella Q5lkg2 silicibacte Q6d2t4 erwinia car Q57fg8 brucella ab Q8u679 agrobacteri Q8y2tz ralstonia s P38765 saccharomyc Q6bvn8 debaryomyce

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P0A5GB; 007215; P28176;
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Hypothetical protein Mb2735.
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PANTHER; PTHR13774; PhzC_PhzF; 1.
Pfam; PP02567; PhzC-PhzF; 1.
Complete proteome; Hypothetical protein.
Complete 228 AA; 24574 MW; PEE2DF0DA8B2A09B CRC64;
                                                                                                                                                    MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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EMBL; AE000516; AAK47105.1; -;
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                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use as long as its content is in no way modified and this statement is no
                                                                                                                                                                                                                                                                                                            Mycobacterium bovis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae, Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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152 NOCFA

Q5YT52 NOCFA

Q5YT52;

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Q5YT52;
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SEQUENCE
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STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino
Shiba T., Hattori M.;
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OrderedLocusNames=nfa37910;
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25-OCT-2004
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NCBI_TaxID=37329;
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                                           IRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVSDGVAQL
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proteome; Hypothetical
215 AA; 23024 MW; '
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Nat. Biotechnol. 21:526-531(2003).
EMBL; BA000030; BAC73641.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; TEA.
GO; GO:0009058; P:biosynthesis; TEA.
InterPro; IPR003719; PhzC PhzF.
PANTHER; PTHR13774; PhzC PhzF; 1.
Pfam; PP02567; PhzC-PhzF; 1.
Complete protecme; Hypothetical protein.
SEQUENCE 214 AA; 23077 MW; 0ED571AD9BFD7
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MEDLINE-21477403; pubmedei-1572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondar."
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OrderedLocusNames=SAV5929;
Streptomyces avermitilis.
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MEDLINB-22608306; PubMed=12692562; DOI=10.1038/nbt820;
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3 (TrEMBLrel. 24,
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il protein SCO2268.
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Pred. No. 2.8e-28;
6; Mismatches 79; Indels
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                          sequence update) annotation updat
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RESULT

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STRAIN-A3(2) / M145;

STRAIN-A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil

Rabbinowitsch E., Rajandram M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill
NUCLEOTIDE SEQUENCE.
STRAIN-CGA009 / ATCC BAA-98;
STRAIN-CGA009 / DOI=10.1038/nbt923;
PubMedCa14704707; DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S.,
Land M.L., Pelletter D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres
Harrison F.H., Gibson J., Harwood C.S.;
                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
phenazine biosynthesis PhzC/PhzF protein.
Name=phzF; OrderedLocusNames=RPA3182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003824; F:catalytic activity; GO; GO:0009058; P:biosynthesis; IEA. InterPro; IPR003719; PhzC_PhzF; PANTHER; PTHR13774; PhzC_PhzF; 1. Pfam; PF02567; PhzC-PhzF; 1.
                                                                                                                                                            Bradyrhizobiaceae;
NCBI_TaxID=1076;
                                                                                                                                                                                                            Rhodopseudomonas palustris.
Bacteria; Proteobacteria; A
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Nature 417:141-147(2002).
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proteome; Hypothetical protein.
214 AA; 23321 MW; A5A53BF5EF9E9C07
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                                                                                                                                                                                        Rhodopseudomonas.
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bred. No. 1.4e-26;
bred. No. 1.4e-26;
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RESULT 7

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CO Rhiz

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MEDLINE-2136507; PubMed=11481430; DOI=10.1073/pnas.161294398;

A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Capela D., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,

Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

T "Analysis of the chromosome sequence of the legume symbiont

T sinorhizobium meliloti strain 1021.",

Proc. Natl Acad. Sci. U.S.A. 98:9877-9882 (2001).

EMBL, AL591791; CAC47347.1; -; Genomic DNA.

GO; GO:0003024; F:catalytic activity; TEA.

GO; GO:0003024; F:catalytic activity; TEA.

R GO; GO:0003058; P:biosynthesis; IRA.

InterPro; IPR03719; Ph2C Ph2F.

R PANTHER; PTHR13774; Ph2C Ph2F; 1.

R Pfam; PF02567; Ph2C-Ph2F; 1.
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EMBL; BX572603; CAR28623.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; TEA.
GO; GO:0009858; F:biosynthesis; IEA.
InterPro; IPR003719; PhzC. PhzF.
PANTHER; PTHR13774; PhzC. PhzF; 1.
Pfam; PF02567; PhzC-PhzF; 1.
TIGRPAMB; TIGR00654; PhzF-family; 1.
Complete nyotecame
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein SMc03984.
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Q92M77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=R02768; ORFNames=SMc03984;
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Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
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PANTHER; PTHR13774; PhzC_PhzF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] MEDLINE=97061201; PubMed=8905231;
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Bacteria; Cyanobacteria; Chroococcales;
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                                                                                                                                   Mismatches
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13-SEP-2005
13-SEP-2005
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ORFNames=XC_1371;
Xanthomonas campestris pv.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qian W., Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F., Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L., Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang
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EMBL; AE012387; AAM42014.1; -; Genomi HSSP, P37757; ISDJ.
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MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
Camargo L.B.A., Camarotte G., Cannavan F., Cardozo J., Chambergo
Clapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J
El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
Ferro M I T. Formichiosi D. Ferreira R.C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PANTHER; PTHR13774; PhzC_PhzF; 1.
Pfam; PF02567; PhzC-PhzF; 1.
TIGRFAMs; TIGR00654; PhzF_family; 1.
Complete proteome; Hypothetical protein.
Complete 292 AA; 30927 MW; DB83DBBB662636CA CRC64;
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OrderedLocusNames=XCC2742;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                              DALAAADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGAA----AIRITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPRTEIPFAGHPTVGASWWLRERG----TPINTL--QVPAGIVQV------
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                                                                                                                           -LAEDRLPGRQGR------YVASQGREVGRDGRVEVE
                                                                                                                                                                                                                                                                                                                                    PRAQCSDTGTHHAAALAQVTRAFAMSAQAPALWNNGPSWWLLELADEAAVRTAVPDLAAI
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PRELIMINARY;
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29.0%;
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-Santos J.R.,
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C101-FEB-2005 (TrEMBLrel. 29, Lav.
C101-FEB-2005 (TrEMBLrel. 20, Lav
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RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J.,
Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Cheepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Brickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Cardyna S., Gnarre S., Graham L., Grand-Pierre N., Hafez N.,
RA Boukhgalter S., Jones C., Kamal M., Kamat A., Karatas A.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Kalls C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Kalls C., Landers T., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauchel E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Milson T., Peterson K., Phunkhang P., Pierre N., Furcell S.,
RA Milson J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Mandyka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Ramasamy U., Raymond C., Tetta R., Rise C., Rogov P.,
RA Ramasamy U., T
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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SEQUENCE 87
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Lander E.;
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Submitted (JAN-2004) to the EMBL/GenBank/DD
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34; Mismatches
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RESULT 13
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ID Q4LTD6,
Q4LTD6;
Q4LTD6;
AC Q4LTD6;
DT 13-SEP-2005 (TTEMBLrel. 31, Last sequence updat
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EMBL; AY59629; AAV47307.1; -; Genomic I GO; GO:0003824; F:catsyltic activity; II GO; GO:0009058; F:biosynthesis; IEA.

InterPro; IPR003719; PhzC PhzF.

InterPro; IPR001412; tRWA-synt I.

PANTHER; PTHR13774; PhzC PhzF; 1.

PANTHER; PTHR13774; PhzC PhzF; 1.

PEGam; PF02567; PhzC-PhzF; 1.

TIGRFAMs; TIGR00654; PhzF family; 1.

PROSITE; PS00178; AA TRNA LIGASE I; UNKO
                                  US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia
                                                                                                                                                                                                                                           Burkholderia cenocepacia HI2424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkho
Burkholderiaceae; Burkholderia; Burkholderia cepacia
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Date S.V., Marcotte E., Hood L
"Genome sequence of Haloarcula
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Ballga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman
Ballga N.S., Mannon P., Chiu Y., Weng R.S., Gan R.R., F
Deutech E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., F
Date S.V., Marcotte E., Hood L., Ng W.V.;
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Haloarcula marismortui (Halobacterium marismortui).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloarcula.
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A Boukhgalter B., Butler J., Calvo S.B., Camarata J., Chang J.,
A Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
A Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
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A Gardyna S., Gnerre S., Jones C., Kamal M., Kamat A., Karatas A.,
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A Kells C., Mauceli E., McCarthy M., Meldrim J., Manning J.,
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A Mihova T., Mlenga V., Murphy T., Naylor J., Muyen C., Nicol R.,
A Milova T., Menga V., Murphy T., Naylor J., Muyen C., Nicol R.,
A Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
A Nielsen C.B., Norbu C., Phunkhang P., Pierre N., Purcell S.,
A Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
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XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

XX Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

XX Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cureino-Santos Jr.,

XX Ciapina L.P., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

Yerro M.I.T., Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

XX Atsuyama A.M., Xishi L.T., Lette R.P., Lemos B.G.M., Lemos M.V.F.,

XX Arating B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

XX Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

XX Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

XX Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

XX Pereira H.A., Rossi A., Sena J.A.D., Tsais S.M., White F.F.,

XX Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

XX A Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

XX Scubal J.C., Xitajima J.P.;

**Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
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Talamas J., Te
Vassiliev H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vanthomonas axonopodis (pv. citri).
Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein XAC29
OrderedLocusNames=XAC2912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
EMBL; AACM01000342; E
Hypothetical protein.
SEQUENCE 309 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Fusarium graminearum genome sequence."; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₩u X.,
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EMBL/GenBank/DDBJ whole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAIEVSVLRVFTDSDGNFGNPLGVI-----NASKVEHRDRQQLAAQSGYSETIFVDLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLGRARISGVSLPVNDLLDDDWRNGLLCKYYYVVNDRREEDGVTVYSIRSRMMB---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALAAADPA-----DFPDD-----IAHYLWTWTDR-----SAGSLRARMFAANLGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tesfaye S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 22, Last (TrEMBLrel. 25, Last protein XAC2912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venkataraman
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        genomes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theodore J., 10p....
Iman V.S., Viel R., Vo A., was a man V.S., Viel R., Zembek L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
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Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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Topham K., Wang S., Wilson
R., Vo A., Wang S., Wilson
Rembek L., Zimmer A., Zodi
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R EMBL; AB011933; AAM37757.1; -; Genomic_DNA.

R HSSP; P37757; ISDJ.

R GO; GO:0003824; F:catalytic activity; IEA.

R GO; GO:0009058; P:biosynthesis; IEA.

GO; GO:0009058; P:biosynthesis; IEA.

R GO; GO:0003719; PhZC_PhZP.

R InterPro; IPR003719; PhZC_PhZP.

R Pfam; PF0Z567; PhZC-PhZP; 1.

R Pfam; PF0Z567; PhZC-PhZP; 1.

R Pfam; F0Z567; PhZC-PhZP; 1.

R TIGRPAMs; TIGR00654; PhZP-family; 1.

W Complete proteome; Hypothetical protein.

G SEQUENCE 292 AA; 31038 MW; 2A9AADFE4816D976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.3%; Score 194; DB 2; Length 292; Best Local Similarity 29.1%; Pred. No. 3.1e-08; Matches 83; Conservative 21; Mismatches 107; Indels 74;
                                                                         248 AQSRYVASQGREV----GRDGRVHVDVDAEGEVWIGGATLQVIDG 288
                                                                                                          190 -----SRDLTITQGKGSLIHTTWSPEG--WVRVAGRVVSDG 223
                                                                                                                                               188 RLTQASAACGLAIYAPMHDHDADLVVRAFCPGDGIPEDPVTGSANACIAARLHGEDRLPG
                                                                                                                                                                                    150 LWTWTDRSAG------SLRARMFAANLGVTEDEATGAAAIRITDYL-----
                                                                                                                                                                                                                        128 RARAIDTGDTYADALRAACAGLGASAQPAALWNNGPNWWLLELADAQAVRQAAPDLAAIA 187
                                                                                                                                                                                                                                                             68 PRTELPFAGHPSVGAAWAAVTHGVTAYKPDGRLRQQCAAGVLPVDVFDRYGALLVRLRAP 127
                                                                                                                                                                                                                                                                                                                   67 PRTEIPFAGHPTVGASWWLRERGT----PINTL--QVPAGIVQVSYHGDLTAISARSEWA 120
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Maximum Match 100%
Listing first 45 s
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// ORGANISM: Acinetobacter baumannii
US-09-328-352-4558

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LENGTH: 292
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APPLICANT: Gary L. Beton et al.
APPLICANT: GARY L. BETON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GT699-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT: Schupp
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                           APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OP INVENTION: Genes for the synthesis of
TITLE OP INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                              COUNTRY: U
                                                                                                                                                 STATE:
                                                                                                                                                                       CITY:
                                                                                                                                                                                      ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
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APPLICATION DATA:
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                                                                                                                                                                     Hawthorne
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                                                                                                                                USA
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Beck, James Joseph
Hill, Dwight Steven
                                                                                                                                                                                                                                                                                                                                                       Gaffney, Thomas Deane
                                                                                                                                                                                                                                                                                                                                                                               Ryals,
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                                                                                                                                                                                                                                                                                                                                          Lam, Stephen Ting
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                           John Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- LRARMFAANLGVTEDEATGAAAIRITDYL 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5643774
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acid
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                   LENGTH: 278 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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 APPLICATION NUMBER:
                                                                                                                                                 COUNTRY:
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ກາ 564377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08456837
                                                                                                                                                                                                                                                                                                                                                                                            Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                 Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip E.
UKnes, Scott Joseph
VENTION: Genes for the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%; Score 145.5; ilarity 28.3%; Pred. No. 2e-(Conservative 33; Mismatches
                                                                                                                                                                                                                         Ciba-Geigy Corporation
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                                                                                           Floppy disk
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US/08/456,837
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Length 278;

41;

160

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RESULT 5
US-08-457-342-20
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/457,205
FILING DATE: 01-7UN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-7UN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip B.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGO
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                                                                                                                             ZIP: 10532
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                               ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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62; Conserv
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Beck, James Joseph
Hill, Dwight Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas
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                            Version
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2e-07;
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US-08-457-646A-20
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-457-342-20
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
PILING DATE: 01.-UN-1995
APPLICATION NUMBER: 08/258,261
PILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEPHONE: 919-541-8614
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 278 amino acid
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                   ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genes for the s
TITLE OF INVENTION: antipathogenic
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                           COUNTRY:
                                                                                                                                                                                       ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08457646A
                                                                                                                                                                                                                                                                                                                                   Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip B.
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Uknes, Scott Joseph
Oknes, Scott Joseph
Genes for the synthesis
Oknation: Genes for the synthesis
                                                                                                                               USA
      PatentIn Release #1.0, Version #1.25
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-457-646A-20
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US-08-458-076A-20
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Best Local S
Matches 62
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Patent No. 5
COUN'IKA.

ZIP: 10532

ZIP: 10532

COMPUTER READLABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

"""" PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Ukneer, Phillip E.
APPLICANT: Uknee, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
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APPLICATION NUMBER: 08/258,261

PILLING DATE: 08-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: CGC 1506/CIP3

TELECOMMUNICATION INFORMATION:
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LENGTH: 278 amino acid
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CORRESPONDENCE ADDRESS:
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                                                                                                                   STREET: 7 Skylin
CITY: Hawthorne
STATE: NY
COUNTRY: USA
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APPLICATION NUMBER: US 08/457,205
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TELEPAX: 919-541-8689
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Similarity 28.3%;
62; Conservative 3
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Beck, James Joseph
Hill, Dwight Steven
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                                                                                                                                                                                                             Ciba-Geigy Corporation
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US-08-457-335A-20
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Best Local Similarity
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APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Blmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatibl
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 278 amino acid
                                                                                                                                                                              TITLE OF INVENTION: Genes to. ....
TITLE OF INVENTION: antipathogenic croffences: 22
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PRIOR APPLICATION DATA:
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                   ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 01-JUN
                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 WRSRMFSPAYGVVEDAXTGSAAGPLAIHLARHGQIEFGQ
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                                                                                                                                                                                                                          Lam, Stephen Ting
Hammer, Phillip E.
UKnes, Scott Joseph
VENTION: Genes for the synthesis of
                                                                                                                                                                                                                                                                                                   Gaffney, Thomas Deane
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Hill, Dwight Steven
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                                                                                                                                                                                                              substances
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HOLECULE TYPE: protein

US-08-457-335A-20
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       APPLICANT: Hammer, Phillip
APPLICANT: van Pee, Karl-He
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes f
TITLE OF INVENTION: antipat
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: C1ba-Ge1gy Corporation
STREET: 520 White Plains Road
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
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FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                  COUNTRY: U
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5817502
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ilarity 28.3%;
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RESULT 10
US-09-028-934-20
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US-08-729-214-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20,
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Best Local Similarity
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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APPLICANT:
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LENGTH: 278 amino acids
TYPE: amino acid
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NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                      CITY: Research Triangle Park
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van Pee, Karl-Heinz
Kirner, Sabine
Young, Thomas R.
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                                                                    US/09/028,934
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Pred. No. 2e-07;
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                                                                                                     Version #1.30
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RESULT 11
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                                                                                                                                                                                                                                                       APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Gregor
TITLE OF INVENTION: CORYNBARCTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CP
CURRENT FILING DATE: 200-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6831165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 242, Application US/09602777A
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Best Local Similarity
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APPLICANT: Kroger, Burkhard
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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LENGTH: 278 amino acid
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                   FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19932125.6
                                                                                                                                                                                APPLICATION NUMBER: DE 19932126.4 FILING DATE: 1999-07-09
                                                                   APPLICATION NUMBER: DE 19932129.9
FILING DATE: 1999-07-19
                                                                                                       APPLICATION NUMBER: DE 19932128.0 FILING DATE: 1999-07-09
                                                                                                                                                                                                                    FILING DATE: 1999-07-09
                FILING DATE:
APPLICATION 1
                                                    APPLICATION NUMBER: DE 19932226.0
                                                                                                                                            FILING DATE: 1999-07-09
                                                                                                                                                               APPLICATION NUMBER: DE 19932127.2
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Zelder, Oskar
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DATE:
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                NUMBER: DE 19932920.6
                                     1999-07-09
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US-09-252-991A-21986

Sequence 21986, Application US/09252991A Patent No. 6551795

Patent No.

GENERAL INFORMATION:
APPLICANT: MAYC J. Rubenfield et al.
APPLICANT: MAYC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

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SEQ ID NO 242
LENGTH: 211
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Best Local Similarity
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APPLICATION NUMBER: DE 19933006.9
FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932973.7
FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932935.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE
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APPLICATION NUMBER: DE 19932924.9
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176 AYPEGAPHAFEVRAFAQGIG--EDPVTGSLNAFIAQWL
                                    160 -----SLRARMFAANLGVTEDBATGAAAIRITDYL 189
                                                                             119 LDÄÄCEALGISPDFIRÄH---QWVDNGPGWAVVELPSAQHVLDLEPDFSAHPTLKLGVIG
                                                                                                                 133 ALAAADPADF-PDDI-AHYLWTWTDRSAG------
                                                                                                                                                      62 TLGTAHVFRELHGEQGTQL-VQECVAGLVAVRAIDGPASGLAFQA--PFTLKDGPLDASD
                                                                                                                                                                                            78 TVGASWWLR----ERGTPINTLQVPAGIVQV-SYHGDLTAISARSEWAPEFAIHDLDSLD
                                                                                                                                                                                                                                                                     19 GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTEIPFAGHP
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Pred. No. 2.1e
26; Mismatches
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  211
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US-09-252-991A-20934
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SEQ ID NO 20934
LENGTH: 270
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21986
LENGTH: 331
TYPE: PRT
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Best Local :
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GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR REPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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Local Similarity 27.6%;
                                     186
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                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                  3 IEVSVLRVFTDSDGNF-GNPLGVINASK-VEHRDRQQLAAQSGYSETIFVDLPSPGSTTA
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                       AVTARSQRFDFVSRWFGPNVGVNEDPVTGSAHTSLAPYWAQRLGKTRLSAEQGGARKGRL
                                                                                                                K-RPEPCATPDGLLEALGIAEAEVLKTD--DYLVVVDDEKTIAALAPDFARLKGLPCRGV 185
                                                                                                                                                   EWAPEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDR-----
                                                                                                                                                                                      RLRWFTPQVBVDLCGHATLATAWVLIHKLDDASPVLRFATRSGELSVRREGDSLAMDFPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNAVAVVIGADRLSSROMLBFÄAWTQLSETTFLLRPTVABADYRVRIFTFLRBLFFÄGHF 144
IHTTWSPEGWVRVAGRVVSDGVAQL 227
                                                                        ---SAGSLR----ARMFAANLGVTEDEATGAAAIRITDYLSRDLTIT----
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Pred. No. 1.6e-05;
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Pred. No. 3.2e-05;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27013
ENOTH: 335
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US-09-248-796A-16787
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US-09-248-796A-16787
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US-09-252-991A-27013
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                                                                                                                                                                                                             Sequence 16787, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                              SEQ ID NO 16787
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Best Local Similarity
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APPLICANT: Marc J.
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Patent No. 6551795
                                                                                                   PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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TITLE OF INVENTION:
FILE REFERENCE: 107
                ORGANISM: Candida albicans
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ORGANISM: Pseudomonas
                                                            LENGTH: 207
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NVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
NVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
ENCE: 107196.136
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Pred. No. 0.00026;
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US-10-156-761-15-210632
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US-10-166-761-14521
US-10-166-087-30
US-10-166-761-13432
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Sequence 66, Appl
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Sequence 110632,
Sequence 210632,
Sequence 6518, App
Sequence 230986,
Sequence 30, Appl
Sequence 30, Appl
Sequence 13419, A
Sequence 1342, Appl
Sequence 52821, A
Sequence 22821, A
Sequence 20127,
Sequence 59131, A
Sequence 7, Appli
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Sequence 10, Appli
Sequence 23012, A
Sequence 23012, A
Sequence 10, Appli
Sequence 23012, A
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	30, App	66693, 1	8, Appli	773, App	1173, A	1172, A	170, App	1977, Ag	1178, Ap	1176, Ag	248384,	72, Appl	19, Appl	•	•	21, Appl	12173, 1	*****

## ALIGNMENTS

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Sequence 66, Application US/09791171

Sequence 66, Application US/09791171

GENERAL INFORMATION:

APPLICANT: ADDERSEN, Peter

APPLICANT: NIELSEN, Rikke

APPLICANT: NIELSEN, Rikke

APPLICANT: RASMUSSEN, Peter Birk

APPLICANT: RASMUSSEN, Peter Birk

APPLICANT: RESIDINGH, Karin

APPLICANT: WELDINGH, Karin

APPLICANT: WELDINGH, Karin

APPLICANT: WELDINGH, Karin

APPLICANT: WELDINGH, Karin

CURRENT FILING DATE: 19001-2002.1

CURRENT FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: US/09/791,171

CURRENT APPLICATION NUMBER: 09/050,739

PRIOR APPLICATION NUMBER: 09/050,739

PRIOR APPLICATION NUMBER: 0376/97

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 1277/97

PRIOR FILING DATE: 1997-04-02

PRIOR APPLICATION NUMBER: 60/044,624

PRIOR APPLICATION NUMBER: 60/044,624

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR FILING DATE: 1998-01-05

NUMBER OF SEQ ID NOS: 173

SEQ ID NO 66

LENGTH: 228

TYPE: PRT

COURSEM: MATCHASTER 1998-01-05

NUMBER: PRT

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US-09-791-171-66
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Best Local S
Matches 228
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hes 228;
121
                                          121 PEFAIHDLDSLDALAAADPADFPDDIAHYLWTWTDRSAGSLRARWFAANI.GVTEDEATGA
                                                                                                                                          61 HATIHTPRTEIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA
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APPLICANT: ORTINICER, THOMAS
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: RELDINGH, Karin
APPLICANT: FILORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1097-11-10
PRIOR APPLICATION NUMBER: 1007-0418
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Publication No. US20030147897A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 66
LENGTH: 228
LENGTH: 228
TYPE: PRT
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US-10-620-246-66
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US-09-804-980-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1192; DB 3; Best Local Similarity 100.0%; Pred. No. 1.8e-116; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: OETTINGER, Tho
FILING DATE: 1997-04-18
APPLICATION NUMBER: 60/070,488
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GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI
APPLICANT: ISEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2001-272697
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                                                                                                                                                                                   ; ORGANISM: Streptomyces avermitilis US-10-156-761-13456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-156-761-13456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUFITE NO 66
; SEQ ID NO 66
rength: 228
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13456
LENGTH: 214
TYPE: PRT
                                                                                           Matches
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13456, Application US/10156761 Publication No. US20030119018A1
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PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/791,171
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.0
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PRIOR FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: 1281/98
PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVVSDGVAQLD 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 HATIHTPRTEIPFAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWA
                             4 EVSVLRVFTDSDGNFGNFLGVINASKV--EHRDRQQLAAQSGYSETIFVDLPSFGSTTAH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAIEVSVLRVFTDSDGNFGNPLGVINASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTA
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                                                                                                                 Similarity
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DYDVLRVFCGPGGGYGNELGVVREGSVLPECADRQALAAKLGFSETVFVDDPERGV----
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                                                                                           Conservative
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                                                                                       35.8%; Score 427; DB 4; L
43.9%; Pred. No. 3.6e-36;
Mismatches 79;
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                                                                                                                                       Length 214;
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US-09-738-626-6518
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; OTHER INFORMATION: Clone ID: MRT4577_123694C.1.pep
US-10-425-115-210632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-10-425-115-210632
                                                                                                                                      RESULT 6
  Sequence 6518, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAXAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 210632
LENGTH: 306
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: unsure
LOCATION: (1).. (306)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAIEVSVLRVFTDSDGNF-GNPLGV--INAS--KVEHRDRQQLAAQSGYSETIFV-DLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                AADPA--DFPDD------IAHYLWTWTD----RSAGSLRARMFAANLGVTEDEA 177
                                                                                                                                                                                                                                                                                          AVNVSSMBFKADNFLXPTGSKALSXFYHVITXLDHGRRRAGXQLRTRMMAHDL---EDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PG-STTAHATIHTPRTEIPFAGHPTVGASWWLRERG-----TPINTLQVPAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAAIRITDYLSRDLTITQGKGSLIHTTWSPEGWVRVAGRVV 220
                                                                                                                                                                                                     TGSASCCLAAYMSIHGADKQTTQTRRYEFTQG 267
                                                                                                                                                                                                                                             TGAAAIRITDYLS---
                                                                                                                                                                                                                                                                                                                                                                           IPHNVHLHATSLASYPGLEPAAHLQRNETIRQLELAAPVFSLVKGMTFVPIELPSLELLA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATNITRTIDIFLITAEIPFÄGHPTIGGAVTLLSQGVTQIITKAGLIPVTPTGPDSVSIG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELPYVTLDVFTRT---RFAGNPLGVRTIPASGPKPTQAQKQSIARBFNFSETIFIHDVAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATIHTPRTEIPPAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWAP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 179.5; DB 4
; Pred. No. 5.8e-10;
30; Mismatches 80
                                                                                                                                                                                                                                           -RDLTITOG 198
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                                                                                                           APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOPTWARE: PatentIn ver. 3.0
SEQ ID NO 6518
LENGTH: 280
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 621
LENGTH: 278
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 621, Application US/10389647
Publication No. US20040033549A1
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JF 00/159162 PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AIHDLDSLDALAAADPADF-PDDI-AHYLWTWTDRSAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 TEIPFAGHPTVGASWWLR----ERGTPINTLQVPAGIVQV-SYHGDLTAISARSEWAPEF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VFS-SEPFMGNPLAVIADADDLSAEQMARIARWINLSETTFLLKPTQEGADYRVRIFTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 VFTDSDGNFGNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGTAIGRAGEIHISIBSHAIW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGSLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDGPLDASDLDAACEALGISPDFIRAH---QWVDNGPGWAVVELPSAQHVLDLEPDFSAH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GELPFAGHPTLGTAHVFRELHGEQGTQL-VQECVAGLVAVRAIDGPASGLAFQA--PPTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTLKLGVIGAYPEGAPHAFEVRAFAQGIG--EDPVTGSLNASIAQWLHRDGRAGEGYLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SIRARMFAANLGVTEDEATGAAAIRITDYLSRDLTITQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 159.5; DB 3
Pred. No. 6.4e-08;
                                                                                              4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VGGSVITIFQGTAB 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-05
PRIOR PILING DATE: 2001-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-156-761-14521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14521, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-08-1
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14521
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.7%; Score 151.5; DB 4; Best Local Similarity 28.1%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                           120
                           188 YLSRDLTITQGKGSLIHTTWSP-EGWVR------VAGRVVS--DG
                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 ALGLKGSTFPIEVYRNGPRHVFVGLESVAALSALHPDHRALCDFP-DLAVNCFAGAGR--
                                                                                             180 RGIIATARAEDPAQGHDFV-------SRCFFPNVGIDEDPVTGSAHTALAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 -HWRSRMFSPAYGVVEDAATGSAAGPLAIHLARHRQIPYGQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 GSLRARMFAANLGVTEDBATGAAAIRITDYLSRDLTITQGK 199
                                                                                                                                                                                                                                       91 ---PINTLQVPAGIVQVSYHGDLTAISARS-----EWAPEFAIHDL-DSLDALA---- 135
                                                                                                                                                                                                                                                                                      60 DWALRWFTPATEVAMCGHATLATAHVLHTSGTHEGPVRFATRSGVLIATPREDGSITLDF 119
                                                                                                                                                                                                                                                                                                                                   61 HATIH--TPRTEIPFAGHPTVGASWWLRERGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LLGTAIALGABTDKDRLFLETRMGTVPFALERQDGKVVÄCSMQQPIPTWEHFSRPABLLA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 TVGASWWL-RERGTPINTLQVPAGIVQVSYH---GDLTAISARS---EW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                    1 MRIRIVDAFTORP-FAGNPAGVLLLDAFPDDAWLÓDVÁREVNHAETAFAHRLPRGEGGEÁ
                                                                                                                                                                                                                                                                                                                                                                                                                                3 IEVSVLRVFTDSDGNFGNPLGVINASKV-BHRDRQQLAAQSGYSETIFVD-LPSPGSTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Conservative
FWSQRL----GRPDLTGLQASPRSGHVRTELRDDRTLLTGRAVTVIDG
                                                                                                                                            ----AADPADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGAAAIRITD
                                                                                                                                                                                         PTAPLTPVEIPEGVAEALGAEPLTACDTGPNVGDLLIELADEKTVRGLAPDLRALARYSE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ADFPDDIAHYLWTWTDRSA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNPVAVFFDCDDLSGERMQRMAREMNLSESTFVLRPQQDG-DARIRIFTPVNELFFAGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 128; DB 4; Length 272; 23.6%; Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches 100; Indels 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 278;
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                                                 223
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APPLICANT: Ecopia Biosciences Inc.
APPLICANT: Ecopia Biosciences Inc.
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
PILE REFERENCE: 3014-2US
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENCTH: 274
TYPE: PATE
CORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-30
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US-10-166-087-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-425-115-230986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO 230986
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Zea mays
                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/10166087 Publication No. US20030077767A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 230986, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                           Local Similarity
151 WTWTDRSAGSLRARMFAANLGVTED------EATGAAAIRI-----TDYLSRDLTITQG 198
                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 RQQLAAQSGYSETIFVDLPSPGS-TTAHATIHTPRTBIPFAGHPTVGASWW----LRERGT 90
                                                                                                                           95 LQVPAGIVQVSYHGDLTAISARSEWAPEFAIHDLDSLDALAAADPADFPD----DIAHYL 150
                                                                                                                                                                                                                      40 AQSGYSETIFVD-----LPSPGSTTAHATIHTPRTEIPFAGHPTVGASWWLRERGTPINT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KÖETAKEFNYSETTFVHPVDPQTPTQQRIDTFTTDRELPFAGHPTTGAASWALYLSPDKG 63
                                                                                                                                                                            AEŚG-ŚQWLWTDGHEVRVPFDGPVVHRGIPHDPALFGPYAGTPYAGGV-----GRAFNL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVTTLLTKAGPIPISLRPSGDEAA 87
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                  9.4%; Score 112.5; DB 4; Length 274;
24.8%; Pred. No. 0.0054;
rative 22; Mismatches 71; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 125; DB 4; Length 120 39.3%; Pred. No. 8.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
                                                                            -------AEDPRTLPAPDPGRMRELGFTDLTVFR 181
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                                                                                                                                                                                                                                                                       65;
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RESULT 12
US-10-450-763-52819
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US-10-733-969A-87
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn version 3.2
SEQ ID NO 87
LENGTH: 288
                                                                                                                                                                                                  Sequence 52819, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: EP 02028058.2
PRIOR PILING DATE: 2002-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHEN, JIE
APPLICANT: HU, LIPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 21525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     192
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                                                                                                                                                                                                                                                                                                                                                          244 HL----GKKEMHAFQCSHRGGELGISLRPDGRVDIRGGAAVVLEG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 TESVFRCTGSARGGSANVTITGRVWTGGTA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAGHPTVGASWWLRERGTPINTLQVPAGIVQVSYHGDLTAISARSEWAPEFAIHDLDSLD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNPAAVCLLENBLDEDMHQKIAREMNLSETAFIRKLHPTDNFAQSSCFGLRWFTPASEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNPLGV-INASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATI-----HTPRTEIP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                               LLQVENTGKVKGLILTLKGEPGGQTQAFDFYSRYFAPWVGVAEDPVTGSAHAVLSSYWSQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DIAHYLWTWTDRSAGSLRA-----RMFAANLGVTEDEATGAAAIRITDYLSR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLYPAHPQDPHEVBDLIKTAIGNTLVQDICYSPDTQKLLVRLSDVYNRSPLENLKVNTEN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGSLIHTTWSPEGW---VRVAGRVVSDGVA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W----DPDRGEVLARVFAPGFGIPEDAGCLPAAAALGVAALRLAADDRTSVTVRQVTV-RG
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                                                                                                                                                                                                                                                                                                                                                                                                     -GSLIHTTWSPEGWVRVAG--RVVSDG 223
                                                                                                                                                           POLYPEPTIDES
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US-10-450-763-52819
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SEQ ID NO 13432
LENGTH: 636
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LENGTH: 375
TYPE: PRT
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Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Query Match
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Best Local
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
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APPLICANT:
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PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOPTWARE: Custom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Local Similarity 22.8%;
hes 53; Conservative 2
                                                                                                                                                                                                                                                                                            Local
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      409
                                                                                           349 VTSVARYAGHLDLFVVGTDSRVYSTWWDQSSGWAAWFRVGTLVARPGSTVNVVSRYSDHL 408
                                                                                                                                                                              296 PISVV-ARYPEHLDVFAVAADGRTMSDWWDAGSGWAGWFQVSGGLASPGGA-----GSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TAISKKIGCNGFFFFOIR------PGKNETDGRMFSPAIGIVEDFVTGNA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 DALAAADPAD--FPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDEATGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AIINALHLTEDDILPGLPIQVATTGHSKVMIPLKPEVDIDALSP------DLNAL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GNSAGVVFPADNLSEAQMQLIARELGHSETAF--LLHSDDSDVRIRYFTPTVEVPICGHA 191
                                                                                                                                  68 RTEIP-FAGH-----PTVGASWWLRERGTP----INTLQVPAG-----IVQVSYHG 108
                                                                                                                                                                                                                         21 PLGVINASKVEHRDRQQLAAQ------SGYSETIFVD--LPSPGSTTAHATIHTP 67
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                                                                                                                                                                                                                                                                                              Similarity
      DLFTTGSDGRTMSTWWDARTGWAADWFHVSGGVAANGATVTAVARHPFHLDVFTVGTDNR 468
                                                  DL-----
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                   8.4%; Score 100.5; Dilarity 24.5%; Pred. No. 0.31; Conservative 29; Mismatches
                                             -TAISARSEWAPE-FAIHDLDSLDALAAADPADFP------DDI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 110; DB 5; Length 375; pred. No. 0.015; 22; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                 DB 4;
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71;

Gaps

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US-10-450-763-52821

/ Sequence 52821, Application US/10450763

/ Publication No. US20050196754A1

/ GENERAL INFORMATION:

/ APPLICANT: Hyseq, Inc

/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO

/ FILE REFERENCE: 790CIP3/US

/ CURRENT APPLICATION NUMBER: US/10/450,763

/ CURRENT PILING DATE: 2003-06-11

/ PRIOR APPLICATION NUMBER: PCT/US01/08631

/ PRIOR APPLICATION OUMBER: PCT/US01/08631

/ PRIOR FILING DATE: 2001-03-30
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US-10-424-599-178493
(Sequence 178493, Application US/10424599
; Publication No. US20040031072A1
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; OTHER INFORMATION: Clone
US-10-424-599-178493
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 178493
LENGTH: 294
TYPE: PRT
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Best Local Similarity
Matches 59; Conserv
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PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDVVELQPDIGAIAKCPGGGILVSGTAPPESGFDYYCRTFFPKVGINEDPITGSAQCALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISLNRFRLRWFTPATEVBLCGHATLASAHVLFSSGLVKSDIIEFVTLSGVLTAKKVSGIN
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                                                                                                                                                                               POLYPEPTIDES
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NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUstom
SEQ ID NO 52821
LENGTH: 217
                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                          IENGTH: 217

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(217)

OTHER INFORMATION: Xaa = X or * as defined in Table :
                                                                                                                                                                                                                               Local
138 NALTAISKKIGCNGFFPFQIR-----PGKNETDGRMFSPAIGIVEDPVTGNA 184
                               132 DALLAAADP-----ADFPDDIAHYLWTWTDRSAGSLRARMFAANLGVTEDBATGAA 181
                                                                  95 TV-AAHYVRAKVLGLGNCTIWQTSLAGKHRVTIEKHND--
                                                                                                      78 TVGASWWLRERGTPINTLQV----PAG--IVQVSYHGDLTAISARSEWAPEFAIHDLDSL
                                                                                                                                       38 GNSAGVVFPADNLSBAQMQLIARELGHSBTAFL-LHSDDSDV--RIRFTPTVBVPICGHA
                                                                                                                                                                           19 GNPLGVI-NASKVEHRDRQQLAAQSGYSETIFVDLPSPGSTTAHATIHTPRTBIPFAGHP
                                                                                                                                                                                                                48;
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                            8.3%; Score 99; DB
27.4%; Pred. No. 0.1.
Live 20; Mismatches
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                                                                                                                                                                                                                                               Length 217;
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                                                                    -DYRI----SL
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                                                                                                                                                                                                                Gaps
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Search completed: April 14, 2006, 18:40:30 Job time : 81.1108 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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seq length: 2000000000
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   A_Geneseq_21:*
1: geneseqp1980
2: geneseqp2000
3: geneseqp2000
4: geneseqp2001
5: geneseqp2002
6: geneseqp2003
7: geneseqp2003
8: geneseqp2003
8: geneseqp2003
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3552
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geneseqn1980s:*
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(c) 1993 - 2006 Biocceleration
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AUX 93 / 36	AAW31855	ABU52942	ABG27250	ABM90225	ABB91504	ADM87156	AA026231	ADX97588	AAW31852	ADZ47759	ABU37030	AB058564	ADX72179	ABB70063	ABU35716	ABU05359	AAY21947	AAW72930	ABU37020	ABU05989	AAB19846	AAY21928	AAW72911	ID	
ACX93/36 Flant ful	Mycoba	Abu52942 Human mam	Abg27250 Novel hum	Abm90225 Rice abio	Abb91504 Herbicida	Adm87156 Human pro	Aao26231 MDDT rela	Adx97588 Pancreati	Aaw31852 Mycobacte	Adz47759 Mycobacte	Abu37030 Protein e	Abo58564 Human gen	Adx72179 Plant ful	Abb70063 Drosophil	Abu35716 Protein e	Ξ.	Aay21947 Amino aci	Aaw72930 Mycobacte	Abu37020 Protein e	Abu05989 M. tuberc	Aab19846 Mycobacte	Aay21928 Amino aci	Aaw72911 Mycobacte	Description	

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M.

africanum or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

Claim 1; Page 183-185; 163pp; English.

N-PSDB; AAV63935.

WPI; 1998-542705/46.

Andersen P, Oettinger T,

Nielsen , Florio

Rosenkrands I,

Weldingh K,

Rasmussen PB;

(STAT-)

STATENS

SERUM INST. ¥,7

45	44	43	42	41	40	39	38	37	36	35	3 4	33	32	31	30	29	28	27	26	25
358.5	359	360.5	363	363.5	364	364	364	364	367.5	367.5	367.5	368.5	369.5	371.5	373	373.5	375.5	375.5	380	381.5
10.1	10.1	10.1	10.2	10.2	10.2	10.2	10.2	10.2	10.3	10.3	10.3	10.4	10.4	10.5	10.5	10.5	10.6	10.6	10.7	10.7
693	262	1579	639	270	408	408	408	330	1151	574	574	325	639	261	693	258	694	261	277	256
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Abp69529	Abu52944	Ads97981	Adn19622	Abu52939	Aab72737	Aab64007	Aaw07539	Aaw57645	Abb61598	Aam52322	Aag67370	Abg21919	Adn21309	Abu52940	Adm05164	Abu52941	Abb92421	Abu52943	Abu52936	Abu52945
Human pol	Human man	. Protein f	<b>Bacterial</b>	Human man	Repetitiv	'CLP prote	_	•	Drosophil	WASP home	_	Novel hun	) Bacterial	) Human man	Human pro	. Human mam	. Herbicida	Human mam	5 Human man	6 Human man

### ALIGNMENTS

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02-APR-1997;
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                                                                                         01-APR-1998;
                                                                                                                                                                     08-OCT-1998.
                                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen RD1-ORF9B.
                                                                                                                                                                                                                                                          AAW72911 standard; protein; 666 AA.
                                                                                                                                                                                 WO9844119-A1
                                                                                                                                                                                                             Mycobacterium tuberculosis; antigen; vaccine;
                                                                                                                                                                                                                                    21-JAN-1999
                                                                                                                                                                                                        infection.
                                                                                                                                                                                                                                   (first entry)
                                                                                                                            97DK-00000376.
97US-0044624P.
97DK-00001277.
98US-0070488P.
                                                                                                                                                                                            tuberculosis.
                                                                                                                                                         98WO-DK000132
                                                                                                                                                                                                             immunological; immunogen;
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RESULT 2
AAY21928
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                                                                   Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A; CFP7B;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
     Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                              AAY21928 standard;
                                                                                                                                                                                              Amino acid sequence of antigen RD1-ORF9B.
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Pred. No. 1.1e-213;
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim:
Matches 666;
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05-JAN-1998;
01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 202-204; 265pp; English.
                         GKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPSPQR
                                                                                                                                                                                                                                                 FVSAPPPPPPPPPPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP
                                                                                                                                                                                                                                                                                                   MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSER
 GKVATGPSIQARLRABBASGAQLAPGTBPSPAPLGQPRSYLAPPTRPAPTBPPPSPSPSPQR
                                                                         HQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNV
                                                                                                            HOPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNV
                                                                                                                                                    IAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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98US-0070488P.
98WO-DK000132.
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The present sequence is that of the Mycobacterium tuberculosis MTBN5 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB1982-49), encoded by 8 open reading frames (see AAB9035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic
                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection.
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         Mycobacterium tuberculosis. Mycobacterium leprae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium tuberculosis and Mycobacterium tuberculosis and mycobacterium tuberculosis and Mycobacterium leprae identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17;
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense concleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibite cellular proliferation; (8) containing a gene required for cellular proliferation or the biological pathway in which a proliferation—required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACA40890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #22547.
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                                                                                        PNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSDDF
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Pred. No. 1.1e-213;
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18-APR-1997;
10-NOV-1997;
                                                                                                                                                                                                                                                                                                                        The present sequence represents a Mycobacterium tuberculosis protu-
products from the present invention, which describes protein frag-
and nucleic acid fragments derived from M.tuberculosis, can be use
the detection of and prevention of mycobacterial infections. In
particular, the proteins and nucleic acids can be used for the dia
of or vaccination against tuberculosis caused by M. tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated mycobacteria polypeptides and nucleic acids - developing products for the diagnosis of or vaccination aga mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                               africanum or M.
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                                                            AGFFDFLTRGVLSTVSGVVVVASVSIDGAQQASVALDMLRNNGYQDLASRACVVINHIMP
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                                                                                                           EKELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQRALSDADWHFIADPASRFYNLVLADCG
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97DK-00001277.
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RESULT 7
ANY21947
ID ANY21947
ANY21947
ANY 21947
AX ANY22
AX AMIN
DE AMIN
WW CEP7
XX IMMU
KW CEP7
XX MYCC
PN WO9:
ANY CEP7
XX MYCC
PN WO9:
ANY CEP7
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                                                                                                                                                                                                     To the tuberculosis complex. The invention provides a (1) fusion one fusion partner; (2) a fusion polypeptide fragment (1) and at least cone fusion partner; (2) a fusion polypeptide fragment (1) and at least cone fusion partner; (2) a fusion polypeptide fragment comprising a T-cell cepitope from M. tuberculosis protein ESAT-6, or MPT59 and a second confiderent amino acid sequence from M. tuberculosis, or MPT59 and a second confiderent which protects the first amino acid sequence from in vivo concepts the above polypeptides. The polypeptides and nucleic acid fragment control of that encodes the above polypeptides. The polypeptides and nucleic acid concepts are useful as pharmaceuticals, for diagnosis of and as antigens for concepts the encodes the above polypeptides. The polypeptides are also useful for diagnosis, africanum or concepts. The polypeptides are also useful for diagnosis of the concepts. The polypeptides are also useful for diagnosis of CFP7A or concepts. The invention also describes the use of CFP7A or concepts. The polypeptides are also describes the use of CFP7A or concepts and mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell concept; use of for diagnosis of TB in a mammal by performing a DTH type skin concept; use of for the preparation of an immunological composition; and concepts and concepts of the preparation of an immunological composition; and concepts and con
Query Match
Best Local Sim
Matches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1997;
05-JAN-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic; Mycobactarium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epidepetis; ESAT-6; MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CPP7A; CPP30A; CPP7B; CPP19; CFP27; CPP30A; RD1-ORF; CPP10A; CPP16; CPP19; CPP23;
                                                                                                                                                   Sequence 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic fragment of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX81047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protective immune response against infections by mycobacteria belonging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 222-223; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of antigen RD1-ORF9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STAT-) STATENS SERUM INST.
                                          Local Similarity
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       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97DK-00001277.
98US-0070488P.
98WO-DK000132.
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                                      Score 1575;
Pred. No. 1.
       Mismatches
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                                                                         Length 308;
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       Gaps
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RESULT 8
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XX ABUG
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                                                   This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases particularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis and M. leprae marker protein #10
   and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 172-174; 874pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterioses; survival; virulence; protective antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-2003
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RESULT 9
ABU35716
ID ABU3
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AC ABU3
DT 19-J
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DB Prot
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KW Anti
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   WO200277183-A2
                               Mycobacterium leprae
                                                                                                                               19-JUN-2003
                                                                                                                                                                                           ABU35716 standard;
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                                                                                                                                                                                                                                                                                                                                                       LASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPI
                                                                                                                                                                                                                                                                                                                                                                                                     TVSKYYNVMLADCGVGLFDPVTRGVLSTASGVVIVTSTSVDAARQAAIALDWLRHNGYQD
                                                                                                                                                                                                                                                                                                                                                                                                                      PASRFYNLVLADCGAGFFDFLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQRALSDADWHFIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHARVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAADYDKI.FRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 AA;
                                                                                                                                                                                                                                                                                                        YKRKVLBLAAALSDDFERAGR 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGRPSEANIADLLADKDVKSYNDIRTHTSVNAVNLEVLPAAEYSTAQHALSGEDWNFAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRTRVRRPPRGSYQIGILGLKGGAGKTTVTVTLGSMFARVRNDRILVVDADTSCGNLADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HARRGHHHRDETQQANPASATEPMIAPRARTAE---LRQAPHAAAEPAP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPP--PAPS---RPSASPAEPPTRPAPQHSR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAGPEPAPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L----PPNPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---PRSPAASLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVSAPPPPPPPPPPPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ
                                                                                                                                                                                                                                                                         YRRRILBLAAALSDDFERAGR
                                                                                                                                                                                                                                                                                                                                        LLSRACVVINHVMPKEPNIASKOLVQQFEQQIQPGRVVVLPWDKHIAAGTBIRLDRLDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GAKKPSKVVAKRGWRHWVHTVTRINLGLSPDERYELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISEPPQWPPABAPEHQPAKABPPSVPIPINEPSP-----AKPATPMPMTPIDGSQR--
                                                               prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                              (first entry)
                                                                                                á
                                                                                              Prokaryotic essential gene #21243
                                                                                                                                                                                           protein; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSPEPSLAEFE-AQPPATPKPSLLPRPMSSPPEAPRPSANQHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TQHLTRPDGLVSHRTALHDS-TATSAIGVQTGRST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1550; DB 5;
Pred. No. 1.3e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc encoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated containing the polypeptide by the cc antisense nucleic acid; (4) an antibody capable of specifically binding cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent convolute acide activity in the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the conductive of an organism. The antisense nucleic acide are useful for identifying proteins or screening for homologous nucleic acide required conduct calls are useful for collentifying proliferation to isolate candidate molecules for rational conductive or cords. or for screening molecules for rational conductive or cords.
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2002.
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                121 IAGPEPAPP----
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                                                                                                                                                                                                                                                                                                             586
                                                                                                                                                                                   MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSER 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio
Trawick
                                                               L----PPNPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---PRSPAASLMP
                                                                                                     FVSAPPPPPPPPPPPPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP
                                                                                                                                             MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                              43.6%;
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Carr G
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----KPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPE 169
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                                                                                                                                                                                                                                              Score 1550; DB 6;
Pred. No. 1.3e-88;
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                             168;
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Forsyth
                                                                                                                                                                                                                                                                 Length 586;
                                                                                                                                                                                                                           Indels 112;
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Xu HH;
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RESULT 10
ABB70063
ID ABB70
XX ABB70
XX ABB70
XX Drosc
XX
                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 36981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB70063;
   interactions
                                                                                                                                                                                                                                                                  (PEKB )
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                                                                                                                 2001-656860/75
DB; ABL14166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADX72179 standard;
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No. 9.4e-21;
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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production, lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; Unidentified yield; plant growth; plant protein content.

US2004034888-A1

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The invention describes a recombinant DNA construct comprising a conjunct polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or byproviding improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert
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Matches 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 697
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05-NOV-2001;
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(TABA/)
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TABASKA J E.
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VSSPPQVEKTSPPPAPLSSPP--LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTP--
                                                                                                                                                                         APQQPESPA-PHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAP-----
                                                                                                                                                                                                                                                PPTPPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPP------RPPTPQTPTG 163
                                                                                                                                                                                                                                                                                    SPPPPAPVASPPPPVKSPPPPTPVAS--PPPPAPVASSPPPMKSPPPPTPVSSP-PPPEK 162
                                                                   SPPPAPLSSPPPAPQVK
                                                                                                   ABPPT-----RPAPQHSRRARRGHRYRTDTBRNVGKVATGPSIQ-ARLRABBASGAQLAP 265
                                                                                                                                         PPSSPEKPSPPKEPVSSPPQTPKSSPPP----APVSSPPPTPVSSPPALAPVSSPPSVKS
                                                                                                                                                                                                                                                                                                                       -PPPP----PPPP---PTPMPIAAGEPPSPEPAASKP----PTPPMPIAGPEPAPPK 113
                                                                                                                                                                                                                                                                                                                                                                                               PHEGMEAPDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSERFVSAPPP---
                                                                                                                                                                                                                                                                                                                                                           PVKSPPPPAPVASPP---PPEKSPPPPAPVASPPPPVKSPPPPT----LVASPPPPVK 105
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Pred. No. 6.9e-18;
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HANZEL D F
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splicing event; genomic alteration.
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gene expression analysis, splicing events, for asse New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues. assessing genomic

Claim 45; SEQ ID NO 32198; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide consequences in the specification, or their complements or fragments, and consequences in the specification, or their complements or fragments, and consequences in the specification, or their complements or fragments, and consequences in the specification, or their complements or fragments, and consequences fully defined in the specification. The probe is a single exon probe that conding at least 8 amino acid sequences conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-care addressable set of single exon nucleic acid probes for measuring human cells or tissues. Also included are a spatially-care addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an constrains and a computer-readable storagen expression data by subscription, and a computer-readable cared methods of selling and/or licensing single exon probes or microarrays to the above-mention and apparatus are useful in gene expression data by subscription, and a computer-readable cated above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying the manual expression of the probes may be used as tools for murveying the manual expression and apparatus are useful in microarrays. specific exon, in constructing genome-derived single exon microarrays that

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Matches 101
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06-SEP-2001; 2001US-0094993.

25-QCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.
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   New antisense nucleic acids, for homologous nucleic acids
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Carr G
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Pred. No. 1.3e
22; Mismatches
   useful for identifying proteins or screening required for cellular proliferation to
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                                                                                                                                                                                                                                 Haselbeck R, Yamamoto R,
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                                                                                                                                                                                                                                 Ohlsen
Forsyth
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                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
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isolate candidate molecules for rational drug discovery programs

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CC (1) a vector comprising a promoter operably linked to the nucleic acid; (2) a host cell containing the vector; (3) an isolated CC encoding a polypeptide whose expression is inhibited by the antieense CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the CC antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway (CC required for proliferation, or that inhibite schlular proliferation; (8) cor a gene on which the test compound that inhibits proliferation; (8) cor a gene on which the test compound that inhibits proliferation of an CC compound; a activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an CC compound; a ctivity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an CC compound; a ctivity; (11) a culture comprising strains in which the gene compound that inhibits are useful for strains; or (13) identifying the target of a compound that inhibits the compound that inhibits are useful for compound; or cellular proliferation of an collaction of an culture or collection of constrains; or screening for homologous nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational constrains; or for screening homologous nucleic acids required constrains and constrains in cells other than S. aureus, S. typhimurium, constrains in proliferation for the printed specification, but was obtained constraint of the printed specification, but was obtained constraint of the printed specification, but was obtained constraints of the constraints. Sequence 598 the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: ftp.wipo.int/pub/published\_pct\_sequences invention relates to an isolated nucleic acid comprising any one A.

S S δ 맑 Ş 밁 S 문 S 뭉 S 片 밁 밁 Matches 134; Query Match Local Similarity 374 434 110 319 AAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVKKVKPQKPKATK----PP 224 124 170 VAPWPPLPPLPNNHP-PAPPSAPVPGVPLAPLPISGRPVRAWVGSLIALRICCCRVCSGV 50 44 -KPNGQTPPPTSDDLSERFVSAPPPPP-----PPPPPPPPPPP--MPIAAGEPPSP--EP ø APPAPPVPPAPAKOP-----PPAPPAPPAPLSRPAFPPAPPASKPSPPTPPAPPEP AASKPPTPPMPIAGPEPAPPKPPTP----PMPIAG-----SRPNPPLPPVPPEPISKAAPPVPPVPPWPVVPMPPDPPVPTPDRIPPAPPDPPSPPSAP SPPFPPDPPAPPVPA----SVAPPAPPTP---RLSMPASPPAPPFPPTLIMLVPPLPPVPPAPNSPPEPPSPPAPPPKMPNPPGPPVPPAPN -----APPPPSGLDPPLPPAPPAAP RRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAP----GTEP--SPAPLGQP QQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEP--PPAPSRPSASPAEPPTRPAPQHS LAGALNPSRPSSCPPKPPAPAVPAGAPVPPLPPLPPLPISTPLPPAPPLPPLPALPTSPG -----PEPAPPKP-----PTPPMPIAGPAPTPTBSQLAPPRPPTPQTPTGAP FAPNPPAPPAPPLANSPPVPPAPAVPPAPIKFWERAAWPPVPAAPRNKPASPPRPPAPPV 109 FRPHEGMEAPDDMAAQPFFDPSASFPPAP------ASANLP-----Conservative 11.7**%**; 28.0**%**; 22; Score 416; DB 6 Pred. No. 1e-17; ---APPTRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQH Mismatches PSANSPPFPPAPPAPPVAPKAAANPP 165, 6; Length 598; Indels 158; Gaps 484 318 277 223 288 165 228 169 3 123

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Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide obtainable from a species of Mycobacterium and is immunoreactive with sera from a human, animal or avian species previously exposed to the Mycobacterium but is not immunoreactive with sera from a human, animal or avian species not previously exposed to Mycobacterium. The composition and methods are useful for diagnosing, preventing or treating tuberculosis or other diseases or conditions associated with M. tuberculosis or related organisms. This sequence represents the Mycobacterial antigen C17 matures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polypeptides derived from Mycobacterium tuberculosis related organisms, useful for diagnosing, preventing or treating tuberculosis or other diseases associated with M. tuberculosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO
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RRARRGHRYRTDTERNVGKVATGPSIQA----RLRAEEAS--GAQLAPGTEPSPAPLGQP
                                                                                                                                                                                                                                                      PPKPPTPPMPIA-GPEPAPPKPPTPPM-----PIAGPAPTPTESQLAPPRPPTPQTPTG 163
                                                                                                                                                                                                                                                                                                              PPAPKRMPALPPAPPAPPSPPTSWLAVPVPPVPPVPPLPVKMPPSPPVPPPPPABPBTPN 173
                                                                                                                                                                                                                                                                                                                                                                                                                              LEAPNPPVPPAPPGPNSAPAPPMPPTPPLPPVPPGSGAPRPVPAVPP------M 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEAPD------DMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSERFVSA
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                                                                                     PPAPPMPPAPNSPAAPP----SPPSPPVPVPPTPPGPPAPPENSSPPAPPAAPP--
                                                                                                                                          APOQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHS
                                                                                                                                                                                                  PPAPPAPPLENSPPPPPVPPVPPLTLNPPVPPAPPAANTSNSPLRPPAPPAPPLKPG
                                                                                                                                                                                                                                                                                                                                                                   PP-----PPPPPPPPPPT-----PMPIAAGEPPSPEPAASKPTPPMPIAGPE-PA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 410.5; DB 9
Pred. No. 1.4e-17;
0; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
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RESULT 15
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                                                                                                                                                     Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                 This novel 74 kDa protein is encoded by an open reading frame of a Mycobacterium tuberulosis DNA fragment (see AAT93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAW31851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and anti-mycobacterial drugs. (Updated on 25-MAI 2003 to correct PR field.)
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Fig 13; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA and related proteins or RNA derived from M. tuberculosis - used for diagnosis of mycobacterial infections, monitoring vaccination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Singh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW31852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                development of anti-mycobacterial agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-549750/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9741252-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibiotic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuberculosis; mycobacteria;
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27-APR-1998
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                                           LANSPPLPPAPPTPAGTPPAAPWPPVPAAPKSKPASPPRPPAPPMPATPMEFPPLPPVPP
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                                                                                                 APNSPPFPPFPPAPKFVPAPPVPPVPNSPPFPPPPAALNPP----
                                                                                                                          APDDMAAQPF----FDPSASFPPAPASANLP--KPNGQTPPPTSDDLSERFVSAPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSYLAPPTRPAPTEPPPSPSPQRNSGR 304
                                                                    ----PPPPPPPPTP--MPIAAGEPPSPEPAASKPPTPPMPIAGPEPA----PPKPPTPP 118
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                                                                                                                                                   Score 410.5; DB
Pred. No. 3e-17;
6; Mismatches 16
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Search completed: April 14, 2006, 17:18:35 Job time: 262.049 Becs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                   US-10-620-246-70
3552
1 MAADYDKLFRPHEGMEAPDD......RKVLELAAALSDDFERAGRR 666
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                                                                                                                                                                                                                                                                           283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                             summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

45 334.5			42 337		40 337.5		38 338.5		36 340		34 341		32 343		30 343.5
9.4	9.4	9.5	9.5	9.5	9.5	9.5	9.5	9.6	9.6	9.6	9.6	9.6	9.7	9.7	9.7
539	369	761	895	1611	328	303	461	353	839	283	240	240	710	416	727
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	8
T28770	S20500	C84672	C86371	T38236	JQ0985	S28264	T10741	S36438	T04859	S13383	A24264	B24264	D96728	JU0465	C84534
hypothetical prote	hydroxyproline-ric	hypothetical prote	99.7K hypothetical	hypothetical prote	hydroxyproline-ric	hydroxyproline-ric	extensin-like prot	EPPT protein - hyd	extensin homolog F	hydroxyproline-ric	proline-rich prote	proline-rich prote	hypothetical prote	extensin precursor	hypothetical prote

## ALIGNMENTS

RESULT 1
B70803
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Dete: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Accession: B70803
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authores: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Cross-references: UNIPROT:069740; UNIPARC:UPI00000D105D; GB:AL1022120; GB:AL123456; NI
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3876
Query Match
Dest Local Similarity 100.0%; Score 3552; DB 2; Length 666;

Matches	666; Conservative 0; Mismatches 0; Indels 0; Gaps	٥,
β	1 MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAPASANLFKPNGQTPPPTSDDLSER 60	
Db	1 MAADYDKLFRPHEGMEAPDDMAAQPFFDPSASFPPAFASANLFKPNGQTPPPTSDDLSER 60	
ş	61 FVSAPPPPPPPPPPPPPPPPPPPPNPIAAGEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP 120	J
DЬ	61 FVSAPPPPPPPPPPPPPTPMPIAAGBPPSPBPAASKPPTPPMPIAGPEPAPFKPPTPPMP 120	J
Qy	121 IAGDEPAPEKPPTPEMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP 180	J
В	121 IAGDEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP 180	٠
Ş	181 HQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHSRRARKGHRYRTDTERNV 240	_
DЬ	181 HOPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPOHSRRARRGHRYRTDTERNV 240	Ŭ
\$	241 GKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPSPSPSPQR 300	_
DЬ	241 GKVATGPSIQARLRABEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQR 300	٠
Ş	301 NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK 360	_
Db	301 NSGRRAERKVHPDLAAQHAAAQPDSITAATTGGRRRKRAAAPDLDATQKSLRPAAKGPKVK 360	_
Ą	361 KVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHARVRBNPRGSYQIA 420	

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Conserved hypothetical protein ML0048 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H86914
C;Accession: H86914
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler,
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.;
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Residues: 1-586 <STO>
A;Residues: 1-586 <STO>
A;Residues: 1-586 <STO>
A;Residues: 1-586 <STO>
A;Residues: Turrosom.common training.common common com
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A;Gene: ML0048
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Matches 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAADYDKLFREHEGMEAPDDMAAQPFFDPSASFPPAPASANLFKPNGQTPPPTSDDLSER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    L----PPNPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---PRSPAASLMP
                                                                                                                                                                                                RARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDFIYKRKVLELAAALSDDF
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                                                                                                TRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD
                                                                                                                                                   HARRGHHRDETQQANPASATEPMIAPRARTAE---LRQAPHAAAEPAP--
                                                                                                                                                                                                                                                                                                                                                                                                  IAGPEPAPP------KPPTPPMPIAGPAPTPTESQLAPPRPTPQTPTGAPQQPB
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ATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELD
                                                 ----TQHLTRPDGLVSHRTALHDS-TATSAIGVQTGRST----
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A.; Hamlin, N.;
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T10030

Typothetical protein MLCB628.11c - Mycobacterium leprae
C;Species: Mycobacterium leprae
R;Eiglmeier, K; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization: Use of an ordered cosmid library to deduce the genomic organization: T10030
A;Reference number: Z16917; MUID:93188700; PMID:8446027
A;Accession: T10030
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-478 < EIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:033082; UNIPARC:UPI00000B6649; EMBL:Y14967; NID:g2370268; C;Genetics:
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     DADTSCGNLADRAGRESEANIADLLADKDVKSYNDIRTHTSVNAVNLEVLPAAEYSTAQH
                                              DADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQR
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R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; Ho; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.; Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0530
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A; Accession: E70545
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                                             HIAAGTBISLDLLDPIYKRKVLBLAAALSDDFBRAGRR 666
                                                                                                                                                                                                                                                                                      ASSDAFSADDYTRTLDILERFYGLVLTDCGTGLLHSAMSAVLPRSDVLVVVSSGSIDGAR
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                                                                                                                        SAAATLDWLQAHGHDDQVRNSIAVVNAVRPRAGKVDVGKVVEHPSRRCRAVRVV--PFDP
                                                                                                                                                                                           QASVALDWLRUNGYQDLASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDR 628
                                                                                                                                                                                                                                                                                                                                                             SAQRALSDADWHFIADPASRFYNLVLADCGAGFFDFLTRGVLSTVSGVVVVASVSIDGAQ 568
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ilarity 29.9%;
Conservative 6;
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; Pred. No. 2.6e-17; 
62; Mismatches 167; Indels 1
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Holroyd, !
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C;Accession: G8441
C;Accession: G8441
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C;Accession: G.W.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
G86441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
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extensin-like protein - maize
C:Species: Zea mays (maize)
C:Species: Zea mays (maize)
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49915
Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
submitted to the EMBL Data Library, June 1994
A;Description: Pex genes: pollen-specific genes with extensin-like domains.
A.Reference number: S49915
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A;Molecule type: DNA
A;Residues: 1-1188 <RUB>
A;Cross-references: UNIPROT:Q41805; UNIPARC:UPI00000A1616; EMBL:Z34465; NID:g600117;
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S49915
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910 PIVKSSPPPAMVSSPPMTPKSSPPPVVVS
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                                                                                                                                                                  SSPPLAPVSSPPQVEKTSPPPAPLSSPP--LAPKSSPPHVVVSSPPPPVVKSSPPPAPVSS
                                                                                                                                                                                                                                                    SPPSVKSSPPPAPLSSPPPAPQVK-------SSPPPVQVSSPPPAPK 799
                                                                                                                                                                                                                                                                                                                                                                             TPQTPTGAPQQPESPA-PHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAP------
                                                                                                                                                                                                                                                                                                                                                                                                                      VSSPPPPEKSPPPPPPAKSTPP-PEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPPQEKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDDMAAQPFFDPSASFPPAPASANLPKPNGQTPPPTSDDLSERFVSAPPP----PPPP--
                                                                                                                      PORNSGRRABRRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGP 357
                                                                                                                                                                                                           SGAQLAP----
                                                                                                                                                                                                                                                                                           SRPSASPAEPPT----RPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQ-ARLRAEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PPPP---PPTPMPIAA-----GEPPSPEPAASKPPTPPMPIAGPEPAPPKPPTPPMP 120
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                                                                               ---KPASPPAHVSSPPEVVKPSTPPAPTTVISPPSEPKSSPPPTPVSLPP
                                    ----PQKPKATKPPKVVS
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938
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PI

#text\_change 09-Jul-2004

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A;Reference number: A86141; MUID:21016
A;Accession: G86441
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1201 <STO>
A;Cross-references: UNIPROT:Q9C6S1; UN
C;Genetics:
extensin homolog T9E8.80 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 C;Accession: T06291 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I submitted to the Protein Sequence Database, April 1 A;Reference number: Z15588 A;Accession: T06291 A;Molecule type: DNA
                                                                                                                                                      RESULT
T06291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                        ASKIELKTL-AEEMQAATKGLEKVEQELMA
                                                                                                                                                                                                                                                        VNAVNLEVLPAPEYSSAQRALSDADWHFIA
                                                                                                                                                                                                                                                                                                                          LDADPGAGN---
                                                                                                                                                                                                                                                                                                                                                            CEQVPRIEAKLRVFGFKITFASQVEELKSCLNTINAATKEVKESAKLRQIMQTILTLGNA
                                                                                                                                                                                                                                                                                                                                                                                             VRRNPRGSYQIAVVGLKGGAGK-----A
                                                                                                                                                                                                                                                                                                                                                                                                                              EIMLTKIKIPL-POMLSAVLALDSLALDIDQVENLIKFCPTKEEMBLLRNYTGDKEMLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHALTRINLGLSPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----rrkkaapdldatq-kslrpaakgpkvkkvkpqkpka-tkppkv--vsqrgwrhw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLAPPTRPAPTEPPPSPSPORNSGRRAERRYH-PDLAAQHAAAQP---DSITAATTGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STPPPPPPPPPKANISNAPKPP---APPPLPPSSTRLGAPPPPPPPPPLSKTPAPPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQPESPAPHVP----SHGPHQPRRTAPAP-PWAKMPIGEPPPAPSRP-SASPAEPPTRPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPSPSQPPPPPPPPPPPTSTTSFSSPSQPPPPPPPPPPTSTTSFSSQPPPPPPPPSFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HESSEEPHEFSHHHHHEIPAKOSVONPLNLPSDPPSSGDHVTLLPPPPPPPPPPPPTSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADTOKQENOPRAPEIDISELESIFSAVSDTTAKKSTGRRGSSISKPEKVQLVDLRRANNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPPPPPPPPPSFGSTGNKRQAQPPPPPPPPPPPTRIPAAKCAPPPPPPPPTSHSGSIRVGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KPPTPPMP---IAGP--EPAPPKPPTPPMPIAG----PEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERFVSAPPPPPPPPP------PPPPPPTPMPI-----AAGEPPSPEPAAS---
                                                                                                                                                                                                                                                                                           LNQGTARGSAVGFKLDSLLKLSDTRARNNKMTLMHYLCKLVGEKMPELLDFANDLVHLEA
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24.6%;
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                                                                                                                                                                                                                                                                                                                         ----LADRVGRQSGATIADVLAE-----KELSHYNDIRAHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 414.5; DB 2;
Pred. No. 1.2e-11;
67; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIPARC:UPI000009C9CB; GB:AE005172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082
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                                                      I.; Mewes, H.W.; Mayer, K.F.X.;
1999
                                                                                                     #text_change 09-Jul-2004
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                                                                       Schue
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A;Residues: 1-760 <BEV>
A;Cross-references: UNIPROT:Q9TOX5; UNIPARC:UPI000009FB81; EMBL:AL049608
A;Rxperimental source: Cultivar Columbia; BAC clone T9E8
C;Genetics:
C;Genetics:
A;Map position: 4
A;Note: T9E8.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                           extensin - Volvox carteri (fragment)
c;Species: Volvox carteri
c;Species: Volvox carteri
C;Date: 04-Dec-1992 #seguence revision 04-Dec-1992
C;Accession: $22697; $21006
                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-464 <HALL>
A;Cross-references: UNIPROT:Q41645; UNIPARC:UPI000009F7C8;
                                                                                                                                                                                                                                                                                                                                                                                                                           R; Brtl, H.; Hallmann, A.; W
EMBO J. 11, 2055-2062, 1992
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                                                                                                                                                                                                                                                                                                                                                                                          A; Title: A novel extensin that may organize extracellular A; Reference number: S22697; MUID:92289669; PMID:1600938
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Best Local Similarity
                                                                                                                                                                                                                                                        Local
                                                                                                   699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393
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                                                                                                                                                                                                                                                       Similarity
                                                                TPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPAPAMAMPIGEPPPA
                                                                                                                               EPPSPEPAASKPPTPPMPIAG-PEPAPPKP-PTPPMPIAGPEPAPPKPPTPPMPIAGPAP
                                                                                                                                                                      STSPPPPARVSSSPPPATRSPPPRRITSPSPVLTASPPLPKTSPPPPPRVPPSPPPPVAS
                                                                                                                                                                                                    SASFPPAPASANLPKPNGQTPPPTSDDLSERFVSAPPP----PPPPPPPPPPPPPPIAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PPVYYSSPPPPPVYYSSPPPPPVHYSSPPPPEVHYHSPPPSPVHYSSPPPPPSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGQPRSYLAPPTRPA-PTEPPPSPSPQRNSGRRAERRVH-PDLAAQHAAAQPDSITAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SPAPH--VPSHGPHQPRRTAPAPPWAKMPIGEPPPAP--SRPSASPA-EPPTRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPPPVYSPPPPPVYSSPPPPPSPAPTPVYCTRPPPPPPHSPPPPPPPPPPPPPPPYYYSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPPTPMPIAAGEPPSPEPAASKPPTPPMPIAGP---EPAPPKPPTPPMPIAGPEPAPPK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPRPPVVTPLPPPSLPSPPPPAPIFSTPPTLTSPPPP-----SPPPPVYSPPPPPP
   PSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRABEASGAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGRRRKRAAPDLDATQKSLRPAAKGPKVKKV---KPQKPKA--TKPPKVVSQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRABEASGAQLAPGTEP-----SPAP
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                                      PSPPPPRSSPSPPPPVVSPPPPPPRASPPPPPASSPPPP-PRPPPPSPPPS
                                                                                                                                                                                                                                                       11.6%;
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                                                                                                                                                                                                                                         27;
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Pred. No. 8.2e-12;
20; Mismatches 145
                                                                                                                                                                                                                                       Score 413; DB 2;
Pred. No. 5.5e-12;
7; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - PCEBSPPPAPVVHHSPPPPMVHHSPPPPVIHQ
                                                                                                                                                                                                                                          101;
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                                                                                                                                                                                                                                                                      Length 464;
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Db 432 HLVSIVGHCISGDRRLLIYDYVSNNDLYFHLHGEKSVLDWATRVKIAAGAARGLAYLH 489	372 KATNGFSQENLLGEGGFGCVYKGILÞDGRVVAVKQLKIGGGQGDREFKAEVETLSRIHHR	350		228SPASSON SANGER STATE	176PSERPTQSPPSBERPTQSPPPSPPSBPSDRPSQSPPPPPBDTKPQPPRR	OV 174 HVDSHGPHOPRRTAPAPPPMAKMPIGEPPPAPSRPSASPARPPTRDAPOHSRRARR 228	degsaacoorangagaatacsatagaatacsatagaatacsatagaasatagasacoorangagasaspapal	21 MAAQPEEDBSASEPPAPASANLEKENGGTEPPTSDDLSEREVSAPPPPPPPPP	Query Match 11.3%; Score 402.5; DB 2; Length 708; Best Local Similarity 24.8%; Pred. No. 2.5e-11; Matches 179; Conservative 80; Mismatches 261; Indels 203; Gaps 32;	A; MOLECULE CYPE: LAWA A; Residues: 1-708 <sto> A; Cross-references: UNIPROT:Q9SX31; UNIPARC:UPI0000048426; GB:AE005173; NID:g5734709; PI C; Genetics: A; Gene: F24U5.8 A; Map position: 1</sto>	A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D96711 A;Accession: D96711 A;Status: preliminary A;Status: preliminary	A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	AKSULT 9 D96711  D96711  hypothetical protein F24J5.8 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: D96711 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000	
Qy 629 HIAAGTEISLDLLDPIYKRKVLELAAALSDDFERAGRR 666	Qy 569 QASVALDWLRNNGYQDLASRACVVINHIMPGEDNVAVKDLVRHPEQQVQPGRVVVMPWDR 628	Qy 509 SAQRALSDADMHFIADPASREYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQ 568 ;	QY 451 ALDADDGAGNLADRVGRQSGATIADVLAEKELSHYNDIRAHTSVNAVNLEVLDAPEYS 508  :    :    :    ::     :      :      :                Db 355 AVDVDADLGDLSARFRERGGPQTNIEHPVSARNAKRYADVRVHTVMNNDRLEMLGAQNDP 414	Qy 393 IGLSPDEKYELDIHARVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADRIL 450	QY 345 ATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALTRIN 392	Oy 292 PPPSPSPQRNSGRRABRRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD 344	Qy 232 YRTDTERNVGKVATGPSIQARLRABBASGAQLAPGTBPSPAPLGQPRSYLAPPTRPAPTB 291 :-  :-	Query Match 11.0%; Score 391.5; DB 2; Length 592; Best Local Similarity 28.0%; Pred. No. 6.6e-11; Matches 129; Conservative 71; Mismatches 201; Indels 59; Gaps 12;	A; Residues: 1-592 < STO> A; Cross-references: UNIPROT:Q9CCI1; UNIPARC:UPI00000C6D14; GB:AL450380; NID:g13092896; C;Genetics: A;Genetics: ML0798		Mycobacterium leprae -Apr-2001 #sequence_revision 20-Apr-2001 n: G87008 T.; Eiglmeier, K.; Parkhill, J.; James, l , R.M.; Devlin, K.; Duthoy, S.; Feltwell Rutherford, K.M.	RESULT 10 G87008 conserved hypothetical protein ML0798 [imported] - Mycobacterium leprae	QY 557 VVVASVSIDGAQQASVALDWLRNNGYQDLASRACVVINHIMPGEPNVAVKDLVR 610	Qy 446 ADRILALDADPGAGNLADRVGRQSGATIADV-LAEKELSHYNDIRAHTSVNAVNLEV 501

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C;Accession: B9636
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                   RESULT
A70598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-907 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 MPIAG--PAPTPTESQLAPPRPPTPQTPTGAPQQPESP----APHVPSHGPHQPRRTAP
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protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPP--PMPMGNSGSGGPPPPPPPMPLANGATPPPPPPPM-----A
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                                                                                             TKKSAYFLQİQADIAKYMTSINELKIEI
                                                                                                                                   -KELSHYNDIRAH----TSVNAVNLEV 501
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 Rv3888c
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27.0%; Pred. No. 1.3e-10;
Mycobacterium tuberculosis (strain
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C;Accession: A70598, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Comnor, R.; Davies, R.; Devlin, K.; Seeger, K.; Skelton, S.; Squares, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-341 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9834230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: Rv3888c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: 005456; UNIPARC: UPI00000D0F8A;
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;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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334 PDAERAAQ 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 PPKVVSQRGWRHWVHALT--RINLGLSPDEKYELDLHARVRRNPRGSYQIAVVGLKGGAG
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                                                                                                           AYLTERFTKVGAIVEAMPFDPHLAKG-----GIIDTVHELNKKSRLRLFBITAGLADKYV
                                                                                                                                                                 RHF-EQQVQPGRVV-VMPWDRHIAAGTBISLDLLDPIY-----KRKVLBLAAALSD---
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                                                     -DFERAGR
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Pred. No. 6.3e-11;
6; Mismatches 126;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230 hypothetical protein Rv3860 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004 C;Accession: A70656

A; Molecule type: DNA A; Residues: 1-390 <COL> Cross-references: UNIPROT:P96217; Experimental source: strain H37Rv

UNIPARC: UPI00000D0F42;

GB: Z83864;

GB:AL123456;

NID:

not shown

genome

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Best Local Si Matches 120; Query Match Similarity Conservative 10.8%; Score 383; DB 2 29.4%; Pred. No. 1e-10; Live 66; Mismatches 1 DB 2; 160; Length 390; Indels 62; Gaps 14;

RESULT 14  RESULT RESUL	Qy 271 PAPLGQPRSYLAPPTRPAPTEPPPSPSPGRNSGRRAERRVHPDLAAQHAAAQPDSITAAT 330 14 PHQPGTPRGYSPRPSGDRCPAPPPGR
RESULT 15  P75518  P75519  P75	Db 188 ASEIPPPPRHLPSPPASERP-STPPSDSEHPSPPPGHPKRREQPPPPGSKR 238  Qy 226 ARRGHRYRTDTERNVGKVATGPSIQARLHABEASGAQLAPGTEPSPAPLGQPRSYLAPPT 285  Db 239 PTPSPPSPSDSKRPVHPSPPSPPP

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	DRVGRQSG 470	463	ફ
560	AAAPRGGASSAAAPSAPAAARĠĠSĠAAGGAAGGAAAGAARPAARPAQTÞĠÁS	512	용
462	RVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLA	408	ફ
511	SAPAAAVPSRAPVSGGSVSAPRTAPTAPVAEQGEVPVSPS	472	₽
407	350 LRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHA .	350	Ş
471	<sup></sup> APAPVSEDRSDVSGLPRREDAPAESSPVAASPARGASSAPS	412	용
349	NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKS:	301	ક
411	352 PVTVTPRGETPDTAASAGTPSAGRVTPAPAPSASEGASAARTPGAGSQTPPIPATPIPAT 411	352	밁
300	249 -IQARLRABBASGAQLAPGTBPSPAP-LGQPRSYLAPTRPAPTBP-PPSPSPQR 300	249	ફ
351	292 ESSTPANPSAQTPPTPTRETAQTEASPAAPNSSAAAPNEPASEPVAGRPGTAASSPESAS	292	용
248	APSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPS	203	ફ

Search completed: April 14, 2006, 17:34:29 Job time: 42.0528 Becs

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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: uniprot_sprot:*
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06974 MYCTU
09CDD8 MYCLE
033082 MYCLE
034082 MYCLE
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035082 MYCHO
052342 NOCFA
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		BASGAQLAPGTBPSPAPLGQPRSYLAPPTRF 	IGEPPPAPSRPSASPAEPPTRPAPQHS 	IAGPAPTPTESQLAPPRPPTPQTPTGAP 	TPMPIAAGEPPSPEPAASKPPTPPMPIAGF 	DMAAQPFFDESASFPPAPASANLI 	; Score 3552; DB 2; ; Pred. No. 4.5e-138; 0; Mismatches 0;	788972; DOI=10.1073/pnas.113 amus JC., Medina N., Manso n S., Lacroix C., Monsempe C t J., Mayes R., Keating L., Cole S.T., Gordon S.V., Hewi ce of Mycobacterium bovis."; A. 100:7877-7882(2003); Genomic DNA. ical protein. W; 752E072FB8B10111 CRC64;	ted) sequence up sequence up amotation ND ALANINE R bacteridae; eae; Mycobac ex.	GNMENTS	2 Q41645 VOLCA 2 Q7XH56 ORYSA 2 Q8W5K6 ORYSA 2 Q9EQ7 ARATH 2 Q9EQ7 ARATH 2 Q9EQ12 MYCTU 2 Q55553 9ALPH 2 Q77CD4 9ALPH 2 Q77CD4 9ALPH 2 Q9C012 HUMAN 2 Q948Y7_VOLCA Q948Y7_VOLCA Q948Y7_VOLCA

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RX MEDLINE-98295997; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Gaznier T., Churcher C.M.,
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RA Cole S.T., Brosch R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
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RA Cole R., Davles R.M., Devlin K., Feltwell T., Rejandream M.A.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Murphy L.D., Cliver S., Seeger K., Skelton S., Squares S., Squares R.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,
RA Murphy L.D., Cliver S., Whitehead S., Barrell B.G.,
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT "Complete genome sequence.";
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT "Complete genome sequence.";
RL Nature 393:537-544(1998).
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laboratory Strains.";
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EMBL; BX842584; CAA17968.1; -; Genc
EMBL; AE000516; AAK48358.1; -; Genc
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069740; Q7D4P3;
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01-AUG-1998 (TYEMBLIPE). 07, Last sequence update)
13-SEP-2005 (TYEMBLIPE). 31, Last annotation update)
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OrderedLocusNames=MT3990,
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Bacteria; Actinobacteria; Actinobacteridae; Actinon
Corynebacterinaes; Mycobacterium;
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ID Q9CDD8;
AC Q9CDD8;
DT 01-UUN-2001 (TrEMBLrel. 17, C;
DT 01-UN-2001 (TrEMBLrel. 26, L;
DT 01-MAR-2004 (TrEMBLrel. 26, L;
DE Hypothetical protein ML0048.
GN OrderedLocusNames=ML0048;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; NCBI_TAXID=1769;
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Complete proteome; Hypothetical
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                                                                                                                                                                                                                                                                                                                                                   PNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSDDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVGLKGGAGKTTLTAALGSTLAQVRADRILALDADPGAGNLADRVGRQSGATIADVLAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAEPPTRPAPQHSRRARRGHRYRTDTERNV
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                                      Mycobacteriaceae;
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                                      Actinobacteridae; Actino
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Pred. No. 4.5e-138;
; Mismatches 0;
                                                                                                                                                                                   PRT;
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752E072FB8B10111
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annotation
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                                                       Actinomycetales;
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420 420 480 480

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Query Match
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RN MEDIJINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

RN MEDIJINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

RN MEDIJINE=21128732; PubMed=11234002; DOI=10.1038/35059006;

RN McOle S.T., Edglmeier K., Parkhill J., James K.D., Thomson N.R.,

RN Mheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.B.,

RN Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,

RN Mungall K.L., Bellin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

RN Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

RN Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

RN Murphy L.D., Oliver K., Ouail M.A., Rajandream M.A., Rutherford K.M.,

RN Murphy L.D., Oliver K., Simon S., Simmonds M., Skelton J., Squares R.,

RN AMIPHY S., Seeger K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RN Leproma, ML008; -.

RN Complete proteome; Hypothetical protein.
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565
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                                                                                                                                                                                                       TVSKYYNVMLADCGVGLFDFVTRGVLSTASGVVIVTSTSVDAARQAAIALDWLRHNGYQD
                                                                                                                                                                                                                                  PASRFYNLVLADCGAGFFDFLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGYQD
                                                                                                                                                                                                                                                                                                        RARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPP
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                                YKRKVLELAAALSDDFBRAGR
                                                                                                                            LASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTBISLDLLDPI
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                                                                                                 LLSRACVVINHVMPKBPNIASKDLVQQFBQQIQPGRVVVLPWDKHIAAGTBIRLDRLDPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L----PPNPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---
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49.2%;
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Pred. No. 4.4e-56;
6; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GAKKPSKVVAKRGWRHWVHTVTRINLGLSPDERYELD
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01-JAN-1998 (101-JAN-1998 (101
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; Y14967; CAA75199.1; -; Genomic_DNA.
PIR; T10030; T10030.
Hypothetical protein.
SEQUENCE 478 AA; 51997 MW; 1CB7DE7EEC1F2EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.

MEDLINE=93188700; PubMed=8446027;

Riglmeier K., Honore N., Woods S.A.,

"Use of an ordered cosmid library to

of Mycobacterium leprae.";

Mol. Microbiol. 7:197-206(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae.
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445
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                                                                                                        ALDWLRNNGYQDLASRACVVINHIMPGEBNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAA
                                                                                                                                                                                              ALSDADWHFIADPASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASV
                                                                                                                                                                                                                                                           LGLSPDEKYELDLHARVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADRILAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKPPTPPMPIAGPEP--APPKPPTPPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                        GVQTGRST-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPSRPSASPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEPPOWP-PARAPEHOFAKARPPSVPIPINEPSPAKPATPMPMTPIDGSORTPVTS----
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ilarity 51.1%;
Conservative 5
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21: 51997
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(TrEMBLrel. 05, Last sequence up
(TrEMBLrel. 25, Last annotation
protein MLCB628.11c.
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STRAIN-A3(2) / M145;

MEDLINE-21996410; PubMed-12000953; DOI-10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., D., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,

Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939124; CAA20252.1; -; Genomic_DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 1083 AA; 112083 MW; AD42EDFE4C
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Bacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. Genomic DNA. EMBL; BA00030; BAC70255.1; -; Genomic DNA. Complete proteome; Hypothetical protein. SEQUENCE 810 AA; 86244 MW; F8D19CDA203F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
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STRALTS-MA-4680 / ATCC 31267 / NCIME 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence and comparative analysis microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
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MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H.,
Sakaki Y., Hattori M., Omura S.;
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OrderedLocusNames=SAV2544;
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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Hypothetical protein.
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STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino
Shiba T., Hattori M.;
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Complete genomic sequence of Nocardia farcinica
Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).

APPO06618; BAD55149.1; -; Genomic DNA.

PEPTO; IPRO00194; ATPASE a/bcentre.

ITTE; PS00152; ATPASE ALPHA BETA; UNKNOWN 1.

Lete proteome; Hypothetical protein.

Lete proteome; Hypothetical protein.

RNCE 525 AA; 55760 MW; P404FE46B85AA09D CRC64
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49pothetical protein.
NUCLEOTIDE SEQUENCE.
STRAIN-IFM 10152;
PubMed=15466710; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino Shiba T., Hattori M.;
                                                                                                                                                                                                                                                                 OrderedLocusNames=nfa8310;
Nocardia farcinica.
                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinol Corynebacterineae; Nocardiaceae;
                                                                                                                                                                      NCBI_TaxID=37329;
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                                    MEDLINE=22803265; PubMed=12923100; DOI=10.1128/JB.185.17.5269-5274.2003; DOI=10.1128/JB.185.17.5269-5274.2003; Stecker C., Johann A., Herzberg C., Averhoff B., Got "Complete nucleotide sequence and genetic organizati kilobase linear plasmid of Rhodococcus erythropolis J. Bacteriol. 185:5269-5274(2003).
EMBL; AY223810; AAP73957.1; -; Genomic_DNA.
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SEQUENCE 446 AA; 47909 MW; 72C2A407D1C7F45C CRC64;
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Plasmid.
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STRAIN=BD2;
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Pred. No. 1.
  E5B072846B634D20
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RESULT 10
Q73SP7 MYCPA
ID Q73SP7;
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AC Q73SP7;
DT 05-UUL-2004 (TREMBLrel. 27)
DT 05-UUL-2004 (TREMBLrel. 27)
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DT 05-UUL-2004 (TREMBLrel. 27)
DE Hypothetical protein.
OR OrderedLocusNames=MAP4026;
OS Mycobacterium paratubercula
OC Bacteria; Actinobacteria;
OC Corynebacterineae; Mycobac
OC Mycobacterium avium comple
OX NCBL_TaxID=1770;
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RP NUCLEOTIDE SEQUENCE.
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RL Submitted (SEP-2003) to th
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Best Local Sim
Matches 191;
                                                                                         Hypothetical protein.
OrderedLocusNames=MAP4026;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium avium complex (MAC).
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Pred. No. 1e-18
77; Mismatches
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EMBL/GenBank/DDBJ databases
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RESULT : Q73VH1 | ID Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 VH1 | Q77 V
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Complete
SEQUENCE
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                                                                                                                                                                                                           Li L., Bannantine J., Zhang
Submitted (SEP-2003) to the
EMBL; AE017238; AAS05591.1;
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05-JUL-2004
                                                                                                                                                               SEQUENCE 388 AA;
                                                                                                                                                                                                                                                                                        STRAIN=k10;
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nes 153; Conserv
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ete proteome; Hypothetical protein.
NCE 434 AA; 46331 MW; 73A47808AD6D13B1 CRC64;
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EMBL/GenBank/DDBJ databases
-; Genomic_DNA.
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                                                    Score 532.5; DB 2;
Pred. No. 1.5e-14;
4; Mismatches 162;
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Pred. No. 6.3e-16;
B; Mismatches 185
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Q8VKJ9_MYCTU
                                                                                                                                 Query Match
Best Local S
Matches 155
                                                                                                                                                                                                                                         Hypothetical SEQUENCE 4
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OBVKJ9 MYCTU PRELIMINARY; PRT; 405 AA.

QBVKJ9;

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STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed-12218036;

MEDLINE-22206494; PubMed-12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

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Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 184:5479-5490(2002).
EMBL; AB000516; AAK44775.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome comparison of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aboratory strains.";
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                                                                         PQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPAPS----RPSASPAEP
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29.9%; Pred. No. 1.9e-14;
tive 62; Mismatches 167
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Cole S.T., Brosch R., Parkhill J., Garrier T., Churcher C.M.,

Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

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A Rogers J., Rutter S., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";

Nature 393:537-544(1998).

Nature 393:537-544(1998).
                                                Query Match
Best Local (
                                   Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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01-JUN-2003
                                                                                                                                PIR; B70545; B70545.
TubercuList; Rv0530; -.
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                                 62;
                                   Score 530; DB
Pred. No. 1.9e-
62; Mismatches
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EMBL; BX248335, CAD93405.1; -; Genomic DNA.

Complete proteome; Hypothetical protein.

Complete proteome; Hypothetical protein.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein Mb0543.
OrderedLocusNames=Mb0543;
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                                                                                                      POTETGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPS----RPSASPAEP
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PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAPL
                                                                                                                                                                     Conservative
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                                                                                                                                                                     62;
                                                                                                                                                               Score 530; DB 2;
Pred. No. 1.9e-14;
2; Mismatches 167
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                                                           -PTVQLPPVPSVGAPPAAAGGET
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74 PPPPTEMPIAAGEPPSPEPAASKPPTEPMPIAGPEPAPPKPPTPEMPIAGPEPAPPKPPT 133	PPSPAPSPPPPPSPBPSPAPPSPPP	PDDMAAQPFFDPSASFPPA	ery Match 13.9%; Score 495; DB 2; Length 3889; st Local Similarity 33.3%; Pred. No. 4.4e-12; tches 125; Conservative 35; Mismatches 143; Indels 72; Gaps 15;	3889 AA;	PR01218; PSTLEXTENSIN.	ATROPHIN.	InterPro; IPR006315; Autogramsporter:	GO; GO:0005199; F:structural constituent of cell wall; IEA.	-; Genomic_DNA.	and Minus	fenschmidt S., Umen J.G.,	STRAIN=CC-621; PubMed=15659633; DOI=10.1105/tpc.104.028035;	NUCLBOTIDE SEQUENCE.		ridiplanta ales: Chla	Name=SAD1; Chlamydomonas reinhardtii.	lutinin.	05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence up	26SSE8;	LT 15  OGSSES CHIRE PRELIMINARY: PRT: 3889 AA.	EEGAŠIALDRLRRETREALTĖLAAVV	629 HIAAGTBISLDLLDPIYKRKVLBLAAALSDDPBRAGRR 666	AHGHDDQVRNSIAVVNAVRPRAGKVDVGKVVEHFSRRCRAVRVVP	569 QASVALDWLKNNGYQDLASRACVVINHIMPGEPNVAVKDLVRHFEQQVQPGRVVVMPWDR 628	244 ASSDAFSADDYTRTLDILBRFYGLVLTDCGTGLLHSAMSAVLPRSDVLVVVSSGSIDGAR 303	509 SAQRALSDADWHFIADPASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQ 568	184 VAVDANPDRGTLSQKVPLETPATVRHLLRDADGIERYSDVRGYTSKGPSGLEVLASDSDP 243	450 LALDADPGAGNLADRVGRQSGATIADVLABKE-LSHYNDIRAHTSVNAVNLEVLPAPEYS 508	124 LINAGEGPRAAHLNDLVAQVNRPLRGCYRIAVLSLKGGVGKTTITATLGATFADLRGDRV 183	VRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTLAQVRADR	97ATTTLLRPVKP	332 GGRRRKRAAPDLDATQKSLRPAAKGPKVKKVKPQKPKATKPPKVVSQRGWRHWVHALT 389	76SPAERPPYRLEPVPHTPYPEL96	275 GQPRSYLAPPTRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATT 331	

Qy 359 VKKVKPQKPKATKPP 373	Qy 302 SGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAAPDLDATQKSLRPAAKGPK 358 :	Qy 247 PSIQAKLRABEASGAQLAPGTE-PSDAPLGQPRSYLAPPTRPAPTEPPPSPSPQRN 301   :	Qy         192 WAKMPIGEPPPAPSRPSASPAEP-PTRPAPQHSRRARRGHRYRTDTERNVGKVATG         246           b         :	Qy 134 PPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPP 191	Db 985 PEPPSPAPLPPPPSSPEPPSPAPPSPPPPSPEPPSPAPPSPPPPSPEPPSPAPPS 1038
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US-07-757-0228-84
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Sequence 10, Appl
Sequence 65, Appl
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Sequence 74, Appl
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Sequence 44, Appl
Sequence 142, Appl
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Sequence 46, Appl
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Sequence 40, Appl
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Sequence 61, Appl
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Sequence 12, Appl
Sequence 13, Appli
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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: OSTTINGER, Thomas
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT FILING DATE: 1998-03-30
EARLIER APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER FILING DATE: 1997-04-02
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EARLIER PILING DATE: 1997-04-03
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EARLIER FILING DATE: 1998-01-05
RUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 70
LENGTH: 666
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Best Local Similarity
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                                                                                           121 IAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP 180
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GENERAL INFORMATION:

APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: PLORIORER, Thomas
APPLICANT: ROSENKRANDS, Ida
APPLICANT: RELDINGH, Karin
APPLICANT: RELDINGH, Karin
APPLICANT: FLORION HULLER
TITLE OF INVENTION: NUCLER
CURRENT SERRORE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/050,739
CURRENT FLING DATE: 1998-03-30
EARLIER FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER FILING DATE: 1997-04-18
EARLIER FILING DATE: 1997-04-18
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EARLIER FILING DATE: 1997-04-18
SARLIER FILING DATE: 1998-01-05
NUMBER OP ESO ID NOS: 173
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ORGANISM: Mycobacterium tuberculosis
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             Conservative
                          44.3%;
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             Score 1575; DB 2;
Pred. No. 6.1e-103;
1; Mismatches 0;
                                         Length 308;
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LPYSSPPAPPACPVPGAPLAPLPISGR
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Sequence 10, Application US/09461774

Patent No. 6897481

GENERAL INFORMATION:
APPLICANT: CHUNG, Maxey Ching Ming
APPLICANT: CHUNG, Maxey Ching Ming
APPLICANT: LIN, Renee Lay Hong
TITLE OF INVENTION: Bacterial-derived molecules and therapeutic and
TITLE OF INVENTION: diagnostic uses therefor
FILE REFERENCE: 1781-0180P
CURRENT APPLICATION NUMBER: US/09/461,774

CURRENT PILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 386
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.6%; Score 410.5; DB 2; Best Local Similarity 33.3%; Pred. No. 4.2e-21; Matches 109; Conservative 20; Mismatches 119;
                                                                                                                                                                                                                                                                                                      114 PPAPKKMPALPPAPPAPPSPPTSWLAVPVPPVPPVPPLPVKMPPSPPVPPFPPABPETPN 173
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                                                 RRARRGHRYRTDTERNVGKVATGPSIQA----RLRAEEAS---GAQLAPGTEPSPAPLGQP
                                                                                                 PPAPPMPPAPNSPAAPP----SPPSPPVPVFPTPPGPPAPPEPNSSPPAPPAAP--
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Best Local Similarity
Matches 101; Conserv
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PATENT NO. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, JOSEPH
APPLICANT: PERRARI, Franco A.
TITTE OF INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TELEX: 910 277299 FHT UR
TELEX: 910 277299 FHT UR
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TOPOLOGY: linear
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TYPE: amino acid
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
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                                                                                                               TGPSIQARLRABEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQRNSG 303
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High Molecular Weight Collagen-Like
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Pred. No. 6.4e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 330;
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Sequence 65, Application US/07609716

301

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; Patent No. 5514581
; GRNERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Functional Recombinal
; TITLE OF INVENTION: Synthetic Protein Po
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
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US-08-475-411A-65
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                                                                                                Sequence 65, Application US/08475411A
Patent No. 6140072
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GENERAL INFORMATION:
APPLICANT: Perrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: rou. _____CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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REFERENCE/DOCKET NUMBER: A
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ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                         258 PGP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GSPGAPGPPG--PPGPPGPPGAPGPPGPPGPPGP-AGPVGSPGAPGPPGPPGPPGP
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Four Embarcadero Center,
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Suite 3400
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RESULT 7
US-08-478-029A-65
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Best Local &
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
APPLICATION NUMBER: US 07/269,716
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/269,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 04-NOV-1986
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
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APPLICATION NUMBER: US 07/114,618
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CURRENT APPLICATION DATA:
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Local Similarity 33.8%;
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TOPOLOGY: linear
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CITY: San Prancisco
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REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/475,411A FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 8.2e-18;
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                                                                                                 -GPPGAPGPPGPPGPPGPAG 301
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Best Local (
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
PRIOR APPLICATION NUMBER: US 07/114,618
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APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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245 TGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPSPQRNSG 303
                                                           194 KMPIGEP----
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Similarity 33.8%;
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Suite 3400
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Best Local Similarity
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: (617)876-5531
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
LENGTH: 941 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: GBEIT, LUBIN
NAME: GBEIT, LUBIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 106(17)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gesner
                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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FILING DATE: 19910910
CLASSIFICATION: 530
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6433142
                                                                                                                                                                           BPAPTTPKEPTPTTPKEPAPTTKEPAPTTP--KEPAPTAPKKPAPTTPKEPAPTTPKEPA 308
                    PAPTTPKKPAPTTPKBPAPTTPKBPAPTTTKKPAPTAPKBPAPTTPKETAPTTPKKLTPT 428
                                                     PTP----PMPIAGPEPAP--PKPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
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87 CambridgePark Drive
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29-JUN-1990
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                                                                                                                                    -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
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US-07-757-022B-84
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Patent No. 64
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                                                                                                                                                                                         PILING DATE: 18-JAN-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10
PILING DATE: 29-JUN-19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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                                                                     APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/643,502
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION
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                REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 29-DEC
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RESULT 10
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TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                              Sequence 74, Application US/07757022B Patent No. 6433142
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02140
                                                        CITY: Cambridge
                                                                          STREET:
                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPTSTTSDKPAPTTPKGTAPTTPKBPAPTTPKBPAPTTPKGTAPTTLKEPAPTTPKKPA-
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                                                                        B: Genetics Institute,
87 CambridgePark Drive
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Pred. No. 3.8e-16;
                                                                                              Inc
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Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 29-JUN-1990
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LENGTH: 1038 amino aci
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CBerr, Luann
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID TOPOLOGY: linear
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 TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR
                                                                        SQRGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
                                                                                                                 --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
                                                                                                                                                  AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV
                                                                                                                                                                                                                             EPS-----PAPLGOPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA
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                                                                                                                                                                                                                                                                                                     P----PTRPAPOHSRRARRGHRYRTDTERNVGKVATGPSIOARLRABEASGAOLAPGT--
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                                                                                                                                                                                                                                                                                                                                                                                                                     PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                PTP----PMPIAGPEPAP--PKPPTP----PMPIA--GPAP-TPTESQLAPPRPPTPQ
                                         SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK------
                                                                                                                                                                                          EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
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ilarity 25.4%; Pred. No. 3.9e-16;
Conservative 58; Mismatches 259;
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                                             -EPGVPTT
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376 720 431

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605 320 493 213 553 267

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-757-022B-58
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US-07-757-022B-58
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Best Local Similarity
Matches 146; Conserv
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APPLICANT: Gesner,
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)876-585
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino aci
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-JUN-1990
PRIOR APPLICATION UNBER: 207/457,196
APPLICATION NUMBER: 1000
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910 CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
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                                                                              EPAPTTPKEPTPTTPKEPAPTTKEPAPTTP--KEPAPTAPKKPAPTTPKEPAPTTPKEPA 416
                                                                                                                     DPSASFP---PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPP-----PPPPPPPPTPM 80
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                                         PIAAGEP---
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PITTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 476
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                   1049 amino acids
                                                                                                                                                            Conservative
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                                                                                                                                                        9.8%; Score 347; DB 2; Length 1049;
25.4%; Pred. No. 3.9e-16;
ative 58; Mismatches 259; Indels 11
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                                     PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
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                                                                                                                                                        Gaps
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US-07-757-022B-104
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                                                                                                                 APPLICATION NUMBER: US/07/
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                     APPLICATION NUMBER:
FILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts COUNTRY: U.S.A.
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SYSTEM: PC-DOS/MS-DOS
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    08-AUG-1989
                                                             29-DEC-1989
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                      US 07/390,901
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Best Local S
Matches 146
                                                                                                                            Sequence 44, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino acids
               TITLE OF INVENTION: ME NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                           APPLICANT: Geener, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
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ee 146; Conserv
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ADDRESSEE:
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Genetics Institute,
                              Megakaryocyte Stimulating : 143
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US-07-757-022B-44
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
PILING DATE: 08-AUG-1989
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CBerr, Luann
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Massachusetts
--PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
                                          AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                          EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
                                                                                                                                  EPS-----PAPLGOPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA 320
                                                                                                                                                                               PAPTTPKEPAPTTPK-----ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
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25.4%; Pred. No. 4.9e-16;
vative 58; Mismatches 259;
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RESULT 14
US-07-757-022B-42
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                                                                                                                                    TOPOLOGY: 11;
; MOLECULE TYPE:
US-07-757-022B-42
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                                                                               Query Match
Best Local (
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                                                           Matches
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                                                                                                                                                                                     TELEPAX: (617)876-5851
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino aci
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPB: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UPPILING DATE: 19910910 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                         al Similarity
146; Conserv
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7: U.S.A.
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                                                                                                                                                                                                           1311 amino acids
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                                                             Conservative
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                                                                                                                                                                                                                                                                                      (617)876-1170
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08-AUG-1989
                                                                         9.8%;
25.4%;
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                                                                                                                                                                                                                                                   42:
                                                       ; Score 347; DB 2; Length 1311;
; Pred. No. 5.1e-16;
58; Mismatches 259; Indels 112; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 64333...

GENERAL INFORMATION:

APPLICANT: Gesner, Thomas G.

APPLICANT: Clark, Stephen C.

APPLICANT: Turner, Katherine

APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-07-757-022B-142
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Patent No. 643
                                   APPLICATION NUMBER: US/07/
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/
PRIOR APPLICATION NUMBER: US 07/
                                                                                                                                                                                                                                                                                                                    STREET: b, STREET: Cambridge CITY: Cambridge CTATE: Massachusetts
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Turner,
APPLICANT: Hewick,
TITLE OF INVENTION:
     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          ZIP:
                       FILING DATE:
                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK------BPGVPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPS-----PAPLGOPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
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                                                                                                                                                                                                                                                                                                                                                                                                       Genetics Institute,
                                                                                                                                                                                                                                                                    Floppy disk
                       29-JUN-1990
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143
                                           US 07/546,114
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                                                                                                US 07/643,502
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Search completed: April 14, 2006, 17:37:56 Job time: 63.5832 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBetr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/INFORMATION:
TELERHONE: (617)876-1170
TELERHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENCTH: 1313 amino acids
TYPE: AMINO ACID
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                                                                              871
                                                                                                                  490 AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                         811 KTPÄÄTKPEMTTTAKÖKTTERÖLRTTPETTTAÄPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                               432 TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 DPSASEP---PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPP-----PPPPPPPPTPM
                                                                                                                                                                                                                                     SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK-----EPGVPTT
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                                                                            STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTE
                                                                                                                                                                                                                                                                          SQRGWRHWVHALTRINLGLSPDEKYELDLHAR----VRRNPRGSYQIAVVGLKGGAGKT
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                                   re greater than or equal to the score of the result beir is derived by analysis of the total score distribution.
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(c) 1993 - 2006 Biocceleration
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US-10-980-190-94
US-10-980-190-10
US-10-620-246-94
US-10-080-170-10
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697	708	521	275	272	241	296	531	554	466	445	270	547	280	298	376	321	
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US-10-425-114-41545	US-10-425-115-313976	US-10-437-963-179715	US-10-425-115-315706	US-10-437-963-197111	US-10-424-599-163337	US-10-424-599-224246	US-10-437-963-112246	US-10-437-963-174151	US-10-437-963-167964	US-10-437-963-161789	US-10-437-963-197222	US-10-437-963-102579	US-10-425-115-231956	US-10-437-963-147019	US-10-437-963-154970	US-10-425-115-202316	CO FO FOR
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## ALIGNMENTS

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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: CONTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 030/50,739
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-01-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
NUMBER OF SCO. TD NOS. 173
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 70
LENGTH: 666
TYPE: PRT
ROGANISM: Mycobacterium tuberculosis
US-09-791-171-70
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Matches
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                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                 Local
                          121 IAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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121
                                                                                                                                                                                                                                                                             666;
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                                                                                                                                                                                                                                                                                                   Similarity
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IAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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Sequence 70, Application US/09804980
Publication No. US20030147897A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
ITITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 70
LENGTH: 666
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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           IAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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Sequence 640, Application US/10080170

; Dendication No. US20030129601A1

; GENERAL INFORMATION:
APPLICANT: COLE, S.T.

APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TRACETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

; CURRENT APPLICATION NUMBER: US/10/080,170

; CURRENT APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 652

; SOFTWARE: Patentin Ver: 2.1

; SEQ ID NO 640

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US-10-080-170-640
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GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malome, Cheryl
APPLICANT: Malome, Cheryl
APPLICANT: Malome, Cheryl
APPLICANT: Malome, Kari
APPLICANT: Consen, Kari
APPLICANT: Consen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
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PRIOR APPLICATION NUMBER: G0/207,727
PRIOR APPLICATION NUMBER: G0/207,727
PRIOR APPLICATION NUMBER: G0/20,335
PRIOR APPLICATION NUMBER: G0/230,335
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RESULT 5 US-10-620-246-70 ; Sequence 70, Application US/10620246 ; Publication No. US20040115211A1

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TITLE OF INVENTION: DERIVED FRAGMENTS AND POLYPEPTIDE FRAGMENTS;
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION UNMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION UNMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 09/10,171
PRIOR APPLICATION NUMBER: 09/10,171
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/115,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 09/415,884
PRIOR APPLICATION NUMBER: 1999-01-21
PRIOR APPLICATION NUMBER: 1999-01-21
PRIOR APPLICATION NUMBER: 1999-01-21
PRIOR APPLICATION NUMBER: 1999-01-21
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Best Local Similarity
Matches 666; Conserv
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NUMBER OF SEQ ID NOS: 173
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                      KVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHARVRRNPRGSYQIA
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WELDINGH, Karin
FLORIO, Walter
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RASMUSSEN, Peter Birk
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NIELSEN, Rikke
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100.0%; Pred. No. 2.5e-180;
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Sequence 640, Application US/10080170

Publication No. US20040121322A9

GENERAL INFORMATION: US20040121322A9

APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS (TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: US/10/080,170

CURRENT APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR APPLICATION NUMBER: 50/270,123

PRIOR PILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 640

LENGTH: 666

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis
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US-10-080-170-640
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KVKPQKPKATKPPKVVSQRGWRHWVHALTRINLGLSPDEKYELDLHARVRRNPRGSYQIA
                                             NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK
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APPLICANT: COLE, STEWART
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 05394,0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 10/080,170
PRIOR APPLICATION NUMBER: 10/080,170
PRIOR RILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
SOFTWARE: PRIOR ASTELLATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
SOFTWARE: PRIOR ASTELLATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
SUMMBER OF SEQ ID NOS: 655
SOFTWARE: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mycobacterium tuberculosis US-10-468-356-640
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US-10-468-356-640
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Best Local S
Matches 666
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NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPKVK
                                                                                          GKVATGPSIQARLRAEEASGAQLAPGTEPSPAPLGQPRSYLAPPTRPAPTEPPPSPSPQR
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Pred. No. 2.5e-180;
Mismatches 0;
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APPLICANT: Brosch, Roland
APPLICANT: Majlessi, Laleh
APPLICANT: Demangel, Caroline
APPLICANT: Demangel, Caroline
APPLICANT: Demangel, Caroline
APPLICANT: Demangel, Caroline
APPLICANT: Demangel, Caroline
TITLE OF INVENTION: Identification of virulence associated regions RD1 and
TITLE OF INVENTION: RD5 leading to improve vaccine of M. bovis BCG and M.
TITLE OF INVENTION: microti
FILE REFERENCE: D20217
CURRENT APPLICATION NUMBER: US/10/510,021
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: BF 02/290864
PRIOR FILING DATE: 2003-04-05
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 66
LENGTH: 666
TYPE: PRT
ORGANISM: mycobacterium tuberculosis
FEATURE:
CONTEND INDEMATION: Drotein segmence By1876
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US-10-510-021-66
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APPLICANT: Cole, St
APPLICANT: Pym, Al
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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121 IAGPEPAPEKPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPESPAPHVPSHGP
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CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOPTWARE: PALENTIN PER. 2.0
SEQ ID NO 94
LENGTH: 308
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; LENGTH: 308
TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-94
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APPLICANT: NIELSEN, I
APPLICANT: OETTINGER,
APPLICANT: RASMUSSEN,
APPLICANT: ROSENKRANI
APPLICANT: WELDINGH,
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APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLERIC ACIDS FRAGMENTS AND POLYPEPTIDE
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
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RASMUSSEN, Peter Birk
ROSENKRANDS, Ida
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Sequence 94, Application US/09804980

Publication No. US20030147897A1

GENERAL INFORMATION:

APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter

TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 67001-2002.4

CURRENT APPLICATION NUMBER: US/09/804,980

CURRENT FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 257

SOFTWARE: Patentin version 3.0

SEQ ID NO 94

LENGTH: 308

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

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Best Local Similarity 99.7%;
Matches 307; Conservative
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Similarity 99.7%; Pred. No. 6.9e-76;
07; Conservative 1; Mismatches C
                  GBPNVAVKDLVRHFEQQVQPGRVVVMPMDRHIAAGTEISLDLLDPIYKRKVLELAAALSD
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Pred. No. 6.9e-76;
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Best Local Similarity
Matches 307; Conserv
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LENGTH: 308
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TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
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PRIOR APPLICATION NUMBER: 1281/98
PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
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APPLICATION NUMBER: 09/791,171
FILING DATE: 2001-02-20
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APPLICATION NUMBER: 10/138,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/116,673
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WELDINGH, Karin
FLORIO, Walter
  GEPNVAVKDLVRHFEQQVQPGRVVVMPWDRHIAAGTEISLDLLDPIYKRKVLELAAALSD
                      GBPNVAVKDLVRHFBQQVQPGRVVVMPWDRHIAAGTBISLDLLDPIYKRKVLELAAALSD
                                                                                                     AGPFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGYQDLASRACVVINHIMP
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RASMUSSEN, Peter Birk
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CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTMARE: PATENTIN Ver. 2.1
SEQ ID NO 10
LENGTH: 586
TYPE: PRT
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US-10-080-170-10
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APPLICANT: COLE, S.T.
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS,
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
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Best Local (
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Publication No.
585 LASRACVVINHIMPGEPNVAVKDLVRHFBQQVQPGRVVVMPWDRHIAAGTBISLDLLDPI
                                                                              525 PASRFYNLVLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLRNNGYQD
                                                                                                                                                         465 VGRQSGATIADVLAEKBLSHYNDIRAHTSVNAVNLEVLPAPBYSSAQRALSDADWHPIAD
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No. US20030129601A1
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49.2%; Pred. No. 2.9e-74;
tive 66; Mismatches 168
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RESULT 13
US-10-282-122A-63640
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63640
LENGTH: 586
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
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APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
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ISEPPQWPPAEAPEHQPAKAEPPSVPIPINEPSP----AKPATPMPMTPIDGSQR--
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Zyskind, Judith
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Malone, Cheryl
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Trawick, John
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Pred. No. 2.9e-74;
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PRIOR FILING DATE: 2001-02-22
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US-10-080-170-10
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
                                                                                                                                                                                                                                         / Match 43.6%; Score 1550; DB 4;
Local Similarity 49.2%; Pred. No. 2.9e-74;
nes 335; Conservative 66; Mismatches 168
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                                                 60 L----PROPPAASKSPLPPMPI--GSSVQPPPASSESPRAPMPVSAP---PRSPAASLMP
                                                                                         1 MAADYDKLERPHEGMEAPDDMAAQPFFDPSASEPPAPASANLPKPNGQTPPPTSDDLSER
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                                                                                                                                               MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ
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    --KPPTPPMPIAGPAPTPTESQLAPPRPPTPQTPTGAPQQPE 169
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SEQUENCE 10, Application US/10468356

Publication No. US20040197896A1

GENERAL INFORMATION:
APPLICANT: COLE, STEWART

ITILE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 05394.0019

CURRENT FILLING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: US/10/468,356

CURRENT FILLING DATE: 2002-02-22

PRIOR PILLING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR PILLING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 655

SEQ ID NO 10

LENGTH: 586

TYPE: PRT

ORGANISM: Mycobacterium leprae

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                                                                                                     h 43.6%; Score 1550; DB 4;
Similarity 49.2%; Pred. No. 2.9e-74;
35; Conservative 66; Mismatches 168;
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                                                                     MAADYDKI.FRPHEGMEAPDDMAAQPFFDPSASFPPAPASANI.PKPNGQTPPPTSDDLSER
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                                    MAADYDKLFRLDDGAYASPDQAAEQLFDDAPLYPPPIIPTCTTTPNGEVASP-MPDWSEQ
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YRRRILELAAALSDDFERAGR
                                  YKRKVLELAAALSDDFERAGR
                                                                                                            TVSKYYNVMLADCGVGLFDPVTRGVLSTASGVVIVTSTSVDAARQAAIALDWLRHNGYQD
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                                                                                                                                                                AGRESEANIADILIADKDVKSYNDIRTHTSVNAVNLEVLPAAEYSTAQHALSGEDWNFAAA
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                                                                                                                                                                                                                                                                                                                                                TRPAPTEPPPSPSPQRNSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKRAAPDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISEPPOWPPARAPEHOFAKAEPPSVPIPINEPSP----AKPATPMPMTPIDGSOR--
                                                                                                                                                                                                                                                                                                                      ----TQHLTRPDGLVSHRTALHDS-TATSAIGVQTGRST----
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Search completed: April 14, Job time: 238.816 secs 2006, 18:40:36

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Result
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Maximum Match 100%
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                388
375.5
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1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/US03_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/US03_NEW_PUB.pep:*
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(without alignments)
991.565 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration
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US-11-169-232-14
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     Sequence 95, Appli
Sequence 96, Appli
Sequence 96, Appli
Sequence 28799, A
Sequence 28799, A
Sequence 29818, A
Sequence 2501, Appl
Sequence 33, Appl
Sequence 84, Appl
Sequence 104, Appl
Sequence 60, Appl
Sequence 44, Appl
Sequence 42, Appl
Sequence 46, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 60, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 51, Appl
Sequence 52, Appl
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298	304	304	304.5	306.5	313.5	315.5	317.5	321	321	321	322.5	322.5	323	328	328	328	337	341	341
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US-10-995-561-988	US-11-036-256-159	US-11-036-256-158	US-11-036-256-31	US-11-108-172-1068	US-10-330-773-661	US-11-059-982-1	US-11-096-568A-12552	US-11-096-568A-30285	US-11-096-568A-30286	US-11-096-568A-30287	US-11-188-298-18316	US-11-087-099-7887	US-10-330-773-663	US-11-096-568A-27755	US-11-096-568A-27756	US-11-096-568A-27757	US-11-096-568A-29626	US-11-096-568A-28958	US-11-096-568A-28959
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
988, App	159, App		31, Appl	1068, Ap	661, App	1, Appli	12552, A	30285, A	30286, A	30287, A	18316, A	7887, Ap		27755, A	27756, A	27757, A	•	28958, A	28959, A

ALIGNMENTS

## ; FEATURE: ; OTHER INFORMATION: This sequence may encompass US-11-036-256-95 RESULT 1 US-11-036-256-95 NUMBER OF SEQ ID NOS: 173 SOFTWARE: PatentIn Ver. 3.3 SEQ ID NO 95 Sequence 95, Application US/11036256 Publication No. US20060026719A1 GENERAL INFORMATION: Matches Query Match Best Local Similarity PRIOR APPLICATION NUMBER: 60/602,562 PRIOR FILING DATE: 2004-08-18 PRIOR APPLICATION NUMBER: 60/582,027 PRIOR FILING DATE: 2004-06-22 PRIOR APPLICATION NUMBER: 60/536,486 PRIOR FILING DATE: 2004-01-14 APPLICANT: KIELISZEWSKI, MARCIA APPLICANT: XU, JIANEMG TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY FILE REPERENCE: 27211/04130 CURRENT APPLICATION UNMBER: US/11/036,256 CURRENT FILING DATE: 2005-01-14 CURRENT FILING DATE: 2005-01-14 LENGTH: 1000 TYPE: PRT ORGANIEM: Artificial Sequence PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid motif 154 RPPTPQTPTGAPQQPESPAPHVPSHGPHQPRRTAPAPPWAKMPIGEPPPAPSRPSASPAE 213 49 34 PPAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPMPIAAGEPPSPEPA 93 94 ASKPPTPPMPIAGPEPAPPKPPTPPMPIAGPEPAPPKPPTPPMPIAGPAPTPTESQLAPP 153 94; μ 48 פֿבּשְׁרֵישִׁישִׁישִׁישִׁישִּישִישִּישִישִישִּישִישִישִישִישִּישִישִישִּישִישִישִּישִישִישִּישִישִישִישִישִי Conservative 12.5%; 0; Score 444; DB 7; Length 1000; Pred. No. 4.4e-18; 0; Mismatches 115; Indels 56; 2-1,000 residues Length 1000; of. Gaps AND

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214 PPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGTEPSPAP 273

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RESULT 3
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US-11-036-256-5
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NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/11036256 Publication No. US20060026719A1 GENERAL INFORMATION:
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Best Local (
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CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR FILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR APPLICATION NUMBER: 60/536,486
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APPLICANT: XU, JIANFENGO
TITLE OP INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REFERENCE: 27211/04130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MOD_RES
LOCATION: (2)...(1001)
OTHER INFORMATION: This region may encompass 2 to 1,000 residues of
OTHER INFORMATION: Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid motif
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OTHER INFORMATION: Lys,
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ORGANISM: Artificial Sequence
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Similarity 35.5%;
                                                                                                       LGQPRSYLAPPTRPAPTEPPPSPSP 298
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Sequence 28799, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILLING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 28799
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US-11-096-568A-28799
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CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR FILLING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR FILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR PILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 173
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JUS: WARE: Patentin Ver. 3.3
SEQ ID NO 96
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Publication No. US20060026719A1
GENERAL INFORMATION:
APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: XU, JIANFENG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REFERENCE: 27211/04130
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LOCATION: (1001)
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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LENGTH: 717
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Indels Length

263;

53 97

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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; HAME/KEY: misc_feature
; LOCATION: (1)...(717)
; OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-28799
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US-11-096-568A-29818
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Sequence 29818, Application US/11096568A Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined
TITLE OF INVENTION: Therby
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Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383
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                                                                                                                                                                       MDQVARVLEGNISPSDL----NQGITPG
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                                                                                                                                                                                                                                                                                                                                                                              KFEAKVADFGLAKIA-------SDTNTHVSTRVMGTFGYLAPBY
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                                                                                                                                                                                                     ----NVAVKDLVRHFEQQVQPG 619
                                                                                                                                                                                                                                          ----LVDWARPLLNQVSELGNFEVVVDKKLNNBYDKBEMARMVACAAACVRSTAPRRPR
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                and Corresponding Polypeptides
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 RESULT 6
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                                                                       ----NQGITPG
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                                                                                                                                                                                                         ----SFGVVLLE----
                                                                                                                                                                                                                                          PASRFYNLYLADCGAGFFDPLTRGVLSTVSGVVVVASVSIDGAQQASVALDWLR-----
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                                                                                                                                                                       -----NIGYOD-----LASRACVVINHIMPGEP-----NVAVKDL
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Pred. No. 2.4e-14;
8; Mismatches 242;
                                                                                                                                                                                                                                                                              -SDINIHVSTRVMGTFGYLAPEYASSGKLTEKSDVF----
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RESULT 7
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PRIOR APPLICATION NUMBER: 60/536,486
PRIOR PILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 173
SOPTWARE: Patentin Ver. 3.3
SEQ ID NO 89
                  NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 2501
LENGTH: 681
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                                                   Sequence 2501, Application US/11096568A Publication No. US20060048240A1
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Best Local Similarity
Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: XU, JIANFENG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REFERENCE: 27211/04130
CURRENT APPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR PILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 60/582,027
                                                                                                                             FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2005-04-01
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FEATURE:
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No. US20060026719A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 366.5; DB 7; 32.0%; Pred. No. 4.4e-14; tive 18; Mismatches 131;
                                                                                                                                                      US/11/096,568A
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                                                                                                                                                                                                               Sequence 33, Application US/11036256
publication No. US20060026719A1
GENERAL INFORMATION:
APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: XU, JIANFENG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REFERENCE: 27211/04130
CURRENT APPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: 60/602,562
PRIOR APPLICATION NUMBER: 60/602,562
                  PRIOR APPLICATION NUMBER: 60/536,486
PRIOR FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTIN Ver. 3.3
SEQ ID NO 33
SEQ ID NO 33
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                      PRIOR FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 60/582,027
PRIOR FILING DATE: 2004-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)..(681)
OTHER INFORMATION: Ceres Seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 SÄVHHRHLVTLVGYCISEQHRLLVYDYVPNNTL-HYHLHAPGRPVMTWETRVRVAAGAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 TRIN-----LGLSPDEKYELDLHARVRRNPRGSYQIAVVGLKGGAGKTTLTAALGSTL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 SYDELSOVTSGFSEKNLLGEGGFGCVYKGVLSDGREVAVKQLKIGGSQGEREFKAEVEII 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 SPSP-PAPTTINPPPKPSPSPPGETPSPPGETPSPPKPSPSTPTP-TTTTSPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 A-----QVRADRIL-----ALDADPGAGNLADRVGRQSGATIADVLAEK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 AAPDIDA----TQKSIRPAAKGPKVKK--VKPQKPKATKPPKVVSQRGWRHW---VHAL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 FVGYTMPPSAYSSPQGSDVVLFNSRSSAPPKMRSHSGSDYMYASSDS---GMVSNQRSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 EPPPAPSR--PSASPAE----PPTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 GPAPTPTESQLAPPRPPTPQTPTGAPQQP-ESPAPHVPSHGPHQPRRTAPAPPWAKMPIG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 PPAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPPPPPPPPPPPPMPIAAGEPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 SPEPAASKPPTPPMPIAGPEPAPPKPPTPPMPIAGPEPA----PPKPP----TPPMPIA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 PPSSNSSTTAPPPLQTQPTT-----PSAPPPVTPPPSPPQSPPPVVSSSPPPPVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DLNTHVSTRVMGTFGYMAPEYATSGKLSEKAD 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSHYNDIRAHTSVNAVNLEVLPAPEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIAYLHEDCHPRIIHRDIKSSNILLDNSFEALVADFGLAKIAQEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPAPTEPPPS-PSPQR-----NSGRRAERRVHPDLAAQHAAAQPDSITAATTGGRRRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SNNGNNTLPSSSPGKSEVGTGGIVAIGVIVGLVFLSLFVMGVWFTRKRKRKDPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPPPSSSPPPSPPV-ITSPPPTVASSPPPPVVIASPPPSTPATTPPAPPQTVSPPPPDA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PPPATSASPPSSNPTDPSTLAPPPTPLPVVPR------
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Pred. No. 1.9e-13;
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491

338

270 285 215

327

172

62 88

Gaps

80

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RESULT 9
US-11-169-232-14
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Best Local Simi
Matches 101;
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Publication No. US20060025570A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Descri
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                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

APPLICATION NUMBER: US 07/643,502

PILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

PILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

PILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PALENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/11/169,232
PILING DATE: 28-Jun-2005
CLASSIFICATION: CURknown>
                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Megakaryocyte Stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 --PPPTLSPSPTPTPPPGVPVSGTPLPTLTPLPAPTPPLLPHPGTPLPTLTPLPAPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VATGPSIQARLRAEKASGAQLAPGTEPSPAPLGQPRSYLAP-PTRPAPT-EPPPSPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTAPAPPWAKMPIGEPPPAPSR--PSASPAEPPTRPAPQHSRRARRGHRYRTDTERNVGK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMPIAGPAPTPTESQLAPPRP-----PTPQTPTG--APQQPESPAP-HVPSHGPHQPR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGEPP---SPEPAASKPP---TPPMPIA-GPEPAPPKPPTPPMPIAGPEPAPPKPPTP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSASFPP-APASANLPKPNGQTPPPTSDDLSERFVSAPPP---PPPPPPPPPPPPTPM-PIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SPPPTLSPSPTPTPPPGPHSPPPPLSPSPTPTPPLGPHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPPLSPSPTPT-PPLGPHSPPPTLSPSPTPTPPPGPHSPPPPLSPSPTPTPPLGPH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHSPPPTLSPSPTPTPPPGPHSPPPPLSPSPTPTPPLGPHSPPPTLSPSPTPTPPPGPHS
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   REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description of Artificial Sequence: amino acid construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 348; DB 7;
Pred. No. 4.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inc
                                                                                                                                                                                                                                                                                                                                       Version
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US-11-169-232-84
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                                                                                                                                                                                    Sequence 84, Application Publication No. US2006 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Sti
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, I
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION
TELEPHONE: (6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPAPSRPS-ASPAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                       Application US/11169232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 941 amino acids
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(617)876-1170
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US-11-169-232-84
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                  160 TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE 213
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                                                                                            AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPTTPKKPAPTTPKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT 509
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SQRGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT 431
                                            --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKBPAPTTPKKPAPTTPETPPPTT
                                                                                                                                                                                          EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA 320
                                                                                                                                                                                                                                         PAPTTPKEPAPTTPK-----ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
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                                                                                                                                           EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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ilarity 25.4%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 347; DB 7; 1
Pred. No. 1.6e-12;
8; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-11-169-232-74
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US-11-169-232-74
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                                           Query Match
Best Local Similarity 25.4
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APPLICANT: Turn
                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             844 STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784 KTPAATKPEMTTTAKOKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       737 SEVSTPTTTKEPTTH--KSPDESTP-ELSAEPTPKALENSPK----
APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                             LENGTH: 1038 amino
                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CBerr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turner, Katherine
Clark, Stephen C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                        (617)876-5851
                                                        9.8%; Score 347; DB 7; Length 1038;
25.4%; Pred. No. 1.6e-12;
vative 58; Mismatches 259; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics Institute,
                                                                                                                                                                74:
                                                                                                                                                                                                                                                                                                                                                                  5190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EPGVPTT
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RESULT 12
US-11-169-232-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION NOMBER: US/11/169,232
PILING DATE: 28-Jun-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                               CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665
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  APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT-- 267
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTE 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTPAATKPEMTTTAKOKTTEROLRTTPETTTTAAPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK-----EPGVPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQRGWRHWVHALTRINLGLSPDEKYBLDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPTSTTSDKPAPTTPKGTAPTTPKBPAPTTPKEPAPTTPKGTAPTTLKBPAPTTPKKPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPTTPKBPAPTTPK------ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPTTPKKPAPTTPKBPAPTTPKBPAPTTTKKPAPTAPKBPAPTTPKBTAPTTPKKLTPT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIAAGEP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacobs, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inc.
                                                                                                                                                                                                                                   Version
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                                                                                                                 RESULT 13
US-11-169-232-104
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                                               Sequence 104, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 58: SEQUENCE CHARACTERISTICS: LENGTH: 1049 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBETT, LUAND
REGISTRATION NUMBER: 31,822
PROPERSION NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                          APPLICANT: Turner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                             764
                                                                                                                                                                                                                                                                                                                                                                                                                                          377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 DESASEP--PAPASANLEKENGQTPPPTSDDLSERFVSAPPPPPPP-----PPPPPPPPTPM 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                           STITODTTPFKITTLKTTTLAPKVTTTKKTITTTE 905
                                                                                                                                                                                                                                                    AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
                                                                                                                                                                                                                                                                                                                                                TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AOPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPAPTTPKEPTPTTPKEPAPTTKEPAPTTP---KEPAPTAPKKPAPTTPKEPAPTTPKEPA
                                                                                                                                                                                                                                                                                                     KTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                                                                                                                                                                                                                                                                                             SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK-----EPGVPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                     SQRGWRHWVHALTRINLGLSPDEKYELDLHAR-----VRRNPRGSYQIAVVGLKGGAGKT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPTTPKEPAPTTPK-----ETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPEKLAPTTPEKPAPTTPEBLAPTTPEBPTPTTPEBPAPTTPKAAAPNTPKBPAPTTPKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPTTPKKPAPTTPKBPAPTTPKBPAPTTTKKPAPTAPKBPAPTTPKBTAPTTPKKLTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTP-----PMPIAGPEPAP---KPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIAAGEP-----
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Clark, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%;
                          Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 347; DB 7; Length 1049;
Pred. No. 1.6e-12;
B; Mismatches 259; Indels 11
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US-11-169-232-104
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 104: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
268
                                           889
                                                                                    214
                                                                                                                                628 TPEKLAPTTPEKPAPTTPEBLAPTTPEBPTPTTPEBPAPTTPKAAAPNTPKEPAPTTPKE
                                                                                                                                                                         160
                                                                                                                                                                                                                     568
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                                                                                                                                                                                                                                                                                                            508
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                                                                                                                                                                                                                                                                                                                                                     81 PIAAGEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          28 DPSASEP--PAPASANLPKPNGQTPPPTSDDLSERFVSAPPPPPPP-----PPPPPPPPTPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-7AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
EPS-----PAPLGQPRSYLAPPTRPAPTEP-PPSPSPQRNSGRRAERRVHPDLAAQHAA 320
                                           PAPTTPKEPAPTTPK-----STAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTK
                                                                                    P----PTRPAPQHSRRARRGHRYRTDTERNVGKVATGPSIQARLRAEEASGAQLAPGT--
                                                                                                                                                                         TPTG-APQQPESPAPHVPSH----GPHQPRRTAPAPPWAKMPIGEPPPAPSRPS-ASPAE
                                                                                                                                                                                                                     PAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPT
                                                                                                                                                                                                                                                              PTP----PMPIAGPEPAP--PKPPTP-----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
                                                                                                                                                                                                                                                                                                              PTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1140 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Hewick, Rodney N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RE: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 347; DB 7;
; Pred. No. 1.7e-12;
58; Mismatches 259
                                                                                                                                                                                                                                                                                                                                                        ------PSPEPAASKPPTP--PMPIAGPEPAP--PKP 114
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US-11-169-232-44
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Publication No. US2006
GENERAL INFORMATION:
                                                                                                                                  INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino a
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MEDIUM TYPE: Floppy disk
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Clark, Stephen C.
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 SEVSTPTTTKEPTTIH--KSPDESTP-ELSAEPTPKALENSPK------EPGVPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
STATE: Massachusetts
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                                             TOPOLOGY: linear
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                            TELEPHONE:
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                                                                  amino acid
                                                                                                                                                       (617)876-5851
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    SEQ ID NO:
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 42, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Turner, Katherine
Clark, Stephen C.
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                                                                                                                            CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAARNTPKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTPAATKPEMTTTAKOKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKLTATTTQVT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKELSHYNDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --PKELAPTTTKGPTSTTSDKPAPTTPKETAPTT--PKEPAPTTPKKPAPTTPETPPPTT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQPDSITAATTGGRRRKRAAPDLDATQKSLRPAAKGPK-VKKVKPQKPKAT---KPPKVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPTTPKEPAPTTPK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTP----PMPIAGPEPAP--PKPPTP----PMPIA--GPAP-TPTESQLAPPRPPTPQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPAPTTPKEPTPTTPKEPAPTTKEPAPTTP--KEPAPTAPKKPAPTTPKEPAPTTPKEPA 373
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INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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hes 146;
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FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
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                                                     AHTSVNAVNLEVLP-----APEYSSAQRALSDAD 518
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                    STTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTB
                                                                                           KTPÄÄTKPEMTTTAKOKTTERDLRTTPETTTAÄPKMTKETATTTEKTTESKITATTTQVT
                                                                                                                            TLTAALGSTLAQVRADRILALD--ADPGAGNLADRVGRQSGATIADVLAEKBLSHYNDIR 489
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 347; DB 7
25.4%; Pred. No. 2e-12;
tive 58; Mismatches 2
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Search completed: April 14, 2006, 18:42:14 Job time : 31.5386 secs

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Aeb91425 Aeb91452 Aeb91456 Abu36423 Abu36623

Aeb91454

Microbial
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Protein e

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present inventon, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - developing products for the diagnosis of or vaccination aga mycobacterial infections, particularly tuberculosis.

against used

for

N-PSDB;

1998-542705/46. DB; AAV63937.

Andersen P, Oettinger T,

₹,70

Rosenkrands I,

Weldingh K,

Rasmussen

PB;

(STAT-)

STATENS SERUM INST. Nielsen Florio

Claim 1; Page 196; 163pp; English.

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75.5	75.5	75.5	75.5	75.5	75.5	75.5	76.5	77.5	78	78.5	79.5	79.5	80	80	80	80	80.5	80.5	80.5	80.5
15.8	15.8	15.8	15.8	15.8	15.8	15.8	16.0	16.2	16.3	16.4	16.6	16.6	16.7	16.7	16.7	16.7	16.8	16.8	16.8	16.8
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Abu36481 Pi		Abu36862 P	Adg15732 M	Abu34417 P	Adn25249 B	Abu05405 M	Abu36981 P	Abu36613 P:	Abu05650 M.		Abu36642 P:	Aau70987 M	Aeb91437 M:	Abu36550 Pi		Abm15820 My	Aeb91427 M	Aeb91450 M	Abu36682 Pi	Aeb91439 M
Protein e	Microbial	Protein e	tubercu	Protein e	Bacterial	M. tuberc	Protein e	Protein e	. tuberc	Protein e	Protein e	M. tuberc	Microbial	Protein e	Microbial	Mycobacte	Microbial	Microbial	Protein e	Microbial

# ALIGNMENTS

RESULT 1 AAW72927

#### 02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 01-APR-1998; 08-OCT-1998 Mycobacterium Mycobacterium tuberculosis; antigen; vaccine; infection. Mycobacterium tuberculosis antigen RD1-ORF3 AAW72927; AAW72927 standard; protein; WO9844119-A1 21-JAN-1999 (first entry) 97US-0044624P. 97DK-00001277. 98US-0070488P. tuberculosis 97DK-00000376 98WO-DK000132 98 Š immunological; immunogen;

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RESULT 2
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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP3OA or a T-cell epitope of for the induction of a strong immune
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01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic fragment of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1998;
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98WO-DK000132.
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Pred. No. 3.3e-46;
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                                        The present sequence is that of the Mycobacterium tuberculosis MTBN2 protein. This is 1 of 8 proteins, i.e. MTBN1-8 (see AAB19842-49), encoded by 8 open reading frames (see AAA89035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BCG strain of Mycobacterium bovis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BCG and, in particular, for diagnostic methods which discriminate between exposure of a subject to M. tuberculosis and vaccination with BCG. The invention features these MTBN polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope of for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, RD1-ORF5, MFT59-ESAT6, ESAT6-MFT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and for the preparation of a subunit vaccine
                                                                                                                                                                                                                                      Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                               Gennaro
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                                                                                                                                                                                                          11; Fig 1; 35pp;
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                              genetic vaccination methods
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Pred. No. 3.3e-46;
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                                                                                              The invention relates to a novel diagnostic reagent comprising a peptide epitope from a protein encoded by the RD1 or RD2 regions of the Mycobacterium tuberculosis, M. Bovis or M. africanum genome. The diagnostic reagents comprised within the kit are selected so that they are able to differentiate between M. Bovis, M. tuberculosis or M. africanum. The polypeptide or its variant or fragment tuberculosis or M. africanum. The polypeptide or its variant or fragment is useful as a medicament provided that the polypeptide is not a MPT-64 polypeptide or a polypeptide encoded by the RV1984c region of the M. Bovis, M. tuberculosis or M. africanum genomes. The nucleic acid which encodes the polypeptide or the diagnostic reagents can be used as a vaccine, especially against Mycobacterium infections. This sequence corresponds to a protein used to derive the peptide epitopes used in the
                                                                                                                                                                                                                                                                                                                                               New diagnostic reagents comprising a peptide having an epitope from polypeptides Rv1986, Rv3878, Rv1983, Rv3873 or Rv3879 derived from I and RD2 regions of Mycobacterium, useful as vaccines against Mycobacterium infections.
                                                          Sequence
                                                                                                                                                                                                                                                                                                                Claim 19; SEQ ID NO 2; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockle PJ,
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27-APR-2002;
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Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial; antitubercular; tuberculostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2003; 2003WO-GB001815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG15730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG15730 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UKEN-) UK SEC FOR ENVIRONMENT FOOD & RURAL AFF
              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 100.0%;
Local Similarity 100.0%;
hes 98; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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              Similarity
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                                                                                   the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reagent; epitope;
lum tuberculosis; N
                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vordermeier HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002GB-00009723.
2002GB-00009724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rv3872
          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein for generating peptide epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordon SV, Hewinson
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          Score 479; DB 7;
Pred. No. 3.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 479; DB 4;
Pred. No. 3.4e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region; RD2 region;
bacterium bovis; Mycobacterium africanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
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                         Length 99;
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Conservative

<u>.</u>

Mismatches

0

Indels

0

Gaps

0

Sequence 102

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RESULT 5
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                              tuberculosis and in preparing a vaccine against tuberculosis caused by civilent mycobacteria. The vaccine or immunogenic/ pharmaceutical composition can be used prophylactically in a subject not infected with a civilent mycobacterium, or therapeutically in a subject not infected with a virulent mycobacterium. The protein is useful for preventing, complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may be used for effecting in vivo expression of the antigen, and in complex (M. tuberculosis in a subject already infected with a virulent mycobacterium of the antigen, and in complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may be used for effecting in vivo expression of the antigen, and in complex the vaccine is an improvement of the living BCG vaccine presently available, where one or more copies of the living BCG vaccine presently cavailable, where one or more copies of the DNA sequence encoding one or microorganism to allow the microorganism to express and secrete the coplypeptide. Incorporation of more than one copy of a nucleotide sequence enhances the immune response. The present sequence represents an M.
                                                                                                                                                                                                                                                                                                                                                      The invention relates to a substantially pure polypeptide comprising an amino acid sequence selected from Rv0284, Rv0285, Rv0455c, Rv0569, Rv1195, Rv1386, Rv3477, Rv3878, Rv3879c or MT3106.1 (also disclosed are ORF13A and Rv0284ct), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% sequence identity to the polypeptide and is immunogenic. The protein is useful in preparing a pharmaceutical composition for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infections caused by species of tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 73-74; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-061970/08.
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21-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis Rv0285 protein
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2001DK-00000283
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Query Match Best Local Similarity

21.4%;

Score 102.5; DB Pred. No. 0.0015;

DB 5;

Length

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CC pharmaceutical composition comprising a fusion polypeptide having comprises after with BCG or to a person who has previously been vaccinated with BCG and are; (1) an immunogenic composition, vaccine or CC pharmaceutical composition comprising a fusion polypeptide which CC comprises two or more immunogenic composition, vaccine or CC pharmaceutical composition comprising a fusion polypeptide which CC comprises amino acid sequences encoding the fusion polypeptides selected CC from Ag85A, Ag85B, TB10.4, ORF2C, Rv0285, Rv0287 and Rv1036C, or CC comprises amino acid sequences encoding the fusion polypeptides selected CC from Ag85A, TB10.4, Ag85B, TB10.4-Ag85A, CC CRF2C-Ag85A, Ag85B-TB10.4-Ag85A, Ag85B-TB10.4-Ag85A, TB10.4-Rv1036, Ag85A-TB10.4-Ag85A, CC CRF2C-Ag85A, Ag85B-TB10.4-Ag85A, TB10.4-Rv1036-Ag85A, TB10.4-CRF2C-Ag85A, CC CRF2C-Ag85A, Ag85B-TB10.4-Ag85A, TB10.4-Rv0287-TB10.4, and their analogues; (2) a vaccine or CC pharmaceutical composition comprising a nucleic acid fragment, comprising a nucleic acid fragment, comprising composition polypeptide as mentioned; and (3) a method for immunizing and/or treating an animal, which has previously been immunized against tuberculosis caused by a virulent mycobacterium, comprising administering to the animal any of the compositioned, received to the animal any of the mentioned. The immunoceasic compositions or pharmaceutical compositions compositions are compositions.
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              immunogenic compositions, vaccines or pharmaceutical compositions mentioned. The immunogenic composition, vaccine or pharmaceutical composition are useful for therapeutic use, prophylactic use, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an immunogenic composition, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 5; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenicity; vaccine; pharmaceutical; fusion protein; Rv0285;
mycobacterium tuberculosis infection; infection; immunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEB26458 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g a fusion polypeptide with antigens administered together with BCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
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from prior
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  BCG vaccination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical compositions from Bacillus Calmette Guerrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for the preparation of an immunogenic composition, vaccine or pharmaceutical composition for a prophylactic or therapeutical vaccination against an infection caused by a virulent mycobacterium, where the immunogenic composition is to be administered to a person has previously been vaccinated with BCG. This sequence represents Mycobacterium tuberculosis Rv0285 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                           AEB26444 standard; protein; 487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 102
                                                                                                                                                                                                                                                                                                                                                                                            AEB26444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 102.5; DB
Pred. No. 0.0015;
7; Mismatches 4
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M. tuberculosis WO2005061534-A2 Synthetic. Mycobacterium tuberculosis. tuberculostatic; mutein. Ag85A; immunogenicity; vaccine; pharmaceutical; fusi
Ag85A; mycobacterium tuberculosis infection; (first entry) fusion polypeptide, TB10.4-Rv0285-Ag85A fusion protein; lon; infection; : Rv0285; TB10.4;

07-JUL-2005

22-DEC-2004; 2004WO-DK000907

23-DEC-2003; 2003DK-00001942.

Jes D, (STAT-) STATENS Andersen P, SERUM INST.

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2005-479440/48.

New immunogenic compositions, vaccines or pharmaceutical compositions having a fusion polypeptide with antigens from Bacillus Calmette Guerrin (BCG) administered together with BCG.

Disclosure; SEQ ID NO 16; 85pp; English.

The invention relates to an immunogenic composition, vaccine or pharmaceutical composition comprising a fusion polypeptide having antigens from Bacillus Calmette Guerrin (BGG) administered to a person together with BGG or to a person who has previously been vaccinated wit BCG. Also described are: (1) an immunogenic composition, vaccine or pharmaceutical composition comprising a fusion polypeptide which comprises two or more immunogenic polypeptide, or its analogue, selecte from Ag85A, Ag85B, TB10.4, ORF2C, RV0285, RV0287 and RV1036c, or comprises amino acid sequences encoding the fusion polypeptides selecte from Ag85B-TB10.4, Ag85B-TB10.4-Ag85B-TB10.4-PR72C, Ag85B-TB10.4-PR72C, selected selected with

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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06-SEP-2001;
25-OCT-2001;
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                                                            Claim 25; SEQ ID NO 64609;
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06-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU36685 standard; protein;
                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                   WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #22212.
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Trawick JD,
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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                                                      1766pp; English.
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                                                                                                                                                                                                                                                                                                                      Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                         Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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                                                                                                                                                                                                                                                                                                                         Zyskind
Xu HH;
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The invention relates to an isolated nucleic acid comprising any one

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                                                                                                                                                                                                                                                                          algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer; antiinflammatory; urinary tract infection; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                     06-FEB-2004; 2004IN-DE000173.
20-JUL-2004; 2004US-0589227P.
                                                                                                         07-FEB-2005; 2005WO-IN000037
                                                                                                                                                     18-AUG-2005
                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                   Microbial pathogen adhesin protein sequence, SEQ ID NO:165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                 WO2005076010-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEB91455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB91455 standard; protein; 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHEQFVQLMSAGAAQYASARAANSSPLQIVGQTALDAINSPVQTLTGRPLIGNGANGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----IQLLASNASA-----QDQLHRAGEAVQDVARTYSQ-----IDDGAAGV 96
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ilarity 27.1%;
Conservative 1
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RESULT 10
ABU36945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sachdeva
21-MAR-2002; 2002WO-US009107
                                                                03-OCT-2002.
                                                                                                                                                                                               Mycobacterium tuberculosis
                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #22472.
                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 27.1
nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IQLLASNASA-----QDQLHRAGEAVQDVARTYSQ-----IDDGAAGV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FHEOFVOLMSAGAAQYASAEAANSSPLQIVGQTALDAINSPVOTLTGRPLIGNGANGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATIGSAIS-----RANAEALVPITALLPAGADDVSAAIAALFATHGQAYQELSAHAVA
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27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 92.5; DB; Pred. No. 0.23; 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 639;
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                                                                                                                                                                                                                                                                drug design.
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ADM40790;

ADM40790

ADM40790 standard; protein; 588

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                                                                                                                                                                                                                                                             cc nucleic acid; (2) a host cell containing the vector; (3) an isolated cc polypeptide or its fragment whose expression is inhibited by the cc antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a cc ompound's activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of contiferation of an organism. The antisense nucleic acids are useful for cellular proliferance or screening for homologous nucleic acids required control discovery programs, or for screening manufaction collection collection of collection of control of a control or callular proliferation to isolate candidate molecules for rational control discovery programs.
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Best Local (
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                           Sequence 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-029926/02.
N-PSDB; ACA40815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 64869; 1766pp; English
                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid
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                                                                                     19
                                                                                                                         11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGI--QLLASNASA 68
                                          69 -QDQLHRAGEAVQDVARTYSQIDDGAAGVFA
72 LHDQ-----
                                                                                                                                                                        30;
                                                                                                                                                                                              Similarity
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                                                                                     ANIGSALS
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Trawick JD,
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                           AA,
                                                                                       ----AANAAAAGTTGLLAAGADEVSAALASLFSGHAVSYQQVAAQATA
                                                                                                                                                                                              18.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malone
Carr G
----FVQALTGAGGSYA
                                                                                                                                                                     ; Score 90; DB
; Pred. No. 0.3:
13; Mismatches
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                                                                                                                                                                                                DB 6
                                            98
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Forsyth
                                                                                                                                                                          24;
                                                                                                                                                                                                                Length 588
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                                                                                                                                                                            Indels
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Xu HH;
                                                                                                                                                                          24;
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ABU36540
ID ABU3
XX
AC ABU3
XX
T19-0
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DB Prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for the early detection of mycobacterial disease or infection in a subject. The method comprises assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies specific for one or more early Mycobacterium tuberculosis antigens. The invention further relates to: a kit for early detection of M. tuberculosis disease; and an antigenic composition for early detection of the M. tuberculosis disease or infection. The compositions of the invention have antibacterial activity. The method is useful for early detection of mycobacterial
   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease or infection in a subject and for preparing a vaccine against M. tuberculosis infection. This sequence represents the protein derived fro the gene RV3167 relating to the mycobacterial disease or infection detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barly detection of mycobacterial infection in a subject by assaying a biological fluid sample from a subject having symptoms of active tuberculosis for the presence of early antibodies for early Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2001; 2001WO-US020545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-2001; 2001WO-US020545
                             Antisense; prokaryotic essential
                                                               Protein encoded by Prokaryotic essential gene #22067
                                                                                                                                                           ABU36540 standard; protein; 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                     588
                                                                                                                                                                                                                                                                       -QDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
                                                                                                                                                                                                                                                                                                                                     ADIGTOVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGI--QLLASNASA 68
                                                                                                                                                                                                                                                                                                        ANIGSALS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zolla-Pazner S;
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigens.
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                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                   18.8%;
                                                                                                                                                                                                                                                                                                       ---AANAAAAGTTGLLAAGADEVSAALASLFSGHAVSYQQVAAQATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection method related Rv3367 protein
                                                                                                                                                                                                                                         ----FVQALTGAGGSYA
                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB 7;
Pred. No. 0.39;
3; Mismatches 2
                               gene; cell proliferation; drug design.
                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 588
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19

QDQLHRAGEAVQDVARTYSQID : | : | : | : FHE--RFIQALSTAAGAYGSAE

-AANAAALAPTTGVLAAGADEVSAAVASLFSGHAQAYQTLGTQAAA

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                                                                                                                                                                                                          cc encoding a polypeptide whose expression is inhibited by the antisense compound for the fragment whose expression is inhibited by the antisense compound that containing the vector; (3) an isolated colypeptide or its fragment whose expression is inhibited by the antisense collect acid; (4) an antibody capable of specifically binding cc antisense nucleic acid; (4) an antibody capable of specifically binding cc proliferation or the activity of a gene in an operon required for cc proliferation; (7) identifying a compound that influences the activity of compound that influences the activity of compound that influences the activity of collentifying a gene required for cellular proliferation or the biological pathway (c) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent cc which each of the strains is present in a culture or collection of conjunction of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required confiction of collection to isolate candidate molecules for rational confiction of for screening for homologous nucleic acids acids are conficient and confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of an organism or screening to homologous nucleic acids required confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confiction of confic
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are of the nucleic acid inhibits promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) a vector comprising a promoter operably linked to the nucleic acid (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a promoter operable (1) and (1) a vector comprising a vector comprising a vector comprising a vector comprising a vector comprising a vector comprising a vector comprising a vector comprising a vector comprising a vector comprising a vector co
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                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25;
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   11
                                                                      Similarity 27; Conserv
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Trawick
ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68
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; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                      Conservative
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Carr G
                                                                                                      18.3%;
                                                               ; Score 87.5; DB
; Pred. No. 0.79;
15; Mismatches
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Forsyth
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                                                                      29;
                                                                                                                                   Length 606;
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Xu HH;
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                                                                      Gaps
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RESULT 13
AEB91453
CC identifying adhesin and adhesin-like proteins, by computing the sequence computed network software, training an artificial neural network (ANN) for ceach of the computed five attributes, and identifying the adhesin and computed five attributes, and identifying the adhesin and ceach of the computed five attributes, and identifying the adhesin and ceach of the computed five attributes, and identifying the adhesin and ceach of the computed five attributes, and identifying the adhesin and ceach of the computed five attributes, and identifying the adhesin and ceach of the computed five attributes, and identifying the adhesin and ceach of ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical ceach of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base ceach of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully connected multilayer feed forward ANN (I) based on (MI). (MI) is useful for identifying adhesin and adhesin-like proteins, of therapeutic potential, and identifying and short-listing ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin and adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypothetical adhesin-like ceach of 105 hypotheti
                                                                        distantly related organisms, and from bacteria belonging to a wide phylogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 algorithm; adhesin; pharmaceutical; vaccine; drug screening; bordetella pertussis infection; antibacterial; pneumonia; antiinflammatory; respiratory-gen.; gastric ulcer; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-2004; 2004IN-DE000173.
20-JUL-2004; 2004US-0589227P.
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                                                protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a computational method (M1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; SEQ ID NO 163; 402pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sachdeva G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbial pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brahmachari SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:163
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The invention relates to a substantially pure polypeptide comprising an acid sequence selected from Rv0284, Rv0285, Rv0455c, Rv0569, CC Rv1195, Rv1386, Rv3477, Rv3878, Rv3879c or MT3106.1 (also disclosed are CRV1195, Rv1386, Rv0284ct), or their immunogenic portion, nucleic acids encoding them and an amino acid sequence analogue having at least 70% cc sequence identity to the polypeptide and is immunogenic. The protein is useful in preparing a pharmaceutical composition for diagnosting cutberculosis and in preparing a vaccine against tuberculosis caused by virulent mycobacterium, or therapeutically in a subject not infected with a virulent mycobacterium, or therapeutically in a subject not infected with a virulent mycobacterium. The protein is useful for preventing, composition and detecting infections caused by species of tuberculosis may be used for effecting in vivo expression of the antigen, and in a compositic assays for detecting the presence of pathogenic organisms in a sample. The vaccine is an improvement of the living BCG vaccine presently available, where one or more copies of the DNA sequence encoding one or more polypeptide has been incorporated into the genome of the composition of more than one copy of a nucleotide sequence enhances the immune response. The present sequence represents an M. cuberculosis protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Mycobacterium tuberculosis antigens, useful for diagnosing tuberculosis, and as a vaccine for treating or preventing infecused by species of tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculosis; Tuberculostatic; antibacterial; vaccine; Rv0284; Rv0285; Rv0455c; Rv0569; Rv1195; Rv1386; Rv3477; Rv3878; Rv3879; MT3106.1; ORF13A; Rv0284ct; Mycobacterium bovis; Mycobacterium africanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis Rv1386 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 77; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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21-FEB-2001; 2001DK-00000283
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ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68

Query Match Best Local S

Local Similarity les 27; Conserv

Conservative

15;

Score 87.5; DB 9; Pred. No. 0.79; .5; Mismatches 29;

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Gaps

Length 606;

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RESULT 15
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CC identifying adhesin and adhesin-like proteins, by computing the sequence-
CC based attributes of protein sequences using five attribute modules of a
CC neural network software, training an artificial neural network (ANN) for
CC each of the computed five attributes, and identifying the adhesin and
CC edhasin-like proteins having probability of being an adhesin (Pad) as
CC equal or greater than 0.51. Also claimed is a set of 274 annotated genes
CC encoding adhesin and adhesin-like proteins, having 274 fully defined 162-
CC (1151 base pair (SEQ ID NO: 385-558) sequences; a set of 105 hypothetical
CC genes encoding adhesin and adhesin-like proteins, having 105 fully
CC defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 279 annotated
CC adhesin and adhesin-like proteins, having 205 fully defined 53-3716 base
CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-
CC 280-384) sequences; and a fully connected multilayer feed forward ANN (I)
CC based on (M1). (M1) is useful for identifying adhesin and adhesin-like
CC proteins, of therapseutic potential, and identifying and short-listing
CC proteins for further testing in development of new vaccine formulations
CC useful for identifying putative adhesins that are important in drug
CC discovery and preventing therapeutics for whooping cough, pneumonia,
CC gastric ulcer and urinary tract infections. (M1) identifies adhesins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches 25
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20-JUL-2004; 2004US-0589227P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2005; 2005WO-IN000037
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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PE-family protein hypothetical glyci	hypothetical glyci hypothetical glyci probable PB protei	conserved hypothet hypothetical prote hypothetical glyci	hypothetical glyci probable PE protei transducer protein	probable PK protei hypothetical glyci hypothetical glyci	halobacterial tran

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# ALIGNMENTS

RESULT 2
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C70799
probable PE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: 17-Uul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004
C;Date: 17-Uul-1998 probable PE protein - Mycobacterium tuberculosis (strain H37RV)

(;Species: Mycobacterium tuberculosis

(;Accession: F70802

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comoor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

Nat R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.S.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genor A;Reference number: A70500; MUID:98295987; PMID:9634230 밁 ð 문 ş A;Molecule type: DNA
A;Residues: 1-99 <COL>
A;Residues: 1-99 <COL>
A;Cross-references: UNIPARC:UPI00000C1571; GB:AL022120;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PE A; Molecule type: DNA A; Residues: 1-111 <COL> C; Accession: C70799 A; Status: preliminary; nucleic acid sequence not shown; A;Status: preliminary; nucleic acid sequence not shown; translation not shown Query Match 100.0%; Score 479; DB 2; Best Local Similarity 100.0%; Pred. No. 3e-37; Matches 61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98 61 ш 1 MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAPTSEGIQ 60 MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQ Conservative 0; Mismatches <u>.</u>. 98 Length Indels translation not shown GB:AL123456; NID:g3261558; PIDN 99 0 Gaps 60 0 Gordon, genome

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probable PE protein - Mycobi
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C;Date: 17-Jul-1998 #sequen
C;Accession: C70836
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C;Accession: D70931
R;Cole, S.T.; Brosch, R.;
; Connor, R.; Davies, R.;
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A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70931
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A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70836
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PE
                                                                                                                                                                                                                                                                                          hypothetical glycine-rich protein Rv1803c - Mycobacterium tuberculosis (strain c;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 31-Mar-2003 C;Accession: D70931
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                                                                                                Status: preliminary; nucleic
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Experimental source: strain H37Rv;
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;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                     strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.2%;
                                                                                                                                                                                                                                                  Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D
Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
                                                                                                    acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 231; DB
Pred. No. 1.9e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102.5; DB
Pred. No. 0.011;
7; Mismatches
                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIPARC: UPI0000043EB2;
                                         GB:AL022021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
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.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shown; translation not
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                                                                                                      shown;
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                                         GB:AL123456;
                                                                                                      translation
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                                         NID:g3250699; PIDN
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                                                                                                                                                                                                                                                       Holroyd,
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                                                                                                                                                                                                                                                                                                                                                                H37RV)
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                                                                                                                                                                    genome
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                                                                                                                                                                 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S. Mature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; A;Title: Deciphering the biology of Mycobacterium tuberculosis fi A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                  hypothetical glycine-rich protein Rv0872c - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003 C;Accession: H70816 C;Accession: H70816 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
F70971
A;Experimental source: strain C;Genetics: A;Gene: Rv0872c
                                                                                                                        A; Status: preliminary; nucleic
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                                                                 A; Cross-references: UNIPARC: UPI00000D3AFD;
                                                                                                                                                  A; Accession: H70816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
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                                                                                   A;Residues: 1-606 <COL>
                                                                                                      A; Molecule type: DNA
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Best Local S
Matches 32
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Best Local :
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acid

sequence not shown; translation

not

.; Barrell, B.G. from the complete

genome

.; Gordon,
Holroyd,

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H37RV)

GB:AL022004;

GB:AL123456; NID:g3261550;

PIDN

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Sature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic
                                                                                                                                                                                                                                                                                                                                                                                                               A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A; Title: Deciphering the biology of Mycobacterium tuberculosis fi A; Reference number: A70500; MUID:98295987; PMID:9834230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical glycine-rich protein Rv3367 - C;Species: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-588 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: uncharacterized glycine-rich protein,
                                                                                                                                                                                                                                                                                                ;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003
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                                                                                                                                                                              Similarity
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                                       -QDQLHRAGEAVQDVARTYSQIDDGAAGVFA
                                                                               ANIGSALS
                                                                                                                ADIGTOVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGI--QLLASNASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IQLLASNASA-----QDQLHRAGEAVQDVARTYSQ-----IDDGAAGV
                                                                                                                                                                                                                                      uncharacterized glycine-rich protein,
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ilarity 27.1%;
Conservative 1
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                     UNIPARC: UPI00000D4F71;
                                                                            ----AANAAAAGTTGLLAAGADEVSAALASLFSGHAVSYQQVAAQATA
                                                                                                                                                                            18.8%; Score 90; DB 33.0%; Pred. No. 1.1;
----FVQALTGAGGSYA
                                                                                                                                                                                                                                                                                                                                                                               acid
                                                                                                                                                           13;
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Pred. No. 0.74;
15; Mismatches
                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis (strain
                                                                                                                                                                                                                                                                                                                     GB:AL009198;
                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                               not shown;
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                                                                                                                                                           24;
                                                                                                                                                                                               Length 58
                                                                                                                                                                                                                                        PB motif containing
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                                                                                                                                                                                                                                                                                                                       GB:AL123456; NID:g3242262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                                          genome
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squax Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70824
                                                                                         A;Cross-references: UNIPROT:053809;
A:Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                             R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical glycine-rich protein Rv0746 - Mycobacterium tuberculosis (stra
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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A;Authors: Squares, S.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable PB protein - Mycobacterium tuberculosis (strain H37RV)
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                                                                     A; Experimental source: C; Genetics:
                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-783 < COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Cross-references: UNIPROT:P71656;
;Experimental source: strain H37Rv
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;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
;Accession: H70898
                                                                                                                                                                                                                                                                                                                                                                                                             Accession: E70824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVSDNALHGVTAGSTALTS------VTGLVPAGADEVSAQAATAFTSEGIQLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVVPESLAGASAAIBAVTARLAAAHAAAAPFIAAVIPPGSDSVSVCNAVBFSVHGSQHVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FHE--RFIQALSTAAGAYGSAE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDQLHRAGEAVQDVARTYSQID 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQIGSTLS-----AANAAALAPTTGVLAAGADEVSAAVASLFSGHAQAYQTLGTQAAA
                      elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                      related uncharacterized
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32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 87; DB
26.6%; Pred. No. 0.29
Live 18; Mismatches
                                                                                                                                                                                           acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycine-rich protein,
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Pred. No. 2;
15; Mismatches
                                                                                                                  UNIPARC: UPI00000D4FCA;
                                                                                                                                                                                           sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIPARC: UPI000011DC87; GB: Z80108; GB: AL123456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.29;
                      glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 102
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                                                                                                                                                                                        translation
                                                                                                                     ନ୍ଥ
                      protein,
                                                                                                                  :AL021958;
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                                                                                                                                                                                           not
                      胺
                                                                                                                  GB:AL123456;
                                                                                                                                                                                                                                                              complete
                      motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                                                                                           Holroyd,
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                   containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H37RV)
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                                                                                                                                                                                                                                                              genome
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                                                                                                                                                                                                                                     Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Square Nature 393, 537-544, 1998
A;Authors: Sqares, F.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A;Title: Deciphering the biology of Mycobacterium tuberculosis from the c A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70806
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                          A; Gene: Rv3508
C; Superfamily:
                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1901 < COL>
                                                                                                                                                                                                                                                                                                                                                        R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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                                                                                                                  A; Experimental
                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: F70806
Query Match
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collagen alpha 1(IV)

18.1%;

Score 86.5;

DB

<u>ب</u>

Length

UNIPROT:053553; ce: strain H37Rv

UNIPARC: UPI000013C2A6;

GB:AL022022;

GB:AL123456;

Z

not shown;

translation

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complete B.G.

.; Gordon, Holroyd,

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A;Gene: Rv3514
C;Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI00000D3AEB; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-1489 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: D70807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar
A;Title: Deciphering the biology of Mycobacterium tuberculosis from
A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical glycine-rich protein Rv3514 - Mycobacterium tubercu
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 393,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: D70807
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                                                                                                                                                                                                                           Query Match
73
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                                        72 LHRAGEAVODVARTYSQIDDGAA
                                                                                                                                12 DIGTOVSDNALHGVTAGSTALTSVTGLVPAGADBVSAQAATAFTSEGIQLLASNASAQDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                     Similarity
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HORFVOALSTGAGAYASAEAAAA
                                                                                        NLGSSIS-----AANASAASATTQVLAAGADEVSARIAALFGGFGLEYQAISAQVAAY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSAATDLAALGSVLGAADAAAATTTGIVAAAQDEVSAAIAALFSAHGRAYQVASAQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGTQVSDNALHGVTAG---STALTSVTGLVPAGADEVSAQAATAPTSEGIQLLASNASAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOLHRAGEAVODVARTYSQIDDGAAGVFA 98
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                   18.1%; Score 86.5;
28.9%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%; Score 86.5; Di
30.3%; Pred. No. 3.3;
                                                                                                                                                                                18; Mismatches
                                          94
95
                                                                                                                                                                                                                                                                                                                                                                   GB:AL022022;
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                                                                                                                                                                                                                           Length 1489;
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                                                                                                                                                                                                                                                                                                                                                                   GB:AL123456; NID:g3261554;
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Recession: P70824

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residuse: 1-961 <COL>
A;Cross-references: UNITROT:053810; UNIPARC:UPI0000139C61; GB:AL021958; GB:AL12
A;Cross-references: UNITROT:053810; UNIPARC:UPI0000139C61; GB:AL021958; GS:AL12
C;Superfamily: elastin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical glycine-rich protein Rv2591 - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis (c;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: F70726 C;Accession: F70726 C;Accession: F70826 C;Connor, R; Brosch, R; Parkhill, J; Garnier, T; Churcher, C; Harris, D; Gordo; Connor, R; Davies, R; Devilin, K; Feltwell, T; Gentles, S; Hamlin, N; Holroyd Rajandream, M.A.; Rogers, J; Rutter, S; Seeger, K; Skelton, S; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell A; Title: Deciphering the biology of Mycobacterium tuberculosis from the A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: F70726
                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical glycine-rich protein Rv0747 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q50630;
Experimental source: strain H37Rv
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                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASAQDQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHHSFVQTLNAAGGAYSSAEAANASAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLHRAGEAVQDVARTYSQIDDGAAGVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANIGTSLS-----AANATAAASTTSVLAAGADEVSQAIARLFSDYATHYQSLNAQAAA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORFVOALSTGAGAYASAEAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLGSSIS-----AANASAASATTQVLAAGADEVSARIAALFGGFGLEYQAISAQVAAY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
              17.8%;
37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 85.5; Di 30.7%; Pred. No. 2.7;
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8; Mismatches
                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI000013BD72;
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                No.
3.5;
4.2;
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A;Title: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70900
A;Ararra. A70900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authbors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authbors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: E70983
                                                                                                                                                                             A;Gene: xv13300
C;Superfamily: uncharacterized glycine-rich
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-576 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rajandream, M.A.; Rogers,
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical glycine-rich protein Rv1396c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
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E70983
hypothetical glycine-rich protein Rv0124 - Mycobacterium tuberculosis (strain
C;Species: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-487 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A70900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Gene: Rv0124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                 Matches
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                                                                                                                         Local
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                          11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68
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                                                                                                                      Score 83; DB Pred. No. 4.9;
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Pred. No. 2.7;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Best Local Similarity
Matches 98; Conserv
O79F93;
O79F93;
O79F93;
O79F93;
O5-JUL-2004 (TERMELrel. 27, Created)
O5-JUL-2004 (TERMELrel. 27, Last sequence update)
O5-JUL-2004 (TERMELrel. 27, Last annotation update)
O5-JUL-2004 (TERMELrel. 27, Last annotation update)
PE FAMILY-RELATED PROTEIN.
Name=PE35; OrderedLocusNames=Rv3872;
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
COrymebacterineae, Mycobacterium;
Mycobacterium tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler I Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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24 MYCBO

27 TVG4 MYCBO PRELIMINARY; PRT; 98 AA.

Q7TVG4;

Q7TVG4;

Q1-OCT-2003 (TREMBLrel. 25, Created)

Q1-OCT-2003 (TREMBLrel. 25, Last sequence update)

Q1-MAR-2004 (TREMBLrel. 26, Last annotation update)

PE FAMILY-LIKE PROTEIN.

MARME-PERS5; OrderedLocusNames=Mb3902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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STRAIN=AF2122/97;
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[1]
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98 AA;
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Q7TY98 MYCBO
PG10 MYCTU
Q7U1D3 MYCBO
Q7U0A9 MYCTU
Q7U2T0 MYCBO
Q79608 MYCTU
Q7U2T0 MYCBO
Q8VRX1 MYCTU
Q8VY59 BRAJA
Q7U1D4 MYCBO
Q6V217 9ENTR
Q6V218 9ENTR
Q6V218 9ENTR
P71664 MYCTU
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Pred. No. 1.
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Q7DW88\_MYCBO
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US-10-620-246-88 479

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STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.I

Salzberg S.L., Delcher A., Utterback T.R., Weldman J.F., Khouri H

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Salzberg S.L., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
J. Bacteriol. 184:547
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AE000516; AAK48354.1; -; Gen
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MEDIJNE=98295987; PubMed=9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Cole S.T., Brosch S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
95-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Name=PE34; OrderedLocusNames=Rv3746C;
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PROBABLE PE FAMILY PROTEIN.
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                                                                                                                                                                                                                STRAIN=H37Rv;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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NCBI_TaxID=1765;
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Q7D4Y1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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OrderedLocusNames=MT3854;
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Nature 393:537-544(1998).
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"Deciphering the biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aboratory strains.";
. Bacteriol. 184:5479-5490(2002).
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Similarity 52.1%;
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Pred. No. 1.5e-
L5; Mismatches
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Pred. No. 1.4e-13;
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Best Local
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                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
PE FAMILY PROTEIN.
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Complete proteome;
SEQUENCE 102 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae; Mycobacteriaceae; Mycobacterium tuberculosis complex.
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Li L., Bannantine J., Zhang Q., Au
Submitted (SEP-2003) to the EMBL/
EMBL; AEO17240; AASO6331.1; -; Gen
InterPro; IPR000084; PB_region_N.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
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OrderedLocusNames=MAP3781;
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                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=PE5; OrderedLocusNames=Mb0293;
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                                                                                                                                   Similarity
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                                                                                                                                                                           proteome.
102 AA;
                                   QDQLHRAGBAVQDVARTYSQIDDGAAGVF
                                                                                          GTQVSDNALHGVT----AGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASA
VEELGRAGVGVGESGASYLAGDAAAAATY
                                                              GLAAASAAVEALTARLAAAHASAAPVITAVVPPAADPVSLQTAAGFSAQGVEHAVVTAEG
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102 AA; 9577 MW; E73DF08A475C2D58
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llarity 31.5%;
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EMBL/GenBank/DDBJ

-; Genomic_DNA.
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Pred. No. 0.08
L4; Mismatches
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                                                                                                                    Mismatches
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RESULT 10
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Q7DA36, Q6MX53;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seque
13-SEP-2005 (TrEMBLrel. 31, Last annot
PE family protein.
Name=PE5; OrderedLocusNames=MT0298, Ra
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TubercuList; Rv0285; -
InterPro; IPR000084; PI
Pfam; PF00934; PB; 1.
Q79rJ9 MYCTU PRELIMINARY;
Q79rJ9;
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98295987; PubMed=9634230; DOI=10.1038/31159; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamli Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamli Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence.";
Nature 393:537-544(1998).
EMBL; AE000516; AAK44522.1;
EMBL; BX842573; CAE55265.1;
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MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
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J. Bacteriol. 184:5479-5490(2002).
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RESULT 11
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Q8VJW1;
01-MAR-2002
01-MAR-2002
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NUCLEOTIDE SEQUENCE.

STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed=12218036;

MEDLINE-22206494; PubMed=12218036;

Pleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,

Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,

Fraser C.M.;
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SEQUENCE
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Corynebacterineae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
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PE-PGRS FAMILY PROTEIN.
Name=PE PGRS32, OrderedLocusNames=Rv1803c;
Mycobacterium tuberculosis
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01-MAR-2004 (TrEMBLrel.
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PRODOM; PD001223; PE region N; 1.
PROSITE; PS00583; PFKB KINASES 1; UNKNOWN 1.
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InterPro; IPR000084; PE region_N.
InterPro; IPR002173; PfkB.
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RESULT 13
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Adhiambo C., Forney J.D., ABai D.J., LeBowitz J.H.;
"Cytoplasmic dynein? isoform is required for flagella a
Leishmania mexicana.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY671898; AAU93603.1; -; Genomic_DNA.
EMBL; AY671898; AAU93603.1; -; Genomic_DNA.
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SEQUENCE
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01-OCT-2003 (TrembLrel.
01-MAR-2004 (TrembLrel.
PE-PGRS FAMILY PROTEIN
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13-SEP-2005 (TrEMBLrel. 31, Las
13-SEP-2005 (TrEMBLrel. 31, Las
Cytoplasmic dynein heavy chain
    Corynebacterineae;
                          Bacteria; Actinobacteria; Actinobacteridae;
                                                  Mycobacterium bovis.
                                                                       Name=PB_PGRS32a;
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Eukaryota; Euglenozoa; Kinetoplastida;
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EMBL; AB000516; AAK46124.1;
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InterPro; IPR000084;
InterPro; IPR002173;
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; PS00583; PFKB_KINASES_1; UNKNOWN_1.
B 650 AA; 56541 MW; CSDS216FD7CCCD87
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  eridae; Actinomycetales;
Mycobacterium;
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flagella assembly
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RESULT 14
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Best Local
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Tubercullist; Rv3367; -.
InterPro; IPR002952; Eggshell
InterPro; IPR000084; PE regio
InterPro; IRR002173; PfkB.
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Q6MWX7;
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COLe S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
COLe S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Biglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin I.
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares R.
Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PB-PGRS FAMILY PROTEIN.
Name=PB_PGRS51; OrderedLocusNames=Rv3367;
Mycobacterium tuberculosis.
                                                                                      PRINTS; PR01228; EGGSHELL.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
                                                                                                                                            Pfam; PF00934; PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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ProDom; PD001223; PE_region_N; 1.
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                                              proteome.
588 AA;
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                                                                                                                                                                  Eggshell.
PE region
PfkB.
                                                 49708 MW;
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Last annotation updat
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Pred. No. 0.96
LO; Mismatches
    Score 90;
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                                                 067B84097F61DAF1 CRC64;
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  Length 588;
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Search completed: April 14, 2006, 17:32:15 Job time : 38.1588 secs
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Best Local S
Matches 30
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A Garnier T., Eiglmester K., Camus J.-C., Medina N., Mansoor H.,
A Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
A Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
A Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
T "The complete genome sequence of Mycobacterium bovis.";
T Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248345; CAD95560.1; -, Genomic DNA.
GO; GO:0005344; F:oxygen transporter activity; IEA.
GO; GO:0015671; P:oxygen transporter activity; IEA.
InterPro; IPR00293; Eggshell.
R InterPro; IPR00293; Eggshell.
R InterPro; IPR002173; PfkB.
R InterPro; IPR002173; PfkB.
R InterPro; IPR002173; PfkB.
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TWN2 MYCBO PRELIMINARY; PRT; 626 AJ
OTTWM2;
O1-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TREMBLrel. 25, Last sequence up
01-MAR-2004 (TREMBLE). 26, Last annotation
PE-PGRS FAMILY PROTEIN.
Name-PE_PGRS51; OrderedLocusNames=Mb3402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1228; EGGSHELL.
PROSITB; PS00583; PFKH_KINASES_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 626 AA; 52577 MW; B538EF2D74B6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium bovis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterinese, Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
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STRAIN=AF2122/97;
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                                                                                                                                72
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                LHDQ---
                                                                                                                                                                                           -QDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
                                                                                                                                                                                                                                                          ANIGSALS-----AANAAAAAGTTGLLAAGADEVSAALASLFSGHAVSYQQVAAQATA 71
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52577 MW; B538EF2D74B6A97B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 18.8%; Score 90; DB 2;
33.0%; Pred. No. 8.8;
Live 13; Mismatches 2
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Last annotation updat
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Result
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Maximum |
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Maximum Match 100%
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Perfect score:
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    No. is the number of results predicted by chance to have
re greater than or equal to the score of the result being pa
is derived by analysis of the total score distribution.

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     US-10-620-246-88
479
1 MEKMSHDPIAADIGTQVSDN......VQDVARTYSQIDDGAAGVFA 98
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/BaCkfiles1.pep:*
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Copyright (c) 1993 - 2006 Biocceleration
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     2 US-09-050-739-88

2 US-09-073-009-32

2 US-09-073-010-33

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2 US-09-073-010-33

2 US-09-125-619-32

2 US-10-222-566-32

2 US-10-143-024A-32

2 US-10-125-619-32

2 US-10-222-566-39

3 US-10-222-162-39

2 US-10-222-162-39

2 US-10-222-162-39

2 US-10-222-162-39

2 US-09-603-208A-292

2 US-09-603-208A-292

2 US-09-603-208A-292

2 US-09-902-540-12224

2 US-09-540-336-3395

2 US-09-540-36-3595

2 US-08-435-991A-20127

2 US-08-435-991A-20127

2 US-09-356-447A-5

2 US-09-356-447A-5

2 US-09-352-267B-5
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Sequence 88, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 292, Appl
Sequence 292, Appl
Sequence 292, Appl
Sequence 2, Appli
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Sequence 5, Appli
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45	44	43	42	41	40	39	38 8	37	36	35	34	<b>3</b> 3	32	31	30	29	28
67	67	67.5	89	68	89	83	68	68	68.5	69	69	69	69	69	69	69	69
14.0	14.0	14.1	14.2	14.2	14.2	14.2	14.2	14.2	14.3	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4
180	180	741	2680	990	370	287	141	138	393	2035	2035	2035	1938	288	259	210	210
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5482709-6	5273901-7	US-09-902-540-15369	US-09-489-039A-7973	US-09-252-991A-32469	US-09-902-540-13987	US-09-107-532A-4761	US-09-252-991A-26729	US-09-252-991A-17846	US-09-252-991A-28810	PCT-US93-11721-5	US-08-393-703-5	US-08-046-585-5	US-09-949-016-6609	US-09-134-001C-4969	US-09-252-991A-30663	US-09-710-279-3320	US-09-710-279-2864
Patent No.	Patent No.	Seguence 1	Sequence 7	Sequence 3	Sequence 1	Sequence 4	Sequence 2	Sequence 1	Seguence 2	Sequence 5	Sequence 5	Sequence 5	Sequence 6	Sequence 4	Sequence 3	Sequence 3	Sequence 2
5482709	5273901	15369, A	7973, Ap	32469, A	13987, A	4761, Ap	26729, A	17846, A	28810, A	i, Appli	•	•	6609, Ap	4969, Ap	30663, A	3320, Ap	2864, Ap

# ALIGNMENTS

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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: NETTINGER, Thomas
APPLICANT: RASMUSER, Peter Birk
APPLICANT: RASMUSER, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
ITTLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
ITTLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
ITILE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
ITILE OF INVENTION NUMBER: US/09/050,739
CURRENT APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER FILING DATE: 1997-04-02
EARLIER FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER APPLICATION NUMBER: 60/070 488
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                                                                                                                                                                                                                                                                    ; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-050-739-88
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                                                                                                                                                                            Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/070,488
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6641814
GENERAL INFORMATION:
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                    61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
61
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                                                                                                               1 MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQ
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                                                                                        MEKMSHDPIAADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQ
LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA
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ilarity 100.0%;
Conservative 0
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Pred. No. 5.6e-50;
Mismatches 0;
98
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RESULT 2
US-09-073-009-32
; Sequence 32, Application
; Patent No. 6555653

US/09073009

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ORIGINAL SOURCE:
ORGANISM: Myc
US-09-073-009-32
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                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6555653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.6%;
Best Local Similarity 39.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Alderso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 206-622-49
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKST NUMBER: 210121.441C1
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 206-622-4900
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                     COUNTRY:
                                                                                                                                                                                 STREET:
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                                                                                                                                                            Seattle
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                                                                                                                                                                               6300 Coumbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                     Alderson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                 701 Fifth Ave.
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RESULT 4
US-09-073-010-32
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Best Local Similarity
Matches 23; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Alderson, Mark
                                                                                                                                                                                                               TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAMB: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                STRANDEDNESS: 811
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                        H: 99 amino acids amino acid
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Pred. No. 0.21;
8; Mismatches 18;
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RESULT 6
US-09-125-619-32
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US-09-073-010-33
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US-09-073-010-32
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Patent No. 6437116
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
                                               Sequence 32, Application US/09125619 Patent No. 6437116
                                                                                                                                                                                                            Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Alders
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.440C1
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Compounds for IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS AND
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STRANDEDNESS:
TOPOLOGY: lin
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Pred. No. 0.21;
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Pred. No. 0.21;
8; Mismatches 18;
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Sequence 32, Application US/10143024A
Patent No. 6740744
GENERRAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
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RESULT 7
US-10-222-566-32
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                                                                                                                                                                                                                                                                SEQ ID NO 32
LENGTH: 212
TYPE: PRT
                                                                                                                                               Query Match 15.6%; Score 74.5; DB Best Local Similarity 26.7%; Pred. No. 0.62; Matches 20; Conservative 21; Mismatches
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LENGTH: 212
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD3
CURRENT APPLICATION NUMBER: US/10/222,566
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR PILING DATE: 1999-01-27
NUMBER: OF SEQ ID NOS: 50
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: JING-RI
APPLICANT: HARDHAN
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 199-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                           ORGANISM: Borrelia burgdorferi
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                                     81 DVARTYSQIDDGAAG 95
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GAGKLFGKVDDAHAG 111
                                                                          GASSGTDAIGEV--VANAGAAKVADKASVTGIAKGIKEIVEAAGGSEKLKVAAATGESNK 96
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
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HOWELL, JERRILYN K.
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26.7%;
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Pred. No. 0.62;
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VWP-LIKE SEQUENCES OF PATHOGENIC BORRELIA FILE REFERENCE: UTSH:234USD4
CURRENT APPLICATION NUMBER: US/10/222,162
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
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APPLICANT: MARBOUR, ALAN G.

APPLICANT: WEINSTOCK, GEORGE M.

FILE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA FILE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA FILE REPERENCE: UTSH:234USD1

CURRENT APPLICATION NUMBER: US/10/143,024A

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: PCT/US97/02952

PRIOR APPLICATION NUMBER: 60/012,028

PRIOR PILING DATE: 1996-02-21

PRIOR FILING DATE: 1996-02-21
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; ORGANISM: Borrelia burgdorferi
US-10-143-024A-32
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US-10-222-162-32
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Best Local 9
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SEQ ID NO 32
LENGTH: 212
TYPE: PRT
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Best Local Similarity
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SEQ ID NO 32
LENGTH: 212
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GAGKLFGKVDDAHAG 111
                                        DVARTYSQIDDGAAG 95
                                                                                     GASSGTDAIGEV--VANAGAAKVADKASVTGIAKGIKEIVEAAGGSEKLKVAAATGESNK 96
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US-09-125-619-39
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US-09-125-619-39
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SEQ ID NO 39
LENGTH: 213
TYPE: PRT
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PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 39
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Patent No. 6437116
GENERAL INFORMATION:
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APPLICANT: WEINSTOCK
TITLE OF INVENTION:
FILE REFERENCE: UTSH
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Best Local Similarity
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Patent No. 6/11.
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APPLICANT:
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APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILLYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
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APPLICANT: JING-RE
APPLICANT: HARDHAM
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CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
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CURRENT FILING DATE: 2002-08-16
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                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Borrelia burgdorferi
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97
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                                 81 DVARTYSQIDDGAAG 95
                                                                                                           24 GVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASAQDQLHRA----GEAVQ 80
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
GAGKLFGKVDDAHAG 111
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VENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
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                                                                                                                                                                     15.6%; Score 74.5; DB 26.7%; Pred. No. 0.63;
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: WPLIKE SEQUENCES OF PATHOGENIC BORRELIA FILE REFERENCE: UTSH:234USD4
CURRENT APPLICATION NUMBER: US/10/222,162
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
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APPLICANT: WEINSTOCK, GEORGE M.

FITTLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA

FILE REFERENCE: UTSH:234USD1

CURRENT APPLICATION NUMBER: US/10/143,024A

CURRENT FILING DATE: 2002-08-23

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR APPLICATION NUMBER: 09/01-27

PRIOR APPLICATION NUMBER: 09/01-202-21

PRIOR APPLICATION NUMBER: 09/012,028

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; ORGANISM: Borrelia burgdorferi
US-10-143-024A-39
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US-10-222-162-39
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Query Match
Rest Local Similarity 20...
20; Conservative
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SEQ ID NO 39
LENGTH: 213
TYPE: PRT
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APPLICANT: JING-RES
APPLICANT: HARDHAM,
APPLICANT: HOWELL,
APPLICANT: BARBOUR,
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LENGTH: 213
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APPLICANT: JING-RI
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SOFTWARE: PatentIn Ver. 2.1
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Local Similarity 26.7%; Pred. No. 0.63;
hes 20; Conservative 21; Mismatches 29;
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JING-REN, ZHANG
HARDHAM, JOHN M.
HOWELL, JERRILYN K.
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                                                                                   15.6%; Score 74.5; DB 26.7%; Pred. No. 0.63;
                                                21;
                                                Mismatches
                                                                                                                 DB 2; Length 213;
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-603-208A-292
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PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/14
PRIOR PILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/15
PRIOR PILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 11
PRIOR PILING DATE: 1999-07-01
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SEQ ID NO 292
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APPLICANT: Kim, Hyung-Joon
TITLE OP INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
TITLE OP INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/603,208A CURRENT FILING DATE: 2000-06-23
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
101
                                 57 EGIQLIASNASAQDQ-LHRAGEAVQDVARTYSQIDDGAA 94
                                                                       41 EFGVRIVDNMLVGFSTLGDGMNQAAEGATTLSDGVGSANDGAVQLADGAVTLRDGIASAN 100
                                                                                                          12 DIGTQVSDNALHGVTA------GSTALTSVTGLVPAGADEVSAQAAT-----AFTS 56
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                                                                                                                                                                    15.4%; Score 74; DB 2; Length 505, 29.3%; Pred. No. 2.4;
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                                                                                                                                                12; Mismatches
                                                                                                                                                42;
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RESULT 15 US-09-605-703B-2330 ; Sequence 2330, Application US/09605703B

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PATERIAL INFORMATION:
APPLICANT: NOT DESCRIPTION:
APPLICANT: KCOSET, Burkhard
APPLICANT: KCOSET, Burkhard
APPLICANT: KCOSET, Burkhard
APPLICANT: KCOSET, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Haberhauer, Gargor
TILE OF INVENTION: ORNAR
APPLICANT: Haberhauer, Gargor
TILE OF INVENTION: ORNAR
APPLICANT: Haberhauer, Gargor
TILE OF INVENTION: PROTEINS
FILE REFERBENCE: BG1-129CP
CURRENT FILING DATE: 2000-06-27
FRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 2330

NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 2330

QUETY MATCH
Best Local Similarity 29-3%; Pred. No. 2.4;
Best Local Similarity 29-3%; Pred. No. 2.4;
Best Local Similarity 29-3%; Pred. No. 2.4;
Best Local Similarity 29-3%; Pred. No. 2.4;
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Best Local Similarity 29-3%; Pred. No. 2.4;
Best Local Similarity 29-3%; Pred. No. 2.4;
Best Local Similarity 29-3%; Pred. No. 2.4;
Best Local Similarity 29
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Sequence 82, Appl
Sequence 62, Appl
Sequence 64869, A
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Sequence 64464, A
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# ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OSTTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter
APPLICANT: RASMUSSEN, Peter
APPLICANT: RASMUSSEN, Peter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
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TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUMBER: US/09/791,171
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 1297/97
PRIOR FILING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NUMBER: 1998-01-0
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Best Local S
Matches 98
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61 LLASNASAODOLHRAGEAVODVARTYSQIDDGAAGVFA
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                                                                                                                                                                                                                                                                                                                            100.0%; Score 479; DB 3; larity 100.0%; Pred. No. 1.4e-42; Conservative 0; Mismatches 0;
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RESULT 2 US-09-804-980-88

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                                                              ; LENGTH: 98
TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-138-473-88
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APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
TITLE OF INVENTION: TB Diagnostic Based On An
PILE REPERENCE: 0459-0710P
CURRENT PELICATION NUMBER: US 10/060,428
PRIOR PELICATION NUMBER: US 10/060,428
PRIOR FILING DATE: 2002-01-29
PRIOR PELICATION NUMBER: US 09/415,884
PRIOR PILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 60/116,673
PRIOR APPLICATION NUMBER: US 60/116,673
PRIOR PILING DATE: 1999-01-21
PRIOR PILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-01-28
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                                                                                                                         NUMBER: Pate
SOFTWARE: Pate
; SEQ ID NO 88
"FNGTH: 98
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LENGTH: 98
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Query Match
Best Local Similarity
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APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                            PRIOR APPLICATION NUMBER: DK 1997 00376
PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 174
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PRIOR FILING DATE: 1997-04-18
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                 FILING DATE: 1997-11-10
APPLICATION NUMBER: US 60/044,624
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                                                                                                                                                                            version 3.1
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100.0%;
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Pred. No. 1.4e-42;
Score 479; DB 4;
Pred. No. 1.4e-42;
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RESULT 5
US-10-510-021-62
; Sequence 62, Application US/10510021
; Publication No. US20050220811A1
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US-10-620-246-88
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CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR PILING DATE: 1998-03-30
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1997-04-18
PRIOR PILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
PRIOR APPLICATION NUMBER: 10/138,473
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
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PRIOR PILING DATE: 2002-05-02
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PRIOR FILLING DATE: 2001-02-20
PRIOR PELLORTION NUMBER: 09/415,884
PRIOR FILLING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR FILLING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: 1281/98
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 173
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SEQ ID NO 88
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
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APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE
TITLE OF INVENTION: DESIVED FROM M. TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ANDERSEN, Peter APPLICANT: NIBLSEN, Rikke APPLICANT: OBTTINGER, Tho
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                     61 LLASNASAQDQLHRAGEAVQDVARTYSQIDDGAAGVFA 98
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RASMUSSEN, Peter I
ROSENKRANDS, Ida
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No. US20040115211A1
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CURRENT APPLICATION NUMBER: US/10/510,021
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: PCT/IB03/01789
PRIOR FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: EP 02/290864
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 75
                                                                   PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential PILE REPERENCE: BLITA, 034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Majlessi, Laleh
APPLICANT: Demangel, Caroline
APPLICANT: Leclerc, Claude
TITLE OP INVENTION: Identification
TITLE OF INVENTION: RD5 leading to
TITLE OF INVENTION: microti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Rv3872-PE35 - PE family-related protein
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                                 APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                 Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                           Trawick, John
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Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                                              Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 479; DB 5; 100.0%; Pred. No. 1.4e-42;
60/242,578
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RESULT 7
US-10-282-122A-64869
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                  OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR PILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR PILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-26
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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OR APPLICATION NUMBER: 60/253,625
OR PILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/269,308
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
OR FILING DATE: 2001-02-16
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32; Conservative
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Zyskind, Jud
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27.1%; Pred. No. 0.63;
tive 15; Mismatches
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Prior Application data removed -

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                                                                                                                                                                                                                                                                                                                RESULT 9
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Best Local S
Matches 30
                                                                                                                                                                                                                                                          Sequence 64464, Application US/10282122A Publication No. US20040029129A1
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Best Local Similarity
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SEQ ID NO 4
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 64869
LENGTH: 588
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TITLE OF INVENTION: MYCOBACTERIAL PROTEINS AS
FILE REFERENCE: 32004-173355
CURRENT APPLICATION NUMBER: US/10/481,563A
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/212,048
PRIOR PILING DATE: 2000-66-16
PRIOR FILING DATE: 2000-66-16
PRIOR PILING DATE: 2000-66-16
PRIOR PILING DATE: 2000-68-16
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APPLICANT:
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              FITLE OF INVENTION: Identification of Essential Genes
                                  APPLICANT:
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REFERENCE: ELITRA.034A
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                                                                                                                   Wall, Daniel
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Zyskind, Judith
                                                Yamamoto, Robert Forsyth, R.
                                                                                                       Trawick, John
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Malone, Cheryl
Haselbeck, Robert
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33.0%; Pred. No. 1;
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33.0%; Pred. No.
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PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-25
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
GENERAL INFORMATION:
                Sequence 64347, Application US/10282122A Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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TYPE: PRT
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FILING DATE: 2000-09-06
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32.9%; Pred. No. 2;
tive 15; Mismatches
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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR APPLICATION NUMBER: 60/230,335
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APPLICANT: Zamudi
APPLICANT: Malone
APPLICANT: Haseli
APPLICANT: Ohlser
APPLICANT: Zyskir
APPLICANT: Wall,
APPLICANT: Trawic
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Malone, Chery
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Forsyth, R.
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US-10-282-122A-64547
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                                      PRIOR APPLICATION NUMBER: 60/29, 6848
PRIOR PILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-07
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR PILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/267,636
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-10-23
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Yamamoto, Robert
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Trawick, John
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Zyskind, Judith
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Malone, Cheryl
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RESULT 12
US-10-282-122A-64514
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US-10-282-122A-64514
                                                                         Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE PatentIn version 3.1
SEQ ID NO 64514
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LENGTH: 576
TYPE: PRT
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Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT FILING DATE: 2003-02-20
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            TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                      ENGTH: 562
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OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Yamamoto, Robert
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Wall, Daniel
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Malone, Cheryl
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US-10-282-122A-64589
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Best Local S
Matches 37
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Publication No. US20040029129A1
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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PRIOR TILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                   LENGTH: 1011
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/253,625
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 59 IQLLASNASA 68
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                                       MSFLLVEPDLVTAAAAN-LAGIRSALSEAAAAASTPTTALASAGADEVSAAVSRLFGAYG 59
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                                                                                                              Score 81; DB Pred. No. 18; 7; Mismatches
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
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US-10-282-122A-62423
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 62423
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                                                                                                                                                                                                                                                                                                               LENGTH: 31
TYPE: PRT
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                                            69 -QDQ-LHRAGEAVQDVARTY--SQIDDGAA 94
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72 FHDOFVHTLTAA----ARWYTATBIANAAA 97
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13; Mismatches
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US-10-282-122A-64606
, Sequence 64606, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

RESULT 15

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APPLICANT: Meschbeck, John
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDS5/ptodata/2/pubpaa/US03_NEW_PUB.pep:*

6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /SIDS5/ptodata/2/pubpaa/US01_NEW_PUB.pep:*
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991.565 Million cell updates/sec
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US-11-082-554A-161
US-11-082-554A-164
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Publication No. US20050288866A1
GRNERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
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Copyright

GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration

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71.5 14.9 597 7 US-11-331-599-6 70.5 14.7 308 7 US-11-188-298-7300 70.5 14.6 186 7 US-11-188-298-7300 70.14.6 30.5 7 US-11-188-298-19377 14.6 30.5 7 US-11-188-298-19377 14.4 210 6 US-10-793-626-2864 6.9 14.4 210 6 US-10-793-626-2864 6.8 14.3 371 7 US-11-057-012-20 6.8 14.3 424 6 US-10-506-454-368 6.8 14.2 411 7 US-11-188-298-17876 6.7 14.1 452 7 US-11-188-298-17876 6.7 14.1 452 7 US-11-188-298-17929 6.7 5 14.1 452 7 US-11-188-298-17929 6.7 5 14.1 452 7 US-11-188-298-17929 6.7 5 14.1 710 7 US-11-188-298-17929 6.7 14.0 114 6 US-10-467-657-6068 6.7 14.0 114 6 US-10-867-662-10 6.7 14.0 511 6 US-10-986-405-307 6.7 14.0 511 6 US-10-986-453-17	14.9 597 7 US-11 14.6 186 7 US-11 14.6 305 7 US-11 14.4 210 6 US-11 14.3 371 7 US-11 14.3 371 7 US-11 14.1 320 7 US-11 14.1 421 7 US-11 14.1 421 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.1 710 7 US-11 14.0 114 6 US-11 14.0 511 6 US-11 14.0 511 6 US-11	45	44	43	42	41	40	39	38	37	36	S	34	33	32	31	30	29	28	27	Č
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# RESULT 1 US-11-052-554A-165 ; Sequence 165, Application US/11052554A ; Publication No. US20050288866A1 ; Publication No. US20050288866A1 ; Publication No. US20050288866A1 ; GENERAL INFORMATION: ; APPLICANT: Sachdeva, et al. ; APPLICANT: Sachdeva, et al. ; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE ; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL ; FILE REPERENCE: 30853/40359A ; FILE REPERENCE: 30853/40359A

ALIGNMENTS

39; 39; YQELS YQELS   IDDGA   :	39; Gaps 58 .YQELSAHAVA 73 IDDGAAGV 96   :         IGNGANGV 131
19.3%; Score 92.5; DB 7; Length 639; 27.1%; Pred: No. 0.086; ive 15; Mismatches 32; Indels 39; HGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGRANAEALVPITALLPAGADDVSAAIAALFATHGOAYQELS [ASAODQLHRAGEAVQDVARTYSQIDDGA   ;   ;   ;   ;   ;   ;   ;   ;   ;	9; G CELSA QELSA DDGAA :   GNGAN

POTENTIAL IDENTIFYING

ADHESIN AND

ADHESIN-LIKE

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GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POT

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20
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                                                                                                                                                                                                                                                RESULT 4
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US-11-052-554A-157
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                                                                                                                                                                               Sequence 135, Application US/11052554A Publication No. US20050288866A1
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Best Local !
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-02-06
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PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
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NUMBER OF SEQ ID NOS: 763
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o. US20050288866A1
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Pred. No. 0.48;
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RESULT 6
US-11-052-554A-166
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US-11-052-554A-162
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                                                                                                                                                                                                 Sequence 166, Application US/11052554A
Publication No. US20050288866A1
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APPLICANT: Sachdeva, et al
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CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL FILE REFERENCE: 30853/40359A CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILING DATE: 2005-02-07 PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR FILING DATE: 2004-07-20 PRIOR FILING DATE: 2004-07-20
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                                                                                                                                                        APPLICANT: Sachdeva, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPUTATIONAL METHOD FOR TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Th 17.8%; Score 85.5; DB Similarity 30.7%; Pred. No. 0.37; 27; Conservative 10; Mismatches
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28.9%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFYING ADHESIN AND ADHESIN-LIKE POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 543;
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                                                                                                                                         AND ADHESIN-LIKE
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GENERAL INFORMATION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION NUMBER: US/11/52,554A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: UN 10/589,227
PRIOR APPLICATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-052-554A-149
; Sequence 149, Application US/11052554A
; Publication No. US20050288866A1
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; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-164
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GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

CURRENT FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: NS 60/589,227
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NUMBER OF SEQ ID NOS: 763
SOPTWARE: PatentIn version 3.3
SEQ ID NO 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.3 SEQ ID NO 164 LENGTH: 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGIGSAIS-----SANAAAAVNTTGLLTAGADEVSTAIAALFGAQGQAYQAASAQA 69
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Pred. No. 0.74;
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APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR ID.
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC PO
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
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                                                                             ; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-137
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APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: UN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
  Matches
                                                                                                                                     SEQ ID NO 137
LENGTH: 1660
                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. US20050288866A1 GENERAL INFORMATION:
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SEQ ID NO 160
                Query Match
Best Local
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Best Local
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Best Local Similarity
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  34; Conservative
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milarity 34.5%;
Conservative 11
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                  16.8%;
37.8%;
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11; Mismatches
                    Score 80.5;
Pred. No. 5
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Pred. No. 2.
red. No. 5.5;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                         IDENTIFYING ADHESIN AND ADHESIN-LIKE POTENTIAL
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  26;
                                      Length 1660;
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  Indels
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  17;
  Gaps
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11 ADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFT--SEGIQLLASNASA 68

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US-11-052-554A-154
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US-11-052-554A-154
                                                                                                                                                                                                                                                                                           Sequence 147, Application US/11052554A
publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
PILE REFERENCE: 30853/40359A
Query Match
Best Local Similarity
                                                                    SOPTWARE: PatentIn version 3.3
SEQ ID NO 147
LENGTH: 923
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
SEQ ID NO 154
LENGTH: 767
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Publication No. US20050288866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
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                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILING DATE: 2005-02-07 PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR FILING DATE: 2004-07-20 PRIOR APPLICATION NUMBER: IN 173/DEL/2004 PRIOR APPLICATION NUMBER: IN 173/DEL/2004 PRIOR FILING DATE: 2004-02-06 PRIOR SEQ ID NOS: 763
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CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR PILICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EAVQ-DVARTYSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSFVVVAPEVLAAAASDLAGIGSTLAQANAAALAPTTAVLAAGADEVSAAIASLFGAHGQ 60
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16.7%;
30.9%;
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Score 80;
Pred. No.
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DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Indels
                   Length 923;
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 Matches
                                  Query Match
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GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
IITLE OF INVENTION: COMPUTATIONAL METHOD FOR ID:
IITLE OF INVENTION: PROTEINS OF THERAPEUTIC POT
IITLE OF INVENTION: PROTEINS OF THERAPEUTIC POT
FILE REFERENCE: 30853/40359A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589, 227
PRIOR PILING DATE: 2004-07-20
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US-11-052-554A-139
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US-11-052-554A-152
                                                                                           US-11-052-554A-139
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 139, Application US/11052554A
Publication No. US20050288866A1
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                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: IN 173/DEL/2004 PRIOR FILING DATE: 2004-02-06
                                                                                                                                      LENGTH: 1306
TYPE: PRT
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                                                                                                                   ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 QDQLH-RAGEAVQDVARTYSQID 90
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Conservative
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15.8%; Score 75.5; ]
34.1%; Pred. No. 13;
tive 11; Mismatches
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31.3%; Pred. No. 4.9;
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20;
                                           Length 1306;
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  Indels
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RESULT 15
US-11-052-554A-159
IS-quence 159, Application US/11052554A
Publication No. US20050288866A1
Publication No. US20050288866A1

Publication No. US20050288866A1

GENERAL INFORMATION:
CART. Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT PAPLICATION NUMBER: US/11/052,554A
CURRENT PILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SEQ ID NO 159
LENGTH: 837
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis H37RV
US-11-052-554A-159
Search completed: April 14, 2006, 18:42:11 Job time : 5.19937 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.7%; Score 75; DB 7; Length 837; Best Local Similarity 36.7%; Pred. No. 8.3; Matches 22; Conservative 7; Mismatches 27; Indels
                                                                                                                                                                                                                                               10 AADIGTQVSDNALHGVTAGSTALTSVTGLVPAGADEVSAQAATAFTSEGIQLLASNASAQ 69 | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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72 HDRFVQTLSAAASS----YVAAEAV 92
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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.

for

WPI; 1998-542705/46. N-PSDB; AAV63938.

Andersen P, Oettinger T,

Rosenkrands I,

Weldingh K,

Rasmussen

PB;

(STAT-)

STATENS SERUM INST. Nielsen R, Florio W;

Claim 1; Page 198; 163pp; English.

102 13.2 135 4 AAM26030 Aam26030 Peptide # 102 13.2 135 4 ABB27414 Abb27414 Human pep 102 13.2 135 4 ABB18062 Abb18062 Protein # 102 13.2 135 4 AAB65771 Aam65771 Human bep 102 13.2 135 4 AAM65771 Aam659771 Human bra 102 13.2 135 4 AAM65171 Aam659771 Aam65995 Human bra 11v Abg47416 Human liv Abg47416 Human pep 101.5 13.1 566 ABB24286 ABG79578 Abg47416 Protein r 101 13.0 1938 6 ABG9849 Abg47416 Protein r 101 13.0 1938 6 ABB98398 Abg47416 Protein r 101 13.0 1938 6 ABB98398 Abg47478 Abg47478 Pseudomon 99.5 12.9 198 7 ABG79582 Abg47478 Human con 97.5 12.6 403 8 Abg116240 Human nuc Abg47478 Human nuc	44	43	42	41	40	39	38	37	36	35	3 <b>4</b>	<u>ω</u>	32	31	30	29	28	27	26	25
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4 AAM26030 Aam26030 4 ABB27414 Abb18062 4 ABB18062 Abb18062 4 AAM65771 Aam65771 4 AAM53395 Abg47416 4 ABG47416 AbM53395 5 ABG35403 Abg35403 6 ADA24286 Ab079578 6 ABB98398 Ab079578 6 ABB98398 Ab079582 8 ABO79582 Ab079582 8 ABO79582 Ab079582 8 ABO79582 Ab079582 8 ABO79582 Ab079582 9 ABA66269 Ab66269 8 ABP76678 Ab976678 7 ADF60212 Aca20959 8 AD116240 Ab059460	12.6 12.5	12.6	12.6	12.7	12.8	12.9	12.9	12.9	12.9	13.0	13.0	13.1	13.2	13.2				13.2	13.2	13.2
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### ALIGNMENTS

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RESULT 1
AAW72928
18-APR-1997;
10-NOV-1997;
05-JAN-1998;
                                                                                     01-APR-1998;
                                                                                                                    08-OCT-1998.
                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                     Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen;
                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis antigen RD1-ORF4.
                                                                                                                                                                                                                                                                                                                                          AAW72928;
                                                                                                                                                                                                                                                                                                                                                                        AAW72928 standard; protein; 139
                                                  02-APR-1997;
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                                                                                                                                                                                                                       infection.
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               97US-0044624P.
97DK-00001277.
   98US-0070488P
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         protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (1) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPTS9 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                             The invention
                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                            WPI; 1999-347282/29.
                                                                                                                                                                                                                                                                                                                                                         05-JAN-1998;
01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis, fusion polypeptide, pharmaceutical; vaccination; M. af CFP7B; CFP29; CFP27; CFP30A; RD1-CCFP25A; CFP30B; CFP7B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of antigen
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                                                                                                                                                                                                                                   immunogenic fragment of Mycobacterium
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                                                                                                                                                                                                        Page 216; 265pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                               n describes a substantially pure immunogenic polypeptide from Mycobacterium tuberculosis that is able to evoke a
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M. africanum; M. bovis; CFP7A; CFP30;
RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
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Pred. No. 6.8e-63;
; Mismatches 0;
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epitope; ESAT-6; MPT59; TB;
                                                                                                                                                                                                                                   tuberculosis
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Best Local (
The invention relates to a novel DNA derived from a human adult brain, tonsil, hippocampus and human fetal brain and its encoded polypeptide, at given in the specification. The novel DNA is useful as a diagnostic agent. The encoded polypeptide is useful as a reagent for screening pharmaceutical compounds which inhibit the biological activity of the polypeptide. A gene containing the novel DNA is useful as a probe for diagnosing the increased expression of damage, mutation or expression reduction in the human DNA. This sequence represents the protein derived from a novel human DNA sequence used in the screening and disgnostic method of the invention. Note: This sequence is an embedded protein taken from the coding DNA shown in the sequence listing of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP3OA or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of TB in a mammal by performing a DTH type skir test; use of CFP27, CFP3OA, RD1-ORF2, RD1-ORF3, RD1-ORF5, MPT99-ESAT6, ESAT6-MPT59, CFP3OA, CFP16, CFP3, CFP23A, CFP3OB, CFP7B or a T-cell epitope of for the preparation of an immunological composition; and for the preparation of a subunit vaccine
                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB86063 standard; protein;
                                                                                                                                                                                                           Claim 4; SEQ ID NO
                                                                                                                                                                                                                                                           hippocampus and
                                                                                                                                                                                                                                                                            Novel DNA derived from human adult brain, human tonsil, human adult
                                                                                                                                                                                                                                                                                                                            WPI; 2003-793311/75
                                                                                                                                                                                                                                                                                                                                                             (KAZU-)
                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2001; 2001JP-00379607.
                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2001; 2001JP-00379607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2003180359-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic; screening; pharmaceutical; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEB86063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 139
                                                                                                                                                                                                                                        gene
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diagnostic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWL
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                                                                                                                                                                                                                                                                                                                                                             KAZUSA DNA
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                                                                                                                                                                                                        20; 87pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA damage detection related human DNA, SEQ
                                                                                                                                                                                                                                                           fetal whole brain and encoding
                                                                                                                                                                                                                                                                                                                                                               KENKYUSHO.
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Pred. No. 6.8e-63;
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                                                                                                                                                                                                                                                           polypeptide, useful
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reticuloendotheliosis viral oncogene-B Rel homology domain (RelB RHD).
The invention also relates to a method of identifying at least one test compound that alters binding of RelB RHD to the RelB-kappa-B sequence involving contacting the nucleotide sequence with the polypeptide sequence in the presence and absence of the test compound and detecting sequence of the test compound and detecting elevance of the test compound and detecting sequence of the test compound and detecting caltered specific binding of the nucleotide with the polypeptide in the presence of the test compound compared to that in the absence of the test compound that alters binding of RelB Rel homology domain (RelB RHD) with RelB-C kappaB sequences and the therapeutic compounds that alter inhibitor of nuclear factor kappa-B kinase alpha (IKK-alpha) subunit related pathologies. The isolated nucleotide segments are effectively and selectively recognized by RelB:p52 in comparison to ReaL:p50 and RelB:p50 domains. The isolated nucleotide sequence does not bind to RelB, ReaL. p50, RelB:p50, ReaL:p50 and ReaL:p50 and RelB; ReaL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                              Isolated nucleotide sequences mediating functions of inhibitor of nuclear factor kappa-B kinase alpha subunit useful for identifying therapeutic compounds that alter the subunit related pathologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reticuloendotheliosis viral oncogene-B Rel homology domain; RelB nuclear factor kappa-B; NFk-B; gene expression.
                                                                                                                                                                                                                                                    The invention
                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 130; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-273503/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003; 2003US-0508349P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2005033284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RVNDPP----APGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAA-----SSSAGL
                                                                                                                                                                                                                                                                                                                                                                           ADZ44699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELP-----
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                                                                                                                                                                                                                                                      relates to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SG----PPLPNGLKPEFALALPPEPPPGPEVKGGSCGLEHGE
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bebien
                                                                                                                                                                                                                                                      an isolated nucleotide sequence
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Pred. No. 0.21
9; Mismatches
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    the specific binding
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                                and RelB:p50
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de in the
                                                                                                                                                                                                                                                      binds
                                                                                                           compound
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RESULT 5
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Best Local
                                                                                                                                           Modulating a steroid receptor or steroid receptor process for treating onset of labor and cancer, comprises administering a polypyridimine tribinding protein-associated splicing factor polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the nucleotide sequence with a polypeptide having a RelB RHD inc: transcription of a required nucleic acid sequence that is operably to the nucleotide sequence and links induction of chemotines to activation of the IKK-alpha-dependent NF-kappa B signaling pathway. sequence represents an NFk-B protein of the invention.
                                                                                                                                                                                      GENBANK;
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                                                                                                                                                                                                                                                                                                                                       WO2005068501-A1
                                                                                                                                                                                                                                                                                                                                                                                parturition;
                                                                                                                                                                                                                                                                                                                                                                                                             Human PSF proline/glutamine rich polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 707
                                                                                                                                                                                                                                                                        15-JAN-2004; 2004US-0536598P
                                                                                                                                                                                                                                                                                             14-JAN-2005;
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                                                                                                                                                                                                                                                                                                                                                                                          Protein-associated splicing factor; PSF; PSF-A; labor; premature labor;
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DB; AEB31356, A
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                                                                                                                                                                                                                                                                                                                                                                                cytostatic; gynecological; tocolytic.
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Pred. No. 0.7;
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The invention relates to a method of modulating a steroid receptor or a process mediated by a steroid receptor in a cell comprising administering a polypyridimine tract binding protein-associated splicing factor (RSF) polypeptide, a polynucleotide encoding a RSF polypeptide (RSF) polymucleotide), an isolated complex of a RSF polypeptide and a steroid receptor (RSF complex) and/or their agonist or antagonist. The invention also relates to a method of inhibiting transactivation domains of a steroid receptor in a cell by administering to the cell a RSF polypeptide, polynucleotide, complex, and/or their agonist, a method of stimulating transactivation domains of a steroid receptor in a cell by administering to the cell a RSF polypeptide, polynucleotide, complex, and/or their agonist, a method of stimulating transactivation domains of a steroid receptor in a cell by

a PSF polypeptide,

polynucleotide and/or a PSF

Claim 22;

SEQ

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91pp;

English.

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CC mediated by a steroid receptor or characterized by an abnormality in a control of interaction between a PSF polypeptide and a steroid receptor by care disrupting or promoting the interaction in cells or inhibiting or complex and/or their agonist or inhibiting or complex in a control receptor by a steroid receptor by a steroid receptor by a steroid receptor by a steroid receptor by administering or complex and/or their agonist or antagonist. The methods care useful for modulating a steroid receptor or process mediated by a condition mediated by a steroid receptor or individual having a condition mediated by a steroid receptor or characterized by an abnormality in a steroid receptor or characterized by an abnormality in a steroid receptor or characterized by an abnormality in a steroid receptor a PSF polypeptide and a progressive or evaluating a condition mediated by a steroid receptor and for evaluating a condition complex and receptor in a subject and for evaluating a condition mediated by a steroid receptor and for evaluating a condition condition the substance of the substance of the substance of the substance of the substance to fearthing and/or treating or treating of the PSF polypeptide and receptor bind to form a complex and comparing to condition the absence of the substance to determine if the substance or reventing and/or treating pre-term or premature labor, for modulating the methods are also useful for conjugate for preventing or treating a condition mediated by a conjugate or stepping labor, for inducing labor, for preventing of the PSF polypeptide to the receptor controlling the timing of parturition in animals, such as domestic conjugate to the preventing of the preventing or treating a condition mediated by a preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the preventing of the 
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                                                                                                                                                          Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; haemophilia; lung disease; emphysema; obstructive pulmonary disease; haemophilia;
      WO2003023002-A2
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO14750 standard; protein; 1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPKQG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPPGAPPPTPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPPPQDSSKPVVAQGPGPAPGVGSTPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein #123.
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Pred. No. 0.7;
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Best Local
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20-SEP-2001;
20-SEP-2001;
25-SEP-2001;
25-SEP-2001;
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17-SEP-2001;
17-SEP-2001;
17-SEP-2001;
17-SEP-2001;
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Lepley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
                                                                                                                                                                                                                 Sequence 1526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a new isolated polypeptide (NOVX). polypeptide, nucleic acid and antibody are useful as there
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07-SEP-2001;
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DB; ACD19443.
                                                   893
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VL,
RA,
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                                                                                                                                                       Similarity
                                                 PPLPGAGIPPPPPLPGVGIPPPPPLPG---AGIPPPPPL----PGAGIPPPPPLPGAGIP
                                                                                         PPAPGSDSARSRPAPALG--PDPPASGWFDSGLVPSRPICAASSSAGLPPP-----VP
        PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWV-----AAGGNWPTGVELPGEGIP 106
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Vernet CAM,
1, Leach MD,
Taupier RJ,
Edinger SR,
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2001US-0318430P.
2001US-032636P.
2001US-0322781P.
2001US-0322816P.
2001US-0322817P.
2001US-0323631P.
2001US-0323631P.
2001US-0323636P.
2001US-0323639P.
2001US-032363P.
2001US-032363P.
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2001US-032363P.
                                                                                                                                    Conservative
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                                                                                                                                                     13.5%;
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Ellerman K, Berght
Catterton B, Kekudt
Shenoy SG, Liu X,
Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                    8
                                                                                                                                                       Score 104.5;
Pred. No. 1.6;
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li L, Anderson ...,

Berghs C, Rothenberg MB, G
Kekuda R, Ji W, Miller CE;
Liu X, Padigaru M, Alsobrook
                                                                                                                                                                           DB
                                                                                                                                    31,
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                                                                                                                                    Indels
                                                                                                                                                                           Length 1526;
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RESULT 7
                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the CC encoded polypeptides (AAM38642-AAM42213) with nootropic, CC immunosuppressant and cytostatic activity. The polypucleotides are useful CC in gene therapy. A composition containing a polypeptide or polypucleotide CC in gene therapy. A composition treat diseases of the peripheral nervous gystem, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central neurous system diseases, such as CC Allaheimer's, Parkinson's disease, Huntington's disease, amyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activity chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CC c.N.S disorders. Note: The sequence data for this patent did not form
Query Match
Best Local Similarity
Matches 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999;
21-JAN-2000;
25-APR-2000;
25-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotrophic thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                     as central nervous system
                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia.
                                                                                                                                                                                                                                                                                                                                                             2001-442253/47
DB; AAI60083.
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                                                                                                                                                                                                                                                                                           2; SEQ ID NO 5858; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
Wang Z,
Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC
                                                     355
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2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
2000US-00623450.
2000US-00662191.
2000US-0063344.
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Wehrman T,
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                                                                              specification
             13.4%;
28.0%;
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                                                                                                                                                                                                                                                                                                                     injuries.
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Score 103.5; | Pred. No. 0.42 6; Mismatches
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Xu C,
IC RT;
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Xue
             0.42;
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                        DB 4;
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Zhang J,
                                                                                                                                                                                                                                                                                                                                   disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
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RESULT 8
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ID AEB3
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The invention relates to a method of modulating a steroid receptor or a CC process mediated by a steroid receptor in a cell comprising administering CC a polypyridimine tract binding protein—associated splicing factor (PSP) CC polypyridimine tract binding protein—associated splicing factor (PSP) CC polypucleotide, a polynucleotide encoding a PSF polypeptide (PSF) CC polynucleotide), an isolated complex of a PSF polypeptide and a steroid receptor (PSF complex) and/or their agonist or antagonist. The invention CC also relates to a method of inhibiting transactivation domains of a steroid receptor in a cell by administering to the cell a PSF polypeptide, polynucleotide, complex, and/or their agonist, a method of CC stimulating transactivation domains of a steroid receptor in a cell by CC complex antagonist, a method of treating a subject with a condition CC mediated by a steroid receptor or characterized by an abnormality in a steroid receptor or characterized by an abnormality in a steroid receptor or characterized by an abnormality or complex and/or their agonist, and a method of complex polypeptide, complex and/or their agonist or inhibiting or complex polypeptide, complex and/or their agonist or inhibiting or complex polypeptide, complex and/or their agonist or antagonist. The methods care useful for modulating a steroid receptor or process mediated by a steroid receptor or individual having a condition mediated by a steroid receptor or individual having a condition mediated by a steroid receptor or characterized by an abnormal level of interaction between a PSF polypeptide and a steroid as a steroid receptor and a steroid as a steroid receptor or characterized by an abnormal level of interaction between a PSF polypeptide and a steroid condition mediated by a steroid receptor or characterized by an abnormal level of interaction between a PSF polypeptide and a steroid condition mediated by a steroid receptor signal transduction pathway and/or an abnormal level of interaction between a PSF polypeptide and a ster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating a steroid receptor or steroid receptor process for treating onset of labor and cancer, comprises administering a polypyridimine trabinding protein-associated splicing factor polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB31354 standard; protein; 525 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPPGAPPPTPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5; 91pp; English.
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RESULT 9
AEB31353
ID AEB3
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Best Local S
Matches 35
                                  binding protein-associated splicing factor polypept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein-associated splicing factor; SFPQ; PSF-A; labor; premature labor; parturition; cytostatic; gynecological; tocolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEB31353 standard; protein; 634 AA.
Claim 22; SEQ ID NO 4; 91pp; English
                                                                                Modulating a steroid receptor or steroid receptor process for treating onset of labor and cancer, comprises administering a polypyridimine tra
                                                                                                                                                                   GENBANK;
                                                                                                                                                                                                WPI; 2005-522812/53.
                                                                                                                                                                                                                                                       Lyes,
                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004; 2004US-0536598P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human SFPQ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
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                                                                                                                                                                                                                                                                                                             MOUNT SINAI HOSPITAL
                                                                                                                                                                                                                                                 Dong X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAPGSDSAR-----SRPAPALGPDPPASG------WFDSGLVPSRPICAA 45
                                                                                                                                                                   AAH04534.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPPGAPPPTPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%;
28.0%;
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Pred. No. 0.63;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SGVPTTPPQAGGPPPPPAAVPGPGP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
                                                            polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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The invention relates to a method of modulating a steroid receptor or

Protein-associated splicing factor; PSF; PSF-F; labor; parturition; cytostatic; gynecological; tocolytic.

premature labor;

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RESULT 10
AEB31352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc steroid receptor signal transduction pathway and/or an abnormal level of interaction between a PSF polypeptide and a steroid receptor by comparing the interaction in cells or inhibiting or promoting the activity of a PSF complex, and a method of preventing or treating a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor by administering a condition mediated by a steroid receptor or process mediated by a condition mediated by a steroid receptor or individual having a condition mediated by a steroid receptor or characterized by an condition mediated by a steroid receptor or characterized by an condition mediated by a steroid receptor or characterized by an condition mediated by a steroid receptor signal transduction pathway and/or an cabnormal level of interaction between a PSF polypeptide and a steroid receptor. The methods are useful for preventing or treating a condition mediated by a steroid receptor in a subject and for evaluating a condition condition and projector in a subject and for evaluating a control in the absence of the substance to flabor by reacting to a control in the absence of the substance to determine if the substance of preventing and/or treating pre-term labor, for inducing labor in a subject, for preventing or treating a condition mediated by a projector for stopping labor preparatory to Cesarean delivery or for controlling the timing of parturition in animals, such as domestic of the invention.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           process mediated by a steroid receptor in a cell comprising administering a polypyridimine tract binding protein-associated splicing factor (PSF) polypsptide, a polynucleotide encoding a PSF polypsptide (PSF polypsptide), an isolated complex of a PSF polypsptide and a steroid receptor (PSF complex) and/or their agonist or antagonist. The invention also relates to a method of inhibiting transactivation domains of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 634
                                                                                                           Human PSF short form, PSF-F.
                                                                                                                                                         06-OCT-2005
                                                                                                                                                                                                   AEB31352;
                                                                                                                                                                                                                                            ABB31352 standard; protein; 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                          124 GPKQG 128
                                                                                                                                                                                                                                                                                                                                                                                                    106 -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                               86 SAPPGAPPPTPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPAPGSDSAR-----SRPAPALGPDPPASG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                       (first entry)
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28.0%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SSGVPTTPPQAGGPPPPPAAVPGPGP 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 634;
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                                                                                                                                                                                                                                                                                                                                                   abnormality in a steroid receptor signal transduction pathway and/or an abnormal level of interaction between a PSF polypeptide and a steroid receptor. The methods are useful for preventing or treating a condition mediated by a steroid receptor in a subject and for evaluating a substance for its ability to regulate the onset of labor by reacting a PSF polypeptide and a progesterone receptor and a test substance, where the PSF polypeptide and receptor bind to form a complex and comparing to a control in the absence of the substance to determine if the substance stimulates or inhibits the binding of the PSF polypeptide to the receptor and thus regulates the onset of labor. The methods are also useful for preventing and/or treating pre-term labor, for inducing labor in a subject, for preventing or treating a condition mediated by a progesterone receptor, for modulating the onset of labor, for preventing pre-term or premature labor, for reducing the risk of pre-term or premature labor, for stopping labor preparatory to Cesarean delivery or for controlling the timing of parturition in animals, such as domestic
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        steroid receptor signal transduction pathway and/or an abnormal level of interaction between a PSF polypeptide and a steroid receptor by disrupting or promoting the interaction in cells or inhibiting or promoting the activity of a PSF complex, and a method of preventing or treating a condition mediated by a steroid receptor by administering a PSF polypeptide, complex and/or their agonist or antagonist. The methods are useful for modulating a steroid receptor or process mediated by a steroid receptor in a cell, for treating a subject or individual having a condition mediated by a steroid receptor or process mediated by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          process mediated by a steroid receptor in a cell comprising administering a polypyridimine tract binding protein-associated splicing factor (PSF) polypeptide, a polymucleotide encoding a PSF polypeptide (PSF) polypeptide), an isolated complex of a PSF polypeptide and a steroid receptor (PSF complex) and/or their agonist or antagonist. The invention also relates to a method of inhibiting transactivation domains of a steroid receptor in a cell by administering to the cell a PSF polypeptide, polymucleotide, complex, and/or their agonist, a method of stimulating transactivation domains of a steroid receptor in a cell by administering to the cell a PSF complex antagonist, a method of treating a subject with a condition mediated by a steroid receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by an abnormality in a second receptor or characterized by a second receptor or characterized by an abnormal receptor or characterized by an abnormal rece
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                                                                                                                                                                                                                                                                                                                                                   Sequence 669 AA;
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                                                                                                                                                           σ
                                                                                                                                                                                                                                                              Similarity
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SSSAGLPPPPVPPTWLNNDVTCCSGWVSCCIGPLISBSWPRVWVAAGGNWPTGVELPGEGI 105
                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a human
                                                                                               PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                           PPAPGSDSAR----SRPAPALGPDPPASG---
                                                                                                                                                                                                                                                       13.4%;
                                                                                                                                                                                                                   Score 103.5; DE Pred. No. 0.82; 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               short
                                                                                                                                                                                                                                                                                     DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                               form PSF, PSF-F.
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                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                           -WFDSGLVPSRPICAA
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RESULT 11
AAM39141
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                              immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
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21-JAN-2000;
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19-JUL-2000;
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                                 The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC which consider the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying an agent CC expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the composition, a method for identifying a method for producing a pharmaceutical composition, a contribution of a method for identifying a compound or small molecule that regulates the contribution of the regulates the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of the contribution of th
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01-NOV-2001;
26-NOV-2001;
polynucleotides, a metnow to polynucleotides, a metnow or method for identifying a compound or method for in an animal of one or more
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segmental nerve injury; chronic constriction injury; CCI;
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RESULT 13
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                       Human;
spinal
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragm derivative or allelic variation of the nucleic acid sequence. Also

fragment

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Claim 1; Page; 1017pp; New composition comprising preparing a medicament for

English

treating

pain

two or more isolated polypeptides, useful treating pain in an animal.

for

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ADE54944
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26-NOV-2001;
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Pred. No. 0.87;
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RESULT 15
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                                                                                                   nerve
                                                                                                                                    pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic cons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPPGAPPPTPP-------SGVPTTPPQAGGPPPPPAAVPGPGP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPAPGSDSAR-----SRPAPALGPDPPASG------WFDSGLVPSRPICAA
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                                                                                                injury;
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                    P23246, SEQ ID NO 752.
                                                                                                SNI; Chung.
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28.0%;
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Pred. No. 0.8
                                                                                                                                    chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                                                                                                             CC claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence comprising the vector, a method for identifying a nucleotide sequence comprising the vector, a method for identifying an appear and a compound to pain and a compound that increases or decreases the expression of the polynucleotide sequence contact is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity in an animal of one or more of the polynucleotides, a method for identifying a compound useful in treating compound that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates the compound to small molecule that regulates or their antibodies. The polynucleotide or the compound that composition comprising a mediciament for treating compound to seem that the polynucleotide or the compound that compound that satisfies the polynucleotide or the compound that compound to seem to stream the polynucleotide or the compound that compound to seem to seem to seem to seem to seem to seem to seem to seem to seem to seem 
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Best Local S
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENBANK; P23246.
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                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                            159
197
                                           106 -PKIG 109
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                                                                                                                                                                                                                                6 PPAPGSDSAR-----SRPAPALGPDPPASG-----WFDSGLVPSRPICAA 45
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GPKQG 201
                                                                                            SAPPGAPPPTPP----
                                                                                                                                        SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI 105
                                                                                                                                                                                         PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
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                                                                                                                                                                                                                                                                                   Conservative
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28.0%;
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                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                      Score 103.5; Di
Pred. No. 0.87;
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                                                                                              ---SSGVPTTPPQAGGPPPPPAAVPGPGP 196
                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                   Indels 43;
                                                                                                                                                                                                                                                                                                                              Length 707;
                                                                                                                                                                                                                                                                                Gaps
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Search completed: April 14, 2006, 17:18:42 Job time : 55.857 secs

Run on:

Title: Perfect score: Sequence: April 14, 2006, 17:19:08; Search time 8.15065 Seconds (without alignments) 1640.866 Million cell updates/sec US-10-620-246-90 774 1 MRVNDPPAPGSDSARSRPAP......RIDAIGSSFSKSVLTAVSAW 139

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26		24	23	22				18	17			14		12			v		7		ທ	.4			ם ב	No. s	Result
84	84.5	85	85	85.5	86	86	86	86.5	86.5	•	87	87	87.5	87.5	88	88.5	89	89	89.5	90.5	91	91.5	91.5	92	92	93.5	•	103.5	Score	
10.9	10.9		11.0	11.0	11.1	11.1	11.1		11.2	11.2		٠	11.3	11.3	11.4	11.4	11.5	11.5	٠	11.7		11.8	11.8	11.9	11.9	•	12.6	13.4	Match	Query
721	745	241	211	1058	907	839	742	520	448	446	1560	533	817	625	1460	451	744	403	924	380	364	1446	502	980	419	365	240	707	Length	
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B70766	S13586	T22216	B89716	T13286	B96636	T04859	F84643	I84718	D41727	A34418	T00080	S37781	S51342	S18420	EDBEIF	A41651	T35192	S52796	F87103	S51797	I48188	A45344	A55197	S54986	G70602	A39481	D70894	A46302	ID	
hypothetical prote		О		æ	hypothetical prote	extensin homolog F	hypothetical prote	RXR-betal isoform	retinoid X recepto	H-2 region II bind	íca	retinoid X recepto	verprolin - yeast	regulatory protein	immediate-early pr	retinoic acid rece	probable ABC trans	prpL2 protein - hu	initiation factor	vasodilator-stimul	gene NKx6.1 protei	immediate-early pr	Wiskott-Aldrich sy	regulatory protein	hypothetical prote	node	H	PTB-associated spl	Description	

RESULT 2 D70894

45	44	43	42	41	40	39	38	37	36	35	3 4	ω G	32	31	30
81.5	81.5	81.5	81.5	82	82	82.5	82.5	82.5	82.5	82.5	83	83	83.5	84	84
10.5	10.5	10.5	10.5	10.6	10.6	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.8	10.9	10.9
1820	373	319	133	1213	907	1278	1255	838	576	129	564	342	670	2357	846
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A55494	A47234	F75420	C86473	A41724	A45560	T27925	T31065	VGBEG1	T36729	T06174	H70804	S18649	F84540	A59249	H70599
latent transformin	homeobox protein H	hypothetical prote	arabinogalactan-pr	limb deformity (ld	sporozoite surface	hypothetical prote	diaphanous protein	glycoprotein H pre	probable serine/th	pZE40 protein - ba	hypothetical prote	homeotic protein H	hypothetical prote	class VII unconven	hypothetical prote

# **ALIGNMENTS**

Db 197 GPKQG 201	Qy 106 -PKIG 109	159	Qy 46 SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI	Db 99 PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT	Qy 6 PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPIC	Query Match 13.4%; Score 103.5; DB 2; Length 707; Best Local Similarity 28.0%; Pred. No. 0.35; Matches 35; Conservative 6; Mismatches 41; Indels 43; Gap:	C;Keywords: alternative splicing; pre-mRNA splicing; surface antigen F;298-359/Domain: ribonucleoprotein repeat homology <rrm1> F;372-438/Domain: ribonucleoprotein repeat homology <rrm2></rrm2></rrm1>	A;Gene: GDB:SFPQ; PSF A;Cross-references: GDB:138275 A:Map position: 4g-4g	A;Molecule type: mRNA A;Residues: 312-707 <gow> A;Cross-references: UNIPARC:UPI000016A1B4; GB:X16850; NID:g23711; PIDN:CAA34747.1; PID:</gow>	A;Accession: A43557 A;Status: preliminary	d characterization of a myoblast cell A43557; MUID:90091812; PMID:2480877	A;NOTE: Bequence extracted from NCB1 Dackbone (NCB1:12/200)  R;Gower, H.J.; Moore, S.E.; Dickbon, G.; Elsom, V.L.; Nayak, R.; Walsh, Davolonment 105 723-731 1080	-references: UNIPROT:P23246; UNIPARC:UPI00001358B9; EMBL:X70944;	A;ACCEBBIOII: AMBJUZ A;Molecule type: mRNA A:Boidines: 1-707 / DBTN	d characterization of PSF, a novel pre-mRNA splicing A46302; MUID:93194059; PMID:8449401	R;Patton, J.G.; Porro, B.B.; Galceran, J.; Tempst, P.; Nadal-Ginard, B. Genes Dev. 7, 393-406, 1993	C;Species: Homo Sapiens (man) C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004 C;Accession: A43302: A4357; S29995	PTB-associated splicing factor, long form - human N;Alternate names: myoblast cell surface antigen 24.1D5; polypyrimidine tract-binding	RESULT 1
			NAGGNWPTGVELPGEGI 105	PGSGPGPTPTPPPAVT 158	WFDSGLVPSRPICAA 45	ngth 707; Nels 43; Gaps 4;	Ce		:g23711; PIDN:CAA34747.1; PID:		surface antigen defined by 24				mRNA splicing factor.	lal-Ginard, B.	change 31-Dec-2004	polypyrimidine tract-binding F	

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probable pra protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: D70894

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Reference number: A70500; MUID:98295987; EMID:9634230

A;Accession: D70894
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S
                                                                                                                                                                                                                                                                                                                      A;Title: Human myocyte-specific enhancer factor 2 comprises a group of tissue-restricted A;Reference number: S25830; MUID:92387551; PMID:1516833 A;Accession: S25832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serum response factor-related protein 2 - human
N;Alternate names: myocyte-specific enhancer factor xmef2; RSRF2
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change (C;Accession: A39481; S25832; S24468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Human SRF-related proteins: DNA-binding properties A;Reference number: A39481; MUID:92084105; PMID:1748287 A;Accession: A39481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Pollock, R.; Treisman, R.
Genes Dev. 5, 2327-2341, 1991
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                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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A; Residues: 1-365 < POL>
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Matches 36
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Keywords: DNA binding; homodimer; transcription factor;
2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                                                                                                    Status: preliminary
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                                         PPVGAEAWARRVPQPAAPPRRP------PQSASSLSASLRPPGAPATFLRPSP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSCVTSISEYDVGQFCVSQPSMIGQLVQWLLSVGGLAYLVWNYGYRQGTIGSSIGKSVL
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                                                                               PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGL-PPPVPPTWLNNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPPPGPSGGHEPPPAA---PPGG----SGYAPPPP---PSSGSGYPPPPPPPGGGAYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPP-----
                                                                                                                      12.1%;
ilarity 32.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
  -WVSCC-IGPLISPSWPRVWVAAGGNWPT---GVELPGEGIPK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.6%;
                                                                                                                    4;
                                                                                                                      Score 93.5; Di
Pred. No. 1.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 97.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4;
                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                              Length 365;
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                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            potential regulatory tax
                                                                                                                        31;
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                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN
                                                                                                                                                                                                                                               PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulatory protein - Emericella nidulans C;Species: Emericella nidulans, Aspergillus nidulans C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #t C;Accession: S54986
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A; Residues: 1-980 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:005589;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: G70602
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A;Residues: 1-419 <COL>
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Best Local S
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        114 WLAPGSRIDAIGSSFSKSVLTAVSAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PGVPDPITGVNTAAAVVNGV 181
                                                                                                                                             PPPPGAGAAPPPPPP---
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                             11.9%;
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26.1%;
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                                                                                                                                                                                                                                             Score 92;
Pred. No.
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Pred. No. 1.9;
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C;Accession: S54986
R;Marhoul, J.F.; Adams, T.H.
Genetics 139, 537-547, 1995
A;Title: Identification of developmental regulatory genes
A;Reference number: S54986; MUID:95229045; PMID:7713416
A;Accession: $54986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E., Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70602
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G70602
G70602
G70602
hypothetical protein Rv1004c - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 17-011-1998 #sequence_revision 17-Jul-1998 #text_c
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI00001688EC; EMBL:L36341; NID:g540283; PID:g540284
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RSTSAAAASYWWCICVPPPPPPPPGTVIGGWRANYLASQG-----
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                                                      LINDVTCCSGWVSCCIGPLISP-----SWPRVWVAAGGNWPTGVELPGEGIPKIGFVVL 113
                                                                                                                                                                                 PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGL---PPPVPPT---W 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTATPSGPAAAEHAVPA--PFEPVADTIAPGLVPRPGVPAAAAVPRVGPPAVPGLPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCSGWVSCCIGP-----LISPSWPRVWVAAGGNWPTGVELPGEGIPKIGFVVLW 114
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                                                                                                                       -GLGGPPPLPSPSSTGWFWWTPAASPSTWWFW 532
                                                                                                                                                                                                                                                                                                            DB 2; Length 980
                                                                                                                                                                                                                                              60; Indels
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   --APSHAIP----VMS
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   581
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SIRPKKKCLKAL--HWDKVDTPQVTVW

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A;Molecule type: mRNA
A;Residues: 1-424, 'PG', 427-502 <DER>
A;Residues: 1-424, 'PG', 427-502 <DER>
A;Cross-references: UNIPARC:UPI000017C422; GB:U12707; NID:g695150
A;Note: the translated sequence in GenBank entry HSU12707 (PINN:AAA62 R;Kwan, S.P.; Hagemann, T.L.; Radtke, B.E.; Blaese, R.M.; Rosen, F.S. Proc. Natl. Acad. Sci. U.S.A. 92, 4706-4710, 1995
A;Title: Identification of mutations in the Wiskott-Aldrich syndrome A;Reference number: 138931; MUID:95273432; PMID:7753869
A;Accession: I38931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Derry, J.M.J.; Ochs, H.D.; Francke, Cell 78, 635-644, 1994
A;Title: Tecl. 1994
             A;Reference number: A45344; MUID:91021039; PMID:2171211
A;Accession: A45344
                                                                 immediate-early protein - suid herpesvirus 1 (strain Kaplan)
[;Species: suid herpesvirus 1
[;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
[;Accession: A45344
[;Vicek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzer, M.
Virology 179, 365-377, 1990
[A;Title: Pseudorabies virus immediate-early gene overlaps with a
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A;Map position: Xp11.23-Xp11.22
A;Note: defects in this gene may result in Wiskott-Aldrich syndrome
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A;RESIQUES: 1-328,'A',330-366,'LIHHPLQLLDVLDHCPLHPLELVGHPCHH','HRHHRHRRPAPGMDQPLPHSLLLWQ
A;Cross-references: UNIPROT:P42768; UNIPARC:UPI000017C421; GB:U12707
A;Note: this sequence is corrected in reference A55197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Isolation of a novel gene mutated A;Reference number: A54747; MUID:94349367; A;Accession: A54747
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A55197
Wiskott-Aldrich syndrome protein WASP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:WAS; IMD2; WASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A55197
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Date: 23-Mar-1995 #sequence revision 24-Nov-1999

Accession: A54747; A55197; I38931
  Status: translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVP----PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGIPKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPIVGGNKGRSGPLPPVPLGIAPPPPTPRGPPPPGRGG-----PPPPPPPATGRSGPLPP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAPGSDSARSRPAPAL-----
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not shown
                                                                                                                                                                                                                                                                                                                                                                                                      118
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27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.5; DB
Pred. No. 2.5;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GPDPPASGWFDSGLVPSRPICAASSSAGLPP 53
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PMID:8069912
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Rosen, F.S.
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                                                                       oppositely oriented
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R;Haffner, C.; Jarchau, T.;
EMBO J. 14, 19-27, 1995
A;Title: Molecular cloning,
A;Reference number: S51796;
                                                                                                                                        vasodilator-stimulated phosphoprotein - human C;Species: Homo sapiens (man) C;Date: 15-7ul-195 #sequence revision 09-Mar-1996 C;Accession: S51797; S55526
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;237-293/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Pancreatic beta cells express a diverse set of homeobox genes. A;Reference number: I48185; MUID:95083670; PMID:7991607 A;Accession: I48188 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: I48188
C;Accession: I48188
R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.;
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene NKx6.1 protein - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
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A;Molecule type: mRNA
A;Residues: 1-380 <HAF1>
                                      A; Accession: S51797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-364 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPAPGSDSARSRPAPALGP-----DPPASGWFDS-------GL-----VPSR 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVASGAALPSASPSGSSSSSSSSASATSASAAAAAAAAAAAAAASSPAGLLAGLPRFSSL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPP----
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                                                                                                                       Reinhard,
                                                            structural analysis MUID:95129547; PMID
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Pred. No.
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                                                                                                                       M.; Hoppe,
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                                                            PMID: 7828592
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                                                                                                                       Lohmann, S.M.; Walter,
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A;Cross-references: UNIPROT:P50552; UNIPARC:UPI0000001C69; EMBL:Z46389; NID:g624963;

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C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: P87103
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holr
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F87103
A;Accession: F87103
A;Residues: 1-924 <STO>
A;Cross-references: UNIPROT:Q9ZSI9; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g1309337
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 11-32;87-96;140-154;255-282;297-303;305-322 <HAP2>
A;Residues: 11-32;87-96;140-154;255-282;297-303;305-322 <HAP2>
A;Cross-references: UNIPARC:UPI000017C415; UNIPARC:UPI000017C416; UNIPARC:UPI000017C417
C;Keywords: phosphoprotein
                                                                                                                                                                                                                prpL2 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 10-Nov-1995
C;Accession: $52796
R;Ruhlmann, A.; Kreideweiss, S.; Nordheim, A.
                                                                                                                                                          A; Reference number: S52796
A; Accession: S52796
                                                                                                                                                                                               submitted to the EMBL Data Library, March 1995
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Query Match
Best Local S
Matches 26
                                                                        ;Molecule type: mRNA
;Residues: 1-403 <RUH>
;Cross-references: UNIPARC:UPI000017C32C; EMBL:X86019; NID:g762950;
                                                                                                                                   Status: preliminary
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42.3%;
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Score 89; DB 2;
Pred. No. 3.3;
1; Mismatches 2
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    Indels
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                                                                               PID:g762951
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C;Accession: A41651
R;Yu, V.C.; Delsett, C.; Andersen, B.; Holloway, J.M.; Devary, O.V.; Naeser, A.M.; Kim, Cell 67, 1551-1266, 1991
A;Title: RXRbeta: a coregulator that enhances binding of retinoic scid, thyroid hormone A;Reference number: A41651; MUID:92103690; PMID:1662118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
T35192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retinoic acid receptor coregulator - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Seeger, K.; Harris, D.; Parkhill, submitted to the EMBL Data Library, A;Reference number: Z21571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable ABC transporter - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35192
                                                               밁
                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UPI0000170BFE; GB:M81766; NID:9206602; PIDN:AAA42025.1; C;Superfamily: retinoic acid receptor alpha; erbA transforming protein homology C;Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  망
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                                                                                                                                                                                                                                F;121-367/Domain: erbA transforming protein homology
                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-451 < YUA>
                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A41651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A41651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:069995;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-744 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T35192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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VTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI--PKIGFVVLMLAP----
                                                               PPSSPPGPPHTPSAPPPPMPPPPLGS-----PFPVISSSMGSPGLPPPAPPGF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAP----GSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSRSGVDSPRSGPRPPLPPDRP---
                                                                                                         PPA--PGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLNND 63
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27.7%; Pred. No. 4;
tive 12; Mismatches
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April 1998
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regulatory protein nifA - Azospirillum brasilense C;Species: Azospirillum brasilense C;Species: Azospirillum brasilense C;Aze: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004 C;Azccession: S18420 R;Liang, Y.Y.; Kaminski, P.A.; Elmerich, C. Rol. Microbiol. 5, 2735-2744, 1991 A;Title: Identification of a nifA-like regulatory gene of Azospirillum brasilense A;Accession: S18420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
S18420
                                                                                                                                                                                                                                                                                  A;Gene: nifA
C;Superfamily: response regulator (sigma54-dependent transcriptional activator), FhlA ty
C;Superfamily: response regulator regulation regulation
C;Keywords: DNA binding; P-loop; transcription regulation
F;205-426/Demain: RNA polymerase sigma factor interaction domain homology <SFI>
F;205-426/Region: nucleotide-binding motif A (P-loop) #status atypical
F;300-304/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1460 <CHS>
A;Residues: 1-1460 <CHS>
A;Cross-references: UNIPROT:P11675; UNIPARC:UPI000017497B
C;Superfamily: herpesvirus immediate-early protein IB175
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies vi A;Reference number: S04713; MUID:89315207; PMID:2546124
A;Accession: S04713
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A;Residues: 1-625 <LIA>
A;Cross-references: UNIPROT:P30667; UNIPARC:UPI000013007F; EMBL:X60714; NID:g38677; PIDN
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Best Local S
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                                                                                             502 PAPVPEPAGAAAARGRPARRVVPRPLAGLRRRPAGG---SG--PPDPACPCPSRAPLPPQ 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
                                             55 VPP 57
                                                                                                                                        7 PAP----GSDSARSRPAPALGPDP-----PASGWFDSGLVPSRPICAASSSAGLPPP 54
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APP 559
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re greater than or equal to the score of the result being printed,
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SULT 2 6VG2 HUMAN Q86VG2 HUMAN PRELIMINARY; Q86VG2; Q80VG2; Q1-JUN-2003 (TrEMBLrel. 24, Q1-JUN-2003 (TrEMBLrel. 24, Q1-MAR-2004 (TrEMBLrel. 26, Splicing factor proline/gluu protein associated). Name=SFPQ;	Query Match Best Local 2 2 Matches 49 177 52 226 104	JUENCE HUMAN PRELIMINARY;  1-JUN-2002 (TrEMBLrel 21, 11-JUN-2002 (TrEMBLrel 21, 11-JUN-2002 (TrEMBLrel 26, 11 11-MAR-2004 (TrEMBLrel 26, 11 11-MAR-2004 (TrEMBLrel 26, 11 11-MAR-2004 (TrEMBLrel 26, 11 11-MAR-2004 (Human).  DI SAPIGNE SEQUENCE SUBJECTION SEQUENCE SUBJECTION SEQUENCE SUBJECTION SUBJ	32 95 12.3 373 1 ZE 33 95 12.3 958 2 Q7 34 95 12.3 1300 2 Q4 35 95 12.3 1300 2 Q4 36 94.5 12.2 298 2 Q5 37 94.5 12.2 298 2 Q5 38 94.5 12.1 370 2 Q8 40 94 12.1 370 2 Q8 41 94 12.1 1754 2 Q4 41 94 12.1 1754 2 Q4 41 94 12.1 365 1 ME 42 93.5 12.0 240 2 Q7 44 92.5 12.0 240 2 Q7 45 92 11.9 419 2 Q0 RESULT 1 RESULT 1
PRT; 707 AA.  Created) Last sequence update) Last annotation update) amine rich (Polypyrimidine	O. 1.7; DB 2; DB 2; DB 2; DB 2; Ind atches 52; Ind DBPASGWFDSGLVPSRP	PRT; 334 AA.  sated) t sequence updat t annotation upd 'raniata; Vertebr [lires; Primates; lires; primates; ances of unidenti w cDNA clones wh mRNA. 65BDED7D0A778E19	ZEN_DROSU Q7JXX2_DROME Q81184_DROME Q81284_DROME Q40297_LEIMA Q531.C9_ORYSA Q50N41_ORYSA Q50N41_ORYSA Q60725_MOUSE Q40714_TEING Q45714_TEING Q45812_TEING Q45812_TEING MEF2B_HUMAN Q7U0Q2_MYCBO Q558M6_CRYME Q05589_MYCTU ALIGNMENTS
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyaki S., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyaki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Butkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RGnerstion and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RD Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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05vu37 HUMAN 1
Q5vu37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensembl; ENSG00000116560; Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0000398; P:nuclear mRNA splicing, via spliceosome;
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Mammalia; Eutheria; E
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HSSP; O08583; 1NO8.
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InterPro; IPR012975; NOPS
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28.0%;
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6; Mismatches
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Matches 33
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EMBL; AL646016; C
GO; GO:0003779; E
GO; GO:0016043; E
GO; GO:0007242; E
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01-FEB-2005
13-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000591; DEP.
InterPro; IPR009408; Drf FH1.
InterPro; IPR003104; FHZ actin bd.
InterPro; IPR001220; LecTin legB.
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Name=FMN2; ORFNames=RP11-90L13.1-001;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wallis J
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AL359342;
AL513342;
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AL590490;
AL513342;
AL646016;
AL646016;
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PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
1865 AA; 194918 MW; 202D47DABE981F11
                                                                                                                 P---
                                                                                                                                                                                     PPLPGAGIPPPPPPPGG---AGIPPPPPP---PGAGIPPPPPLPGAGIP
                                                                                                                                                                                                                          PPAPGSDSARSRPAPALG--PDPPASGWFDSGLVPSRPICAASSSAGLPPP-----VP
                                                                                                                                                  PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWV-----AAGGNWPTGVELPGEGIP
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                                                                                                                                                                                                                                                                Conservative
                       PRELIMINARY;
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CAH170921.1; -; Genomi

CAH17092.1; -; Genomi

CAH17093.1; JOINED; G

CAH70931.1; JOINED; G

CAH70931.1; JOINED; G

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CAH17121.1; JOINED; G

CAH17093.1; JOINED; G
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P:intracellular sign
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Last sequence
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Pred. No. 13;
8; Mismatches
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Genomic_
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Genomic_DNA.
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Primates; Catarrhini; Hominidae;
                       836
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ng cascade;
                       B
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                                                                                                                                                                                                                                                                                                                                          CRC64;
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Best Local S
Matches 48
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05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
SFPQ protein (Fragment).
Name=SFPQ;
Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; APO
Complete
                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas
                                                                                                                                                                                                                                                                      Bukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                 Q6PIX2;
                                                                                                                                                                                                                                                                                                                                                                                                 Q6PIX2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15466710; DOI=10.1073/pnas.0406410101; Ishikawa J., Yamashita A., Mikami Y., Hoshino Shiba T., Hattori M.;
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OrderedLocusNames=nfa54870;
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                   TISSUB=Placenta;
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                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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Euarchontoglires; Primates; Catarrhini; Homin
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27,
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Pred. No. 6.6;
L5; Mismatches
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Ensembl; ENSG00000116560; Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IE
InterPro; IPR012677; a.b. plait_nuc_bd.
InterPro; IPR012975; NOPS.
InterPro; IPR000504; RNP1_RNA_bd.
Pfam; PF00076; RNP1_RNA_bd.
Pfam; PF00076; RRM 1; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
            TISSUB-Placenta;

WEDLINB-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

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NON TER 525 525
SEQUENCE 525 AA; 55469 MW;
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     Fahey
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Pred. No. 4.6;
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GO; GO:0003676; F:nucleic acid binding; IB
GO; GO:000166; F:nucleotide binding; IBA.
InterPro; IPR012677; a b plait_nuc_bd.
InterPro; IPR012975; NOPS.
InterPro; IPR000504; RNP1_RNA_bd.
Pfam; PP00075; NOPS; 1.
Pfam; PP00076; RRM 1; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
  Patton J. "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full and mouse cDNA sequences.";
                                                                                           NUCLEOTIDE SEQUENCE (MI
SPLICING, AND FUNCTION
                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                            TISSUE=Fetal brain;
MEDLINE=93194059; P
                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                           NCBI_TaxID=9606;
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L; BC004534; AAH04534.2;
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008583; 1NO8.
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  Porro B.B., Galceran characterization of I
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Euarchontoglires; Primates; Catarrhini;
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         Lutz C.S., Cooke C., (
"The snRNP-free UIA (S
subunit as PSF, the po
splicing factor.";
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                       Westergaard O., Boege F.;
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by a direct interaction.";
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MEDLINE=93176127; PubMed=8439294;
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a DNA-binding heterodimer
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                                                                                                                                                                                                                  SNRNP SND SPLICEOSOME COMPLEXES.
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                                                                                                                                                                                                                                                                                                                   INTERACTIONS WITH NONO AND US SNRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11259580; DOI=10.1128/MCB.21.7.2298-2311.2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11514619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION IN HOMOLOGOUS DNA PAIRING, MBDLINE=20392247; PubMed=10931916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straub T., Knudsen B.R., Boege F., "PSF/p54(nrb) stimulates 'jumping' separate DNA helices.", Biochemistry 39:7552-7558(2000).
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PubMed=10858305; DOI=10.1021/b1992898e;
                                                                                                                                               FUNCTION IN
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rejoining
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                                                                                                                                               IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOI=10.1093/nar/28.16.3022
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Matches
Howden P.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL590434; CAI12467.1; -; Genomic_DNA.
Ensembl; ENSG00000116560; Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR012677; a_b_plait_nuc_bd.
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01-FEB-2005 (TrEMBLrel. 29, Last ar
Splicing factor proline\/glutamine
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Q5SZ71;
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                                                                                                                    NUCLEOTIDE
                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                      Name=SFPQ; ORFNames=RP11-181E22.2-001;
                                                                                                                                                                                                                                                                                                                            01-FBB-2005
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                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 280: - FUNCTION: DNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      establish a functional preligation complex. SPPQ is involved in transcriptional regulation. Transcriptional repression is probably mediated by an interaction of SFPQ with SIN3A and subsequent recruitment of histone deacatylases (HDACs). The SFPQ-NONO/SF-1 complex binds to the CYP17 promoter and regulates basal and cAMP-dependent transcriptional avtivity. SFPQ isoform Long binds to the DNA binding domains (DBD) of nuclear hormone receptors, like RXRA and probably THRA, and acts as transcriptional corepressor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          involved in homologous DNA pairing; in vitro, promotes the invasion of ssDNA between a duplex DNA and produces a D-loop formation. The SFPQ-NONO heteromer may be involved in DNA unwinding by modulating the function of topoisomerase I/TOP1; in vitro, stimulates dissociation of TOP1 from DNA after cleavage and enhances its jumping between separate DNA helices. The SFPQ-NONO heteromer may be involved in DNA nonhomologous end joining (NHEJ) required for double-strand break repair and V(D)J recombination and may stabilize paired DNA ends; in vitro, the complex strongly stimulates DNA end joining, binds directly to the DNA substrates and cooperates with the KU70/G22P1-KU80/XRCS (KU) dimer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypyrimidine tracts. Interacts with U5 snRNA, probably by binding to a purine-rich sequence located on the 3' side of U5 snRNA stem 1b. May be involved in a pre-mRNA coupled splicing snRNA stem 1b. May be involved in a pre-mRNA coupled splicing polyadenylation process as component of a snRNP-free complex w SNRPA/U1A. The SFPQ-NONO heteromer associated with MATR3 may parallel in nuclear retention of defective RNAs. SFPQ may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear processes. Essential pre-mRNA splicing factor requearly in spliceosome formation and for splicing catalytic
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                                                                                                                                                                                    Eutheria;
                                                                                                                  SEQUENCE
                                                                                                                                                                                                      Metazoa;
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Euarchontoglires; Pr
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                                                                                                                                                                                                                                                                                        Last sequence update)
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Wallend S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Malcaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Malcaud S., Jaffe D., Fischer S., Boudet N., Castellano S.,
Malcaud C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Malcaud C., Jubin C., Castelli V., Katinka M., Vacherie B.,
Malcaud C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Malcaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,
Malcaud C., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
Malcaud C., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
Malcaud T., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Malcaud V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Malcaud V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander B.S., Walssenbach J., Roest Crollius H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                  Submitted (FEB-2004) to the
                                                                                                                                                                                       NUCLEOTIDE SEQUENCE. Genoscope; Whitehead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=GSTENG00022009001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA splicing.
SEQUENCE 707 AA;
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InterPro; IPR000504;
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mitosis. Co
repetitive
MPF (By sim
                                                   oscope; whitehead Institute Centre for Genome Research; mitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

FUNCTION: Plays a key role in the control of the eukaryotic cycle. It is required in higher cells for entry into S-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
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                   RNA
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                                    higher cells for entry into S-phase and kinase complex that phosphorylates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome
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                     component
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RESULT 11
Q4S6R8\_TETNG
ID Q4S6R8\_T
AC Q4S6R8;
DT 13-SEP-2
DT 13-SEP-2

Q4S6R8; Q4S6R8; 13-SEP-2005 (13-SEP-2005 (14)

(TrEMBLrel. 31, (TrEMBLrel. 31,

Created)
Last sequence update)

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Matches 35
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Best 1
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EMBL, AKI23968; BAC65736.1; -; mRNA.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6ZVX4;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Wagateuma M., Murakawa K., Kanehori K., Sugiyama A., Kawata Y., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama K., Karehori K., Sugiyama A., Kawata K., Karehori K., Sugiyama K., Karehori K., Sugiyama K., Karehori K., Sugiyama K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Karehori K., Kareh
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ41974.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo.
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SMART; SM00498; FH2; 1.
NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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InterPro; IPR010473; Drf_GTPase_bd
InterPro; IPR003104; FH2_actin_bd.
InterPro; IPR001265; Formin.
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L; CAAE01014700; CAG02796.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               641
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                                                                                                                                                                                       PPAPGSDSARSRPAPALGPDPPAS-GWFDSGLVPSRPICAASSSAGLPPPVPPTWLNNDV
                                                                                                                                 PPTEG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLSPAPASDVCDSAPPPPPALGGVPPPPPPPPPPPPALGAMGA---PPPPPPPPPSAAGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDPPAPGSDSARSR--PAPALG------PDPPASGWFDSGLVPSRPICAASSSAGLP
HTAPSGGGCCVTGPACSIAWAGRSPPSRWIFQRGLTATST-LPG
                                                                -TCCSGWVSCCIGPLISPSW-----PRVWVAAGGNWPTGVELPG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1204 AA;
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                 -AAVTPASSPGPQASLAWRSSG---SRPCCPLTASLTSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                             12.8%;
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AM Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
AM Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
AM Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
AM Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
AM Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
AM Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
AM Anthouard V., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
AM Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
AM Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
AM Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
AM Cruaud C., Duprat S., Brottier P., Kckennan K.J., McEwan P., Bosak S.,
AM Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
AM Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
AM Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
AM Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
AM Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
AM Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
AM Haudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
AM Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
The early vertebrate proto-karyotype.";
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Best Local :
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                                                                                                             Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;
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Bukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
   Sasaki T.,
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Name=P0026A08.31-1; Synonyms=CJ1003_E05.5-1;
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                                                              NUCLEOTIDE
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   Yamamoto K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. Frankia sp. CpI1. Plasmid pFQ12.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004556; BAC99532.1; -; Genomic DNA.
EMBL; AP003936; BAC99403.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002586; CbiA_P_syntĥ. Pfam; Pf01.656; CbiA; 1. Hypothetical protein; Plasmid. SEQUENCE 396 AA; 39916 MW; 566
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SMART; SM00498; FH2; 1.
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InterPro; IPR001265; Formin.
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NUCLEOTIDE SEQUENCE.
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GO:0003779; F:actin binding; IEA
GO:0016043; F:cell organization
GO:0007275; P:development; IEA.
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   CVGCCGPALRPGPLPAWPSADAAAPPAGDAPS-FSVPGSGGASPRLG--
                                                               ---CIGPLIS----
                                                                                                                                   RPARCCG---
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29.6%;
                                                                                                                                   ----SGGAVGARPGCAAVSCR---TPSPPT-----
                                                               PSWPRVWVAA--GGNWPTGVELPGEG--IPKIGFVVLWLAPGS-RI 121
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                                                                                                                                                                                                                                                               14;
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-APCTVSV
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ID Q59GF6 H
AC Q59GF6 F
AC Q59GF6 F
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DT 10-MAY-2
DT 10-MAY-2
CAN Name=for
OS Homo sap
OC Eukaryot
OC Mammalia
OC MOBI_Tax
RN [1]
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STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

MEDLINE=22206494; PubMed=12218036;

Pol=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.I

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H

Salzberg S.L., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae, Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
       TISSUE=Brain;
                               NUCLEOTIDE SEQUENCE.
                                                                         NCBI_TaxID=9606;
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Q59GF6;
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Similarity 29.3%;
39; Conservative 1
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6; AAK45283.1; -; Genomic_DNA.
                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ
EMBL; AB209153; BAD92390.1; -; mRNA.
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            2006, 17:32:28
                                                                                               -----PPPLPGVGIPPPPPLPGAGIPPPPPLPGMGIPP----
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-518-022-993
US-09-528-092-993
US-09-252-991A-2854
US-09-252-991A-2856
US-09-252-991A-2866
US-09-252-991A-23688
US-09-252-991A-2385
US-09-299-2991A-23285
US-09-299-2991A-23285
US-09-2999-391A-21454
US-09-252-991A-27851
US-09-252-991A-27851
US-09-252-991A-27851
US-09-252-991A-27851
US-09-252-991A-23664
US-09-499-016-9978
US-09-499-016-9978
US-09-499-016-9978
US-09-417-197-125
US-09-252-991A-23769
US-09-252-991A-23664
US-09-252-991A-23664
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Sequence 90, Appl Sequence 278, App Sequence 931, App Sequence 28324, A Sequence 28324, A Sequence 28569, A Sequence 21648, A Sequence 21648, A Sequence 2185, App Sequence 21854, A Sequence 21854, A Sequence 21854, A Sequence 21854, A Sequence 27851, A Sequence 27851, A Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7291, App Sequence 7291, App Sequence 7291, App Sequence 7291, App Sequence 7356, A Sequence 2356, App Sequence 23564, A Sequence 23664, A Sequenc
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US-09-252-991A-20613	US-09-252-991A-18097	US-09-252-991A-30156	US-09-252-991A-24927	US-09-252-991A-32485	US-09-518-914-2	US-08-899-595-3	US-09-323-735-2	US-09-080-897-2	US-09-252-991A-19331	US-10-078-547-24	US-09-599-287A-24	US-09-949-016-11282	US-10-078-547-2	US-09-599-287A-2	US-08-660-963-12	US-09-518-914-4	US-09-489-039A-12891
Sequence 20613,	Sequence 18097,	Sequence 30156,	Sequence 24927,	Sequence 32485,	Sequence 2, Appli	Sequence 3, Appl	•	Sequence 2, Appli	Sequence 19331,	Sequence 24, Appl	Sequence 24, App	Sequence 11282,	Sequence 2, Appl:	Sequence 2, Appl:	Sequence 12, Appl	Sequence 4, Appl	Sequence 12891,
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## ALIGNMENTS

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APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: NIELSEN, Rikke
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
ITTLE OF INVENTION: NUCLEIC ACIDS PRAGMENTS AND POLYPEPTIDE FRAGMENTS
ITITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
ITITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
ITITLE OF INVENTION NUMBER: US/09/050,739
CURRENT APPLICATION NUMBER: 0376/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER APPLICATION NUMBER: 1277/97
EARLIER FILING DATE: 1997-04-02
EARLIER FILING DATE: 1997-04-02
EARLIER FILING DATE: 1997-04-03
EARLIER FILING DATE: 1997-04-03
EARLIER FILING DATE: 1997-04-03
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; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 90
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-90
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Best Local
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EARLIER FILLING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
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  121
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5. 6641814
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                                                                                                                                                                                                1 MRVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWL
                                                                                                                                                                                                                                                                                     Similarity
                         IDAIGSSFSKSVLTAVSAW 139
                                                                                  NNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIGFVVLWLAPGSR 120
                                                                                                                                                                         MRVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWL
IDAIGSSFSKSVLTAVSAW
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No. 2.3e-66;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                        Length 139;
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 1387
SOPTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 993
LENGTH: 707
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US-09-538-092-993
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; OGRANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No.
US-09-919-039-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-919-039-278
                                                                                                                                    US-09-538-092-993
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Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OP INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 278
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APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 278, Application US/09919039 Patent No. 6727066
                                                        Matches
                                                                                          Query Match
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Best Local Similarity
                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P23246
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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                                                                          Local Similarity
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                  6 PPAPGSDSAR-----SRPAPALGPDPPASG---
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                                                        Conservative
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Pred. No. 0.11;
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Pred. No. 0.11;
                                                        Mismatches
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                    ----WFDSGLVPSRPICAA 45
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US-09-949-016-10120
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                         CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 199-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 28324
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         Sequence 28324, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                FILE REFERENCE:
                   LENGTH: 273
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 SAPPGAPPPTPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 -PKIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 GPKQG 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 SAPPGAPPPTPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI 105
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                                                                                                                                                                                                                                107196.136
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Pred. No. 0.12;
6; Mismatches
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 30843
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US-09-252-991A-28328
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28328
LENGTH: 198
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                                                                                                                                                                                                                                               Sequence 30843, Application US/09252991A Patent No. 6551795
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APPLICANT: Marc J.
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Best Local Similarity 29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                       66 CCSGWVSC---CIGPLISPS-WPRVW------VAAGGNWPTGVELP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWLNNDVT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVBLPGEGI 105
                                                                                                                                                                                                                                                                                                                                                      AATTWKACGSRCRGSATSATHWPSNWRRSAPSCWSATSIPAGCNWPSSSSVP
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27.7%;
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Pred. No. 0.064;
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US-09-252-991A-28569
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                                                                                                                                                                   Sequence 28569,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30843
                                                                                                                                                                                                                Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 28; Conserv
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SEQ ID NO 21648
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ASKUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
EILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
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                                                                                                                                                                                                                                                                                                                                                                                      113 SASSPWP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                     89 AAGGNWP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 SCSSTSATPMPSSKACRESPPPAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 ICAASSSAGL-----PPPVPPTWLNNDVTCCSGWVSC----CIGPLISPSWPRVWV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 NVAGRSATDAWSSAPAPANCCCLFPAGP--SPASPAPAACRRWPRAACHWPAS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 12.4%;
1 Similarity 27.8%;
37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSTVPKASRHSSGPASPPSSPASAWSCRDVPSMSTCARGTCTCSPYRAGCWYASSPPCRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marc J. Rubenfield et al.
NVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
NVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DV---TCCSGWVS-----CCI---GPLISPSWP----RVWVAAGGNWPTGVELPGEG 104
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                                                                                                                                                                                                                                                               Application US/09252991A
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1998-02-18
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Pred. No. 0.53;
9; Mismatches
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US-09-949-016-10372
Sequence 10372, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
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                                                                                                                                                                                                                                 RESULT 11
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT ELIUNG DATE: 199-03-17
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 43688
LENGTH: 313
TYPE: PRT
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Best Local S
Matches 44
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NUMBER OF SEQ ID NOS:
SEQ ID NO 28569
LENGTH: 794
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Best Local (
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPGSDSARSRPA----PALGPDPPASGWFDSGLVPSRPIC--AASSSAGLPPP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AASAASTPWPAPWPWATNRGRSASPWPTSVSMASSRSTTWPSATGAPARPWYSPTRWATP
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                                                                                                                                                                                                                                                                                      VQPQNPQQPQNPQQPGNSNPETAESVEQAAPVPPANVPASNENASV 182
                                                                                                                                                                                                                                                                                                                                                                  VPPTWRPLLPGQNGSGAPGSGLINGIVNPPQRPHPFWPN-WQSWVNSWRPTKPVPSTEAP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGGAPAGSNVPAGSSPGSSVLGPNPPA----GSVVPSIPVLPGGAGSWPWHPRPNIPI
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25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 95; DB 2; Length 313; Pred. No. 0.28;
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OF DETECTION AND
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RESULT 13
US-09-199-637A-287
; Sequence 287, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Pseudomonas
US-09-252-991A-23285
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US-09-252-991A-23285
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; ORGANISM: Human
US-09-949-016-10372
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10372
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Best Local Similarity
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SEQ ID NO 23285
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                              196
                                                                                                                                                              130 KSVLTAVSA 138
                                                                                                                                                                                                   138 WPARRGWRSAVRPSLARQDGPPACPRPRPCRTGAARRRTGPARAWFT--SPAPAQGASLA 195
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                                                                                                                                                                                                                                                                        85 --GTVSSCSRRSRDLPAGTRESRAHSFSGSAGRHAGARRRSRFAEPGW-----RPGRSPG 137
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                                                                                                                                                                                                                                                                                                                                             32 PPLAAGCAAPG--RAARYPPPATGRSRPAAGWSPPGCRSPRAVLQAIRSCPAPPP----
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                                                                                                                                                                                                                                      WP--RVWVA-----AGGNWPTGVELP----
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                                                                                                                                                                                                                                                                                                           -----GWVSCCIGPLISPS 82
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Pred. No. 0.65;
9; Mismatches
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PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOPTWARE: PASTSEQ for Windows Version 4
SEQ ID NO 287
LENGTH: 187
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-21454
                                                                                                                                                                                                                                    US-09-252-991A-21454
                                                                                                                                                                                                                                                                                                     APPLICANT: MATE J. Rubenfield et al.
TITLE OF INVENTION: NUCLBIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21454
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                                                                                                                                            Query Match
Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21454, Application US/09252991A Patent No. 6551795
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APPLICANT: T80ngalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
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                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                               LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 12.0%;
Local Similarity 32.5%;
121 RPSAGCVPGPGWSGTGCAPCSRGRPCA-APPPSPAWPA--RSSAGSAPSPAPRP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RPSAGCVPGPGWSGTGCAPCSRGRPCA-APPPSPAWPA--RSSAGSAPSPAPRP 171
                                    51
                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LPPP--VP-PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 PPAPGSDSARSRPAPALGPD---PPASG-----WFDSGLVPSR-PICAASSS----AG
                                  LPPP--VP-PTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELP 101
                                                                                                       PPAPGSDSARSRPAPALGPD----PPASG------WFDSGLVPSR-PICAASSS----AG
                                                                           PPRPGRSLADAAPAPCAAASRARPRASSTPGYRSTWKPLRRPPRRSPCCAATGSRSCRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPRPGRSLADAAPAPCAAASRARPRASSTPGYRSTWKPLRRPPRRSPCCAATGSRSCRAG
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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Pred. No. 0.27;
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RESULT 15 US-09-252-991A-25096

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Search completed: April 14, 2006, 17:37:59
Job time: 13.853 secs
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                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 25096
LENGTH: 414
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25096, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                               75
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                                                                                                                      61 NNDVTCCSGWVSC 73
                                                                                                                                                                                                     7 PAPGSDSARSRPAPALGPDPPASGW-----FDSGLVPSRPICAASSSAGLPPPVPPTWL 60
                                                                                                                                                                                                                                             26; Conservative
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                                                                                                                                                              PAACSNRARCRPERMPG---PAAGWRSTTAPWPGSRRPSGPICQASSSSTRRSPATAS--
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35.6%;
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Pred. No. 0.83;
                                                                                                                                                                                                                                             26;
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US118_PUBCOMB.pep:*

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774
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### SUMMARIBS

Result

No.	Score	Query Match	Length	BB	ID	Description
_	774	100.0	139	ω¦	US-09-791-171-90	Sequence 90, Appl
N	774	8	139	ω	-09-804-	о 9
w	774	100.0	139	4	-10-620-246	90,
4	112	14.5	377	4.	-10	e 1331
ហ	110	4	123	4	-10-767-701-5349	
σ	103.5		707	w	-09-919-039	e 278, Ap
7		13.2	135	w	-09-864-761	e 33360
8		13.1	285	4	-10-437-963	
9	•	12.9	179	4	US-10-437-963-169481	æ
10	99.5		199	4	US-10-029-386-33093	Sequence 33093, A
11	99.5	12.9	212	w	US-09-925-302-741	
12	99.5	12.9	212	w	US-09-925-302-741	Sequence 741, App
13	99.5	12.9	297	4	US-10-437-963-163320	16332
14	99	12.8	327	4	US-10-437-963-114935	Sequence 114935,
15	98	•	155	4	US-10-767-701-40674	Sequence 40674, A
16	98	12.7	457	4	US-10-437-963-141396	Sequence 141396,
17	97.5	12.6	252	4	US-10-437-963-151853	Sequence 151853,
18	97.5	12.6	19662	4	US-10-084-846A-6	Sequence 6, Appli
19	97	12.5	198	4	US-10-029-386-33094	33094,
20	97	12.5	354	Δ	US-10-437-963-163219	Sequence 163219,
21	٥.	12.5	196	4	US-10-425-115-292580	
22	٥.	12.5	304	4	-10-437-963-	æ
23	96.5	12.5	1049	4	US-10-317-835-16	Sequence 16, Appl
24	٥.	12.5	1049	4		
25		12.4	170	4	-10-767-70	
26	96	12.4	387	5		
27		12.4	1507	4	US-10-437-963-143963	Sequence 143963,

95 12.3 1612 4 US-10-425-115-283342 95 12.3 1612 6 US-11-097-143-5022 95 12.3 1612 6 US-11-097-143-5022 95 12.3 19725 4 US-10-0437-963-173295 94 12.1 149 4 US-10-437-963-204838 94 12.1 149 4 US-10-437-963-204838 12.1 149 4 US-10-767-701-58165 12.1 149 4 US-10-767-701-58165 12.1 149 4 US-10-767-701-58165 12.1 1460 5 US-10-739-930-8672 12.1 460 5 US-10-739-930-8672 12.1 460 5 US-10-739-930-8672 12.1 460 5 US-10-739-931-8672 12.1 475 4 US-10-82-122A-51472 12.1 632 4 US-10-82-122A-51472 12.1 19695 4 US-10-84-846A-3 12.1 19695 4 US-10-87-124769 13.5 12.1 240 4 US-10-437-963-144769 13.5 12.1 365 3 US-09-876-187-4 13.5 12.1 365 3 US-09-876-187-4 13.5 12.1 365 5 US-10-732-923-16081 13.5 12.1 365 5 US-10-763-57757	45	44	43	42	41	40	39	38	37	36	35	3 <u>4</u>	33	32	31	30	29	ď
197525 197525 197525 197525 197525 197525 19853 19853 19853 19853 19853 19853 19853 19853 19853 19853 19853 19853 19853 19853	93.5	93.5	93.5	93.5	93.5	93.5	94	94	94	94	94	94	94	94.5	95	95	95	90
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4 US-10-437-963-137-94 4 US-11-097-143-5022 4 US-11-097-143-5022 4 US-10-043-63-173295 4 US-10-437-963-204838 4 US-10-437-963-204838 4 US-10-437-963-204838 4 US-10-437-963-18672 5 US-10-767-701-58165 5 US-10-739-930-8672 4 US-10-82-122A-51472 4 US-10-82-122A-51472 4 US-10-82-122A-51472 4 US-10-984-846A-3 4 US-10-767-701-37061 4 US-10-767-701-37061 5 US-09-876-187-4 5 US-09-876-187-4 5 US-10-732-923-16081 5 US-10-450-763-57757	914	365	365	365	240	217	19695	632	475	460	198	157	149	254	19725	1612	295	7107
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	57757, A	16081, A	15, Appl	4, Appli	144769,	37061, A	3, Appli	51472, A	187947,	8672, Ap	58165, A	156311,	204838,	173295,	4, Appli	5022, Ap	283342,	FUF - C -

# ALIGNMENTS

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APPLICANT: NIBERSEN, Peter
APPLICANT: NIBERSEN, Peter Birk
APPLICANT: OETTINGER, Thomas
APPLICANT: ROSENKRANDS, Ida
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WICKERT ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT PILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: U9/09/791,171
CURRENT PILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTIN VET. 2.0
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US-09-791-171-90
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mycobacterium tuberculosis US-09-791-171-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 90
LENGTH: 139
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 774; DB 3; Best Local Similarity 100.0%; Pred. No. 3.2e-55; Matches 139; Conservative 0; Mismatches 0;
121 IDAIGSSFSKSVLTAVSAW 139
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121 IDAIGSSFSKSVLTAVSAW 139
                                                                                                                                           61 NNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIGFVVLWLAPGSR 120
                                                                                                           61 NNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGIPKIGFVVLWLAPGSR 120
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Sequence 90, Application US/09804980
Publication No. US20030147897A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 139
TYPE: PRT
                                                                                                                                                                                       APPLICANT: ROSENKRADS, ICA
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT APPLICATION NUMBER: US/50/57.39
PRIOR APPLICATION NUMBER: 09/05,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR APPLICATION NUMBER: 0376/97
PRIOR PILING DATE: 1997-04-02
PRIOR PILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-01-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
PRIOR PILING DATE: 1998-01-05
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US-10-620-246-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90, Application US/10620246 Publication No. US20040115211A1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: OBTTINGER, Tho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
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                    APPLICATION NUMBER: 09/415,884 FILING DATE: 1999-10-08 APPLICATION NUMBER: 60/116,673
                                                                                            APPLICATION NUMBER: 09/791,171 FILING DATE: 2001-02-20
                                                                                                                                              APPLICATION NUMBER: 10/138,473 FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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RASMUSSEN, Peter Birk
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1999-01-21
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100.0%; Pred. No. 3.2e-55;
tive 0; Mismatches 0;
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US-10-620-246-90
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LENGTH: 139
TYPE: PRT
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LENGTH: 377
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                                                                                                                                          Matches
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                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(377)
OTHER INFORMATION: unsu
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PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                                                         LENGTH: 37
TYPE: PRT
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139; Conserva
77
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                                                                    17 APSSSPGGRRATPTSSPTPPASSGWATSSSSPSRPPARRPCSASSGCSAPPSLSSASSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRVNDPPAPGSDSARSRPAPALGPDPPASGWFDSGLVPSRPICAASSSAGLPPPVPPTWL
                                                                                          8 APGSDSARSRPAPALGPDPPA-SGWPDSGLVPSRP----ICAASSSAGLPPPV-----
                                                                                                                                          34:
                                                                                                                                                         h 14.5%;
Similarity 29.8%;
RWPGVLPATARTPASSPPTWRP---
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                                                                                                                                          Conservative
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                                 PPTWLNNDVTCCSGWVSCCIGPLISPSWPRV--WVAAG 91
                                                                                                                                          <u>.</u>
                                                                                                                                                         Score 112; DB 4; Length 377; Pred. No. 0.46;
                                                                                                                                          Mismatches
                                                                                                                                        33; Indels
PPPSPPTWPAPPRWSGAG 116
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RESULT 5 US-10-767-701-53499

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US-09-919-039-278
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                                                                                                                 Best Loc
Matches
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CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 53499
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PERL
SEQ ID NO 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 278, Applic Publication No. US20 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kaser, Matthew R. TITLE OF INVENTION: GENES EX PILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kovalic, Davi
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 401
                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                             NAME/KEY: misc_feature
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LOCATION: (1)..(12:
OTHER INFORMATION:
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SSSAGLPPPVPPTWLNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGVELPGEGI 105
                                     PPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPTPTPPPAVT 158
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                                                                        PPAPGSDSAR-----SRPAPALGPDPPASG-----WFDSGLVPSRPICAA 45
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p. US20030108871A1
                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
                                                                                                             Score 103.5; | Pred. No. 4.2; | 6; Mismatches
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                                                                                                                                                Length 707;
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
OTHER INFORMATION: MAP TO ACOO6111.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER,
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL
OTHER INFORMATION: EXPRESSED IN BONE MARROW,
                                                                                                                                                                                                                                                                                    SOFTWARE: Annomax Sequence
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
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OR APPLICATION NUMBER: US 60/236,359

OR PILING DATE: 2000-09-27

OR APPLICATION NUMBER: PCT/US01/00666

OR FILING DATE: 2001-01-30

OR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00662
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US20020048763A1
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Hanzel, David K.
Chen, Wensheng
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                                                                                                                                                                                                                                                                                Listing Engine vers.
  HEART, SIGNAL = 11
PLACENTA, SIGNAL =
BONE MARROW, SIGNAL
                                                                                           SIGNAL
= 17
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US-10-437-963-185237
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                                                                                                                                            RESULT 9
                                                                                                                       US-10-437-963-169481
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Best Local S
Matches 34
                                                                     Sequence 169481, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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SEQ ID NO 185237
LENGTH: 285
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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NAME/KEY: unsure
LOCATION: (1)..(285)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
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R INFORMATION:
R INFORMATION:
R INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 RWLSSCRAACAPMPQSVHGPSTCCTACMSCS----TPSWPAAWRRPWRAGPWP 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGPGWASSRISGAQPSGPCRQRTGGWTCSCASSPASCLRGSMPSWPAPCWPKASTRPTGP
                                                                                                                                                                                                                                  LNNDVTCCSGWVSCCIGPLISPSWPRVWVAAGGNWPTGV 98
                                                                                                                                                                                                                                                                                                         PPA--PGSD-SARSRPAPALGPDP---PASGWFDSGLVPSRPICAASSSAGLPPPVPPTW 59
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Li, Ping
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EXPRESSED IN BT474, SIGNAL = 13
EXPRESSED IN HBL100, SIGNAL = 18
SWISSPROT HIT: Q01705, EVALUE 9.30e-02
EST_HUMAN HIT: AW003023.1, EVALUE 2.00e-06
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Pred. No. 2.5;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: ASOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33093
LENGTH: 199
THEORY OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE PROBES OF THE 
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APPLICANT: Boukharcy, Andrey A.
APPLICANT: Boukharcy, Andrey A.
APPLICANT: Boukharcy, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANTON: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 169481
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Best Local Similarity
                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens

PEATURE:

OTHER INFORMATION: MAP TO AL049853.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

OTHER INFORMATION: SWISSPROT HIT: P23206, EVALUE 3.00e-08
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                           37; Conservative
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PGSDSARSRPAPA----LGPD-----PPASGWFDSGLVPSRPICAAS-----SSAGLPP 53
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28.0%;
                                                                                                                  15;
                                                                                                           Score 99.5; DB
Pred. No. 2.5;
15; Mismatches
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Pred. No. 2.
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                                                                                                                  56;
                                                                                                                                                                               Length 199;
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Ant
TITLE OF INVENTION: Nucleic Acids, Proteins and Ant
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCTT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 741
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US-09-925-302-741
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US-09-925-302-741
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                                    ; ORGANISM: Homo sapiens
US-09-925-302-741
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US-09-925-302-741
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Best Local (
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Query Match
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
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                                                                             TYPE: PRT
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                                                                                                 LENGTH:
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Local Similarity 29.7%;
Les 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 GSPSSGLEPLVPPS-------VCPRGPL--PRWPLGIKAWAALREGGRGWSG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVPQTGAPQTAWGLAWHAP 197
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o. US20030064072A9
  12.9%;
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Pred. No. 2.7;
9; Mismatches
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  Score 99.5;
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RESULT 14
US-10-437-963-114935
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US-10-437-963-163320
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Sequence 114935, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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SEQ ID NO 163320
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Best Local :
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 386-21 (5321) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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Barbazuk, Brad
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9; Mismatches
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US-10-767-701-40674
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US-10-437-963-114935
                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40674
LENGTH: 155
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(52221)B
FILE REPERENCE: 38-21(52221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 114935
LENGTH: 327
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Publication No. US20040172684A1
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                     Local Similarity
143
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R-----RWPTSVPL 151
                                          RVWVAAGGNWPTGVBL 100
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                                                                                                                                                                               PPAPPPPPRAPPPPLAPPAPRGARRPRGRPPAAP--PAGRAAAPAPPVRPPWAGGRPG 82
                                                                                    PGAAPEPPPSRAAFTRRPRAPPAPPPPTAPRGRCGGVSPGSCQRSALGSCFSPGFFWAWP 142
                                                                                                                                                                                                                                                                12.7%; Score 98; DB 4; Length 155; ilarity 22.8%; Pred. No. 2.6; Conservative 7; Mismatches 48; Indels
                                                                                                                                  ----NDVTCCSGWVSCCIGPLISPSWP 84
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Search completed: April 14, 2006, 18:40:39
Job time: 49.8785 secs

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2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

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Gapop 10.0 , Gapext 0.5
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US-11-150-487-20
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Sequence 324, App
Sequence 368, App
Sequence 11981, A
Sequence 10, Appli
Sequence 14, Appli
Sequence 14, Appli
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Sequence 20, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 7887, Appl
Sequence 18316, A
Sequence 18, Appl
Sequence 18, Appl
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Sequence 11, Appl
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Sequence 13, Appl
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Sequence 16, Appli
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RESULT 2 US-11-043-806-368 ; Sequence 368, Application US/11043806 ; Publication No. US20060051774A1 ; GENERAL INFORMATION: ; APPLICAUT: Compugen Ltd ; TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and PILLE OF INVENTION: thereof for Diagnosis of Prostate Cancer ; FILE REFERRICE: 1847-1003 ; CURRENT APPLICATION NUMBER: US/11/043,806 ; CURRENT APPLICATION NUMBER: 2005-01-27 ; NUMBER OF SEQ ID NOS: 575 ; SEQ ID NO 368	Db 371 PDPPPGPGTGWGPTLPSRAVLARSSAEGGPRGTVSTAPGMGLGCSPGLCVG 425  Qy 77	SULT 1 -11-051-720-324 -11-051-720-324 Sequence 324, Application US/11051720 PRINTICATION OF US20060046257A1 GENERAL INFORMATION: APPLICANT: Compugen Ltd TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER TITLE REFERENCE: 1847.1002 CURRENT FILING DATE: 2005-01-27 NUMBER OF SEQ ID NOS: 1780 SEQ ID NO 324 LENGTH: 584 TYPE: PRT ORGANISM: Homo sapiens -11-051-720-324  Query Match Best Local Similarity 26.3%; Fred. No. 0.13; Matches 41; Conservative 16; Mismatches 58; Indels 41; Gaps	26 90.5 11.7 505 7 US-11-150-845-4 27 90.5 11.7 505 7 US-11-150-845-2 28 90.5 11.7 505 7 US-11-150-87-4 29 90.5 11.7 638 7 US-11-150-87-2 30 90.5 11.7 638 7 US-11-150-487-2 31 88 11.4 667 7 US-11-150-487-2 32 87.5 11.3 277 7 US-11-087-99-9879 33 87.5 11.3 277 7 US-11-096-568A-27199 34 87 11.2 412 7 US-11-096-568A-27199 Sequence 27199, Appl 34 87 11.2 533 7 US-11-096-568A-27131 Sequence 27191, Appl 35 86 11.1 253 7 US-11-072-512-3048 Sequence 3040, Appl 36 86 11.1 315 7 US-11-072-512-307 39 85.5 11.0 716 7 US-11-072-512-307 Sequence 3040, Appl 40 83 10.7 137 6 US-10-644-807-349 Sequence 16, Appl 41 82.5 10.7 283 7 US-11-150-487-16 Sequence 16, Appl 43 82 10.6 1870 7 US-11-1086-568A-2123 Sequence 349, Appl 43 82 10.6 1870 7 US-11-188-298-7764 Sequence 349, Appl 56 US-10-644-807-349 Sequence 349, Appl 56 US-10-644-807-349 Sequence 349, Appl 56 US-10-644-807-349 Sequence 349, Appl 56 US-10-644-807-349 Sequence 3170-45, Appl 56 US-10-644
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US-11-043-806-368
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                                                                                                                                                                                                                                                                      RESULT 4
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US-11-087-099-11981
                                                                                                                     GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: YANG, Junming

APPLICANT: BURFORD, Neil

APPLICANT: BURFORD, Neil
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Matches 41
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TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450)B BP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11981
LENGTH: 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11981, Application US/11087099
Publication No. US20060041961A1
                                                                                                                                                                                                                   Sequence 7, Application US/10979095 Publication No. US20060068481A1
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 OF INVENTION: HUMAN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 PDPPPGPGVPPTGW--GPTLPSRAVLARSSAEGGQPRGTVSTAPGMGLGCSPG---LCVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 CTPAPAPPLPGHRPPGTARDRSGDKDLPS-LAALSA 520
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                                                                                                                                                                                                                                                                                                                                                       123 AIGSSFSKSVLT 134
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                                                                                                                                                                                                                                                                                                                       85
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                                                                                                                                                                                                                                                                                                                                                                                        62 -- VCGGGSVAPCSG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 13.0%;
Similarity 28.8%;
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                                                                              AU-YOUNG, Janice
LU, Dyung Aina M.
REDDY, Roopa
                                 LAL, Preeti
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ilarity 26.3%;
Conservative 1
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                                               Monique G.
                 Farrah A.
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Pred. No. 0.13;
.6; Mismatches
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SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 1049
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FRATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 3210906CD1
US-10-979-095-7
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
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                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                               Query Match
                                                                                                                                                                      IENGTH: 398

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1). -(398)
OTHER INFORMATION: 105WASP
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/150,845
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/673,444
PRIOR FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/578,949
PRIOR FILING DATE: 2004-06-10
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PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILE REFERENCE: PI-0002 PCT
CURRENT APPLICATION NUMBER: US/10/979,095
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/10/168,582
PRIOR FILING DATE: 2002-06-20
PRIOR FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cytokinetics, Inc
APPLICANT: Tomasevic, Nenad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 27.3
mes 38; Conservative
                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 PARAAAQGYPAP-----PPAPAW-----PSRPVPRSGAHWSHGPPPPGMPPPAWRQPSL
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                                     6 PPAPGSDSARSRPAPAL------GPDPPASGWFDSGLVPSRPICAASSSAGLPP 53
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 PPIVGGNKGRSGPLPPVPLGIAPPPPTPRGPPPPGRGG-----PPPPPPPATGRSGPLPP
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                                                                             Conservative
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27.3%;
                                                                                             11.8%;
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                                                                         ; Score 91.5; DB
; Pred. No. 0.68;
5; Mismatches
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Pred. No. 0.64;
10; Mismatches
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                                                                                                               DB 7;
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                                                                               Indels
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, NAME/KEY: misc_feature
; LOCATION: (1). (398)
; OTHER INFORMATION: 105WASP
US-11-150-487-10
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US-11-150-487-10
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Publication No. US20050287518A1
GENERAL INFORMATION:
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SEQ ID NO 10
LENGTH: 398
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: WASP AND N-WASP CONSTRUCTS AND METHODS OF EXPRESSING SUCH
TITLE OF INVENTION: CONSTRUCTS
FILE REFERENCE: 020552-007910US
CURRENT APPLICATION NUMBER: US/11/150,487
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/578,913
PRIOR PILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 70
                                                                                                                     APPLICANT: Hahn, I
APPLICANT: Toutch
APPLICANT: Muthy:
APPLICANT: Krayno
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Best Local Similarity
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              APPLICANT: Kraynov, Vadim
APPLICANT: Burton, Dennis R.
APPLICANT: Chamberlain, Chester
APPLICANT: The Scripps Research Institute et al.
TITLE OF INVENTION: Labeled Peptides, Proteins and
TITLE OF INVENTION: Useful for their Preparation
FILE REFERENCE: 1361.007US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cytokinetics, APPLICANT: Tomasevic, N
CURRENT APPLICATION NUMBER: US/11/122,795
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                                                                                                                      Muthyala, Rajeev
Kraynov, Vadim
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Russell, Alan
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Toutchkine, Alexei
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27.9%;
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                                                    Antibodies and Processes
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US-11-150-845-2
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; ORGANISM: Homo sapiens
US-11-122-795-14
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SOPTWARE: FastSEQ for
SEQ ID NO 14
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Best Local :
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TYPE: PRT
ORGANISM: Homo sapiens
PEATURB:
PEATURB:
NAMB/KSY: misc_feature
LOCATION: (1)...(502)
OTHER INFORMATION: FL-WASP
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Best Local
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CURRENT FILING DATE: 2005-06-10
FRIOR APPLICATION NUMBER: US 60/673,444
PRIOR FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/578,949
PRIOR FILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 78
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APPLICANT: Pierce, Daniel
APPLICANT: Finer, Jeffrey
TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION
FILE REFERENCE: 020552-007720US
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APPLICANT: Tomasevic, Nenad
APPLICANT: Jia, Zhiheng
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Similarity 27.9%;
                                                  FVVLWLAPG 118
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                  -----LAPG
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27.9%;
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                                                                                                                                                                                                                               Score 91.5; DB 7;
Pred. No. 0.85;
5; Mismatches 43;
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; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-149-945-1
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US-11-149-945-1
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US-11-150-487-2
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                                                                US-11-150-487-2
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Publication No. US20060014266A1
Query Match
Best Local Similarity
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Best Local (
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APPLICANT:
APPLICANT:
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APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: WASP AND N-WASP CONSTRUCTS AND METHODS OF EXPRESSING SUCH
TITLE OF INVENTION: CONSTRUCTS
TILE REFERENCE: 0.205-2-007910US
CURRENT APPLICATION NUMBER: US/11/150,487
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/578,913
PRIOR PILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 70
NUMBER OF SEQ ID NOS: 70
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.3
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APPLICANT: Sakowicz, Roman

TITLE OF INVENTION: PURIFICATION OF ARP2/3 COMPLEX AND COMPOSITIONS CONTAINING

TITLE OF INVENTION: PURIFIED ARP2/3 COMPLEX

FILE REFERENCE: 020552-007810US
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APPLICANT: Tomasevic, Nenad
APPLICANT: Sakowicz, Roman
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APPLICANT: Tomasevic, Nenad
APPLICANT: Russell, Alan
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CURRENT FILING DATE: 2005-06-10
CURLENT PILICATION NUMBER: US 60/578,969
PRIOR FILING DATE: 2004-06-10
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                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(502)
OTHER INFORMATION: FL-WASP
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Pred. No. 0.85;
5; Mismatches
Score 91.5; DB Pred. No. 0.85;
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RESULT 12
US-11-150-845-20
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SEQ ID NO 28
LENGTH: 502
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                FILE REFERENCE: 020552-007720US
CURRENT APPLICATION NUMBER: US/11/150,845
CURRENT FILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/673,444
PRIOR FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: 60/578,949
PRIOR FILING DATE: 2004-06-10
                                                                                                                                         APPLICANT: Pierce, Daniel
APPLICANT: Finer, Jeffrey
TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION ASSAY
                                                                                                                                                                                               APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/079,907
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/552,663
PRIOR FILING DATE: 2004-03-12
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APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Live Cell Biosensors
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NUMBER OF SEQ ID NOS:
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Jia, Zhiheng
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Pred. No. 0.85
5; Mismatches
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CURRENT APPLICATION NUMBER: US/11/150,487
CURRENT PILING DATE: 2005-06-10
PRIOR APPLICATION NUMBER: US 60/578,913
PRIOR PILING DATE: 2004-06-10
PRIOR PILING DATE: 70
NUMBER OF SEQ ID NOS: 70
SOPTWARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 609
TYPE: prom
RESULT 14
US-11-087-099-7887
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FRATURE:
COTHER INFORMATION: Myc-105WASP-TAP
US-11-150-845-20
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; PEATURE:
; OTHER INFORMATION: Myc-105WASP-TAP
US-11-150-487-20
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Best Local :
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Best Local Similarity 27.9%;
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SEQ ID NO 20
LENGTH: 609
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: WASP AND N-WASP CONSTRUCTS AND METHODS OF EXPRESSING SUCH
TITLE OF INVENTION: CONSTRUCTS
FILE REFERENCE: 020552-007910US
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APPLICANT: Tomasevic, Nenad
APPLICANT: Russell, Alan
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Local Similarity 27.9%;
hes 36; Conservative
                                                                       343
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                                                                                                                                           302 PPPGAGGP----
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                                                                     -----LAPG 346
                                                                                                       FVVLWLAPG 118
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SEQ ID NO 18316
LENGTH: 647
TYPE: PRT
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                            Sequence 18316, Application US/11188298

Publication No. US20060075522A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53452)B

CURRENT APPLICATION NUMBER: US/11/188,298

CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/592,978

PRIOR PILING DATE: 2004-07-31

PRIOR FILING DATE: 2004-07-31
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# ALIGNMENTS

02-APR-1997; 18-APR-1997; 10-NOV-1997; 05-JAN-1998; 01-APR-1998; 08-OCT-1998 Mycobacterium Mycobacterium Mycobacterium tuberculosis antigen CFP7B. 21-JAN-1999 AAW72934; AAW72934 standard; protein; 67 WO9844119-A1 infection. (first entry) tuberculosis. tuberculosis; antigen; vaccine; 97DK-00000376. 97US-0044624P. 97DK-00001277. 98US-0070488P. 98WO-DK000132 A immunological; immunogen;

(STAT-) STATENS SERUM INST.

Andersen P, Oettinger T, Nielsen Florio ≅,⊽ Rosenkrands I, Weldingh K, Rasmussen PB;

WPI; 1998-542705/46.

N-PSDB; AAV63944.

New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis. for

Claim 1; Page 222; 163pp; English.

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis

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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (I) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP3OA or a T-cell epitope of for the induction of a strong immune
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Best Local S
Matches 67
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05-JAN-1998;
01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic; Mycobacterium tuberculosis; immune response; infection; tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6, MPT59; TB; pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP3OA; CFP7B; CFP10; CFP27; CFP3OA; RD1-ORF; CFP1OA; CFP16; CFP19; CFP23;
                                                                                                                                                                                                                                                                  Example 3;
                                                                                                                                                                                                                                                                                           New immunogenic fragment of Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of antigen CFP7B
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Best Local :
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08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1999;
01-JUL-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation.
                                                                                                                                                                                                                       Pompejus
Lee H, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope of for diagnosis of TB in a mammal by performing a DTH type; test; use of CPP27, CPP30A, RD1-ORF2, RD1-ORF3, RD1-ORF3, RD1-ORF3, RD1-ORF3 or a ESATG-MPTS9, CPP10A, CPP16, CPP39, CPP23, CPP3BA, CPP3B or a cell epitope of for the preparation of an immunological composition;
                                                               New isolated Corynebacterium glutamicum nucleic acid encoding a stress, tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum; stress; resistance; fine chemical production; organic acid; protein
                                           production of carbohydrates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. glutamicum
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                                                                                                                                                        N-PSDB;
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27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium
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                                                                                                                                                                                                                                                                                           BASE
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99DR-01030429
99US-0142692P
99US-01031413
99DE-01031457
99DE-01031249
99DE-01032209
99DE-01032230
99DE-01032314
99DE-01032914
99DE-01040764
99US-0151214P
99US-01041382.
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                                               or
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                                           enzymes.
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.. No. 2.4e-36;
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Claim 20; Page 231-232; 526pp; English

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Best Local
                               25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide, lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP70984 to AAP71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) probeins given in AAB78871 to AAB7020. The C. glutamicum SRT genes (I) can be used in vectors (II) for expression in host cells and production of fine chemicals, such as, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. glutamicum
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                                                                                                                                                                                                                                                                                                                                               23-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB78911 standard; protein; 67
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                                                                                                                                                                                                                                                                                                                                               2000WO-IB000922
                                   99US-0141031P.
99DB-01030429.
99US-0142692P.
99US-01031413.
99DB-01031457.
99DB-01031541.
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77.6%;
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Pred. No. 7.5e-27;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vitamin; cofactor; polyketide; enzyme; l hazard; fermentation.
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RESULT 5
AAG89941
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14-JUL-1999;
27-AUG-1999;
27-AUG-1999;
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Lee H, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-061972/07.
N-PSDB; AAF71024.
                                                                                                                                                                                              AAG89941 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            culture may be increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 230-231; 526pp; English
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99DE-01032914.
99DE-01040764.
99US-0151214P.
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77.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 282; DB
Pred. No. 7.5e
5; Mismatches
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7.5e-27;
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Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.

C glutamicum protein fragment SEQ ID NO: 3695.

26-SEP-2001

(first entry)

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Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino particularly L-lysine. The present sequence and organic acids, operation of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium
                                                                              Abiotic stress tolerance; transgenic heat tolerance; cold tolerance; salt
                                                                                                                        Corynebacterium
                                                                                                                                                                                                       ADZ21478 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1999;
07-APR-2000;
                                       Corynebacterium glutamicum
                                                                                                                                                   30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK
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DB; AAH65160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   point of a gene, measuring expression of a gene, analyzing on profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                       AQQVRAL 67
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2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda
                                                                                                                       glutamicum
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77.6%;
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da M,
                                                                                                                        cold shock protein.
                                                                                                                                                                                                                                                                                                                                                                              Score 282; DB Pred. No. 7.5e 5; Mismatches
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Ozaki A;
                                                                                plant; crop improvement;
tolerance; drought tolerance;
                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
.5e-27;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein sequence of a Corynebacterium CC glittamicum cold shock protein (sp). The invention provides a plant that CC shows improved abiotic stress tolerance as a result of the expression of a Csp in its cells. In one embodiment, a polynucleotide encoding a Csp is CC operably linked to a plant promoter and plant terminator. The polynucleotide preferably encodes a protein comprising a specified Csp conserved motif ADZ21430, particularly Bacillus subtilis CspB ADZ21429 or its homologues, Escherichia coll CspA ADZ21428 out its homologues, a Csp is conserved motif ADZ21430, particularly Bacillus subtilis CspB ADZ21429 or its homologues, Escherichia coll CspA ADZ21429 or its homologues, a Csp is conserved motif ADZ21430, particularly Bacillus subtilis CspB ADZ21429 or its homologues, Escherichia coll CspA ADZ21429 or its homologues, a Csp is constitutive, temporally-regulated, developmentally-regulated, tissue-specific constitutive, temporally-regulated, developmentally-regulated, tissue-specific preferred, cold enhanced, cold-specific, stress enhanced, stress-correct with a DNA molecule that expresses a Csp is claimed. The CC plant may be a crop plant, a monocot or dicot, and is especially selected from soybean, corn, canola, rice, cotton, barley, oat, turf grass, cotton cand wheat. The transgenic plant that has been transformed what tolerance, cold colerance, salt tolerance, drought tolerance and survival after cold shock than the corresponding non-transformed plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                     nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carboblydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme evolutionary study; environmental hazard; fermentation.
                                                                                Corynebacterium glutamicum; stress; resistance; tolerance; SRT; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA molecule comprising a DNA polynucleotide promoter and a DNA that encodes a cold shock protein, useful producing plants with increased tolerance to abiotic stress.
                                                                                                                                                                                                                                                                                         AAB78914 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67 AA;
                                                                                                                                                                C. glutamicum SRT protein sequence SEQ ID NO:88.
                                                                                                                                                                                                             30-APR-2001
                                                                                                                                                                                                                                                   AAB78914;
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DB; ADZ21477.
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2003US-0530453P.
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77.6%;
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No. 7.5e-27;
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Corynebacterium

glutamicum.

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CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine chemical production can be modulated. The presence of (I) or the SRT croteins (II) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I), (II), (III) and host cells containing them can be used to map the genomes of organisms related to C. Compound them can be used to map the genomes of organisms related to C. Compound them can be used to map the genomes of organisms related to C. Compound the compound the compound of containing an in modulating the sRT protein activity, and in modulating the sRT protein activity, and in modulating the sRT protein activity, and in modulating the sRT protein activity, and in modulating compound that is normally environmentally or chemically because to it. (I) and protein molecules encoded by it increase the CC survival of C. glutamicum to chemical and environmental hazards and compound the conditions. By increasing the growth rate or conditions, the yield, production and/or efficiency or production of fine chemicals from a
                                                                                                                                                                            Matches
                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                  Query Match
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01-JUL-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. The C. glutamicum SRT genes (I) can be used in vectors (II) for expression in host cells and production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic
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Lee H, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Corynebacterium glutamicum nucleic acid encoding a stress, tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                         Sequence 67
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N-PSDB; AAF71027.
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27-AUG-1999;
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08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                  culture may
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ATGVRSL
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99DB-01031413.
99DB-01031457.
99DB-01031541.
99DB-01032209.
99DB-01032230.
99DB-01032914.
99DB-01032914.
99US-0151214P.
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                                                                                                                                                                      Score 275; DB 4;
Pred. No. 5.5e-26;
4; Mismatches 11
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RESULT 9 ABU34189 ID ABU3

ABU34189 standard; protein;

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Best Local :
                                                                                                                                                                                               sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lygine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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Tateishi
                                                                                                                                                                        Sequence 67
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N-PSDB; AAH65310.
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO 3845; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
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acid synthesis.
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AQAVRAI 67
                            ATGVRSL
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2000JP-00159162
2000JP-00280988
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Senoh A, Ikeda M,
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77.6%;
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Pred. No. 5.5e-26;
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Ozaki A;
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ABU34189;

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the 613 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of the biological pathway in which a proliferation-required gene or a gene on which the test compound that inhibits proliferation of a gene or which the test compound that inhibits proliferation of a gene on which the test compound that inhibits proliferation of a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the confound that inhibits the gene condition of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational conditions.
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 62113; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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Xu HH;
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Query Match Best Local Similarity

71.3**%**; 64.2**%**;

Score Pred.

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                                                                                                                                                                                                                                                                                                                            polypeptides. The invention also relates to a recombinant expression vector comprising a polymucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polymucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                Sequence
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treating E.
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N-PSDB; ADH82881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to Enterococcus faecalis polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 4171; 193pp; English
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           61 ATGV
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                                                                                                                    1 MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
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Pred. No. 5.6e-20;
                                                                                                                                                                            Mismatches
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RESULT 11
ABM78962
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                                                                                                                                                                                             CC nucleotide sequence encoding the heterologous polypeptide and a promoter cc and 5' untranslated region (UTR) from a cold shock inducible gene, such cc as cspG, which directs its expression. An AT-rich sequence that enhances cranslation under cold shock inducible conditions is present either in cc the coding sequence of the heterologous polypeptide or in an additional cc element inserted between the coding sequence and the cold shock inducible cc promoter and 5'-UTR. The DNA molecule preferably also includes the cspA cc yrong sequence. Inducing expression by cold shock eliminates the need cc for chemical induction, and under cold conditions all ribosomes in the close are forced to express the single target protein, which simplifies cc purification. When used to prepare isotopically labelled proteins; the cculture size, and thus amount of expensive labelled reagent, can be creduced. The method can also be used to produce proteins native to cold-crimate organisms at high yield
                                                                                                                                            Query Match
Best Local :
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the protein sequence of Escherichia coli cold shock protein CspG. The invention provides a DNA molecule or vector and a host cell containing the DNA molecule or vector for use in the production of a heterologous polypeptide under conditions that elicit a cold shock response in the host cells. The DNA molecule and vector include a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding heterologous protein, useful particularly for producing isotopically labeled proteins, includes a cold-shock inducible promoter.
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14-AUG-2002; 2002US-0402921P
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 73; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isotopically labeled
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                                                                                                                                              Local Similarity
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67
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                              VRSL 67
                                                                                 GTVKWFNAEKGFGFIAFEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSFKGFQATG 63
                                                                                                                                                                                             70
                                                              GLVKWFNADKGFGFITPDDGSKDVFVHFTAIQSNEFRTLNENQKVEFSIEQGQRGPAAAN 66
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Pred. No. 1.5e-19;
5; Mismatches 17;
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                                                                                                                                                          Length 70;
                                                                                                                             Indels
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                                                                                                                             Gaps
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RESULT 12
ADZ21446
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                                                                                                                                                                                     Matches
                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                             constitutive, temporally-regulated, developmentally-regulated, tissue-preferred, cold enhanced, cold-specific, stress enhanced, stress-specific, drought inducible, water deficit inducible or tissue-specific promoter. An abiotic stress-tolerant transgenic plant that has been transformed with a DNA molecule that expresses a Csp is claimed. The plant may be a crop plant, a monocot or dicot, and is especially selected from soybean, corn, canola, rice, cotton, barley, oat, turf grass, cotton and wheat. The transgenic plant shows improved heat tolerance, cold tolerance, salt tolerance, drought tolerance and survival after cold shock than the corresponding non-transformed plant.
                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of a cold shock protein (Csp) from Escherichia coli. The invention provides a plant that shows improved abiotic stress tolerance as a result of the expression of a Cs in its cells. In one embodiment, a polynucleotide encoding a Csp is operably linked to a plant promoter and plant terminator. The polynucleotide preferably encodes a protein comprising a specified Csp conserved motif ADZ21430, particularly Bacillus subtilis CspB ADZ21429 its homologues, Escherichia coli CspA ADZ21428 or its homologues, a csp from Agrobacterium tumefaciens or other Csp protein of the invention, such as the present Csp. The promoter is selected from an inducible, constitutive, temporally-regulated, developmentally-regulated, tissue-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA molecule comprising a DNA polynucleotide promoter and a DNA that encodes a cold shock protein, useful producing plants with increased tolerance to abiotic stress.
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 19; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-285434/29.
N-PSDB; ADZ21445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2003; 2003US-0506717P.
17-DEC-2003; 2003US-0530453P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-2004; 2004WO-US031856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abiotic stress tolerance; transgenic plant; crop improvement; heat tolerance; cold tolerance; salt tolerance; drought tolerance; cold shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADZ21446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MONS ) MONSANTO TECHNOLOGY LLC.
         64 VRSL 67
                                            7
                                                                                                                 l Similarity 65.0
42; Conservative
                                                                                                                                                                                       70
                                          GLVKWFNADKGFGFITPDDGSKDVFVHFTAIQSNEFRTLNENQKVEFSIEQGQRGPAAAN 66
                                                                          GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG
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                                                                                                                               62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shock protein.
                                                                                                               Score 223; DB 9;
Pred. No. 1.5e-19;
5; Mismatches 17;
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67

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RESULT 14
ADH54477
ID ADH54
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AC ADH54
XC ADH54
XC ADH54
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DT 25-MJ
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DE Eschi
XX
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CS Eschi
XX
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ABO66959
ID ABO66
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                     New nucleic preparing a
                                                                                                                                                                                                                                                                           The invention describes a new isolated nucleic acid encoding a Klebsiel pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
           Escherichia coli
                                              Escherichia
                                                                                  ADH54477;
                                                                                                                                                                                                                                                            Sequence 131
                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 13476; 932pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO66959 standard; protein; 131 AA
                           Cold shock inducible gene; physiological
                                                                25-MAR-2004
                                                                                                  ADH54477 standard; protein; 70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6610836-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella
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                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                   GVRSL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                             Osborne
                                                                                                                                                                                                                                                                                                                                                                      acid encoding a Klebsiella pneumoniae polypeptide, useful vaccine composition against Klebsiella pneumoniae.
                                              coli cspG
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression vector;
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                                                                (first entry)
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                                                                                                                                                                                                                                61.8%;
                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide
                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                        Score 222; DB 7;
Pred. No. 4.4e-19;
7; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription regulatory element; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     веqid 13476
                                                                                                                                                                                                                                                                                                                                                      English.
                            stress;
                                                                                                                                                                                                                                         Length 131;
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RESULT 15
ABB07338
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Best Local :
                                                                    13-FEB-1989;
09-MAR-1992;
01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid molecule which prolongs the expression of cold shock inducible genes under conditions that elicit the cold shock (cs) response in a bacterium, comprises the 5-UTR of cspI operably linked to a non-native promoter. The nucleic acid is useful for regulating expression of cold shock inducible genes to elicit the cold shock response in bacterium under conditions of physiological stress. The present sequence is Bacherichia coli cspG protein used in the exemplification of the invention.
Inouye M, Jo
Goldstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid comprising the 5-UTR of capI operably linked to a native promoter, useful for regulating expression of cold shock inc genes to elicit the cold shock response in bacterium under conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                          Streptomyces
                                                                                                                                                                                                                                                               S. clavuligerus CspA-like protein SC7.0.
                                                                                                                                                                                                                                                                                             09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2000; 2000US-00516667
                                                                                                                           03-FEB-1998;
                                                                                                                                                                                US6333191-B1
                                                                                                                                                                                                                                       Cold-shock induced protein;
                                                                                                                                                                                                                                                                                                                        ABB07338;
                                                                                                                                                                                                                                                                                                                                               ABB07338 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physiological stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inouye M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2000; 2000US-00516667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6610533-B1
                                           (UYNE-) UNIV
                                                                                                                                                     25-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                       YIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLVKWFNADKGFGFITPDDGSKDVFVHFTALQSNEFRTLNENQKVEFSIEQGQRGPAAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG
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               Jones
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                                            NEW JERSEY MEDICINE &
                                                                                                                                                                                                           clavuligerus
                                                                                                                                                                                                                                                                                             (first
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                                                                    89US-00310332.
92US-00852013.
94US-00203806.
                                                                                                                           98US-00017754
              ָי,
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                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.6%;
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               Etchegaray J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86pp;
                                                                                                                                                                                                                                    Csp;
                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 221; DB 7;
Pred. No. 2.6e-19;
6; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                       prokaryotic;
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                                            DENTISTRY.
                 Jiang W,
                                                                                                                                                                                                                                       stress;
                 Pollitt
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                                                                                                                                                                                                                                       desaturase; SC7.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Search completed: April 14, 2006, 17:18:45
Job time : 28.9599 secs
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                                                                                                                                                                                                                                                                                                                                         The invention relates to a family of stimuli-induced in particular stress cc or cold-shock induced genes and proteins. An isolated DNA molecule (I) is provided that comprises a prokaryotic promoter that is induced under conditions eliciting a cold shock response (Csp), or the promoter that is comprise a cc conditions eliciting (Sp, where the conditions comprise a cc decrease in temperature below the normal physiological growth temperature cc of the prokaryotic cell, preferably bacterium. (I) is useful for encoding proteins under stimuli-induced, particularly stress or cold-shock induced conditions. The encoded proteins are useful in staining DNA and in the creatilization of DNA and RNA, and thus increasing the efficiency of DNA cand RNA in various in vitro reactions. The encoded protein is also useful as desaturase to denature DNA irrespective of temperature. The proteins care also useful for commercial purposes. The present sequence represents a s. clavuligerus CspA-like protein SC7.0
                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA molecules useful for encoding proteins under stress or cold-induced conditions, comprising a prokaryotic promoter that is induced under conditions eliciting a cold shock response.
                                                                                                                                                                                                                                                                                                                                         Sequence 66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 10; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-129568/17.
                                                                                                                                                                                                                                                y Match 60.9%;
Local Similarity 65.6%;
hes 42; Conservative
                                                                                 60 AENV 63
                                                                                                                         61 ATGV 64
                                                                                                                                                                 Score 218.5; DB 5;
Pred. No. 4.9e-19;
6; Mismatches 15;
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Maximum Match 100%
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Perfect score:
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                          US-10-620-246-147
359
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                                                                                                                                                                                                                                                                                                          1 MPQGTVKWFNAEKGFGFIAP.....VEFEIGHSPKGPQATGVRSL
                                                                                                                                                                                                                            283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                            Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                        April 14,
                                                PIR_80:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyright
pir1: *
pir2: *
pir3: *
                                                                                                                                                                                                                                                                                                                                                                                                        2006, 17:19:08 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                             Gapext 0.5
                                                                                 summaries
                                                                                                                                                                                                                                                                                                                                                                        Search time 3.92873 Seconds (without alignments) 1640.866 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	v	4	w	N	1	No.	Result
207	207.5	207.5	209.5	210	211	211	211	211	215	216	216	216	216	217	217	218.5	219	220	220	220	221	221	222	222	223	223	352	359	Score	
57.7	.7	57.8			58.8		.8		59.9		60.	60.	60.2	60.			61.	61.3	61.3	61.3	61.6	61.6	61.8	61.8	62.1	62.1	98.1	100.0	Match	
67	66	99	65	70	70	70	70	70	69	69	69	69	69	70	69	66	70	69	69	69	70	69	69	69	70	70	67	67	Length	
N	N	N	N	N	N	N	N	-	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	BB	
G82568	AH1607	AD1245	H86645	D70412	E86030	A91184	AG0981	OCECJ	AG0316	H85793	S43618	E90945	AE0727	C64910	AI0212	S26378	AD0755	F90711	849050	B85562	E85634	F84967	AH0579	A84987	D64840	A90772	F86933	A70564	ID	
cold shock protein	cold shock protein	cold shock protein	cold shock protein	<b>shock</b>	shock	shock	Bhock	8	O	gho ode	cold shock protein		shock-	cold shock protein	Bhock	<b>Bhock</b>	shock	cold shock protein	cold shock protein	cold shock protein	homolog of Salmone	cold shock-like pr	shock-like	shock-	cold shock protein	Š	probable cold shoc	cspA pr	Description	

44	2 42	42	4 6	39	38	37	36	35	34	33	32	31	30
199.5	199.5	199.5	200.5	200.5	201	201	202.5	202.5	204	206	206.5	206.5	206.5
55.4	55.6	55.6	55.8	55.8	56.0	56.0	56.4	56.4	56.8	57.4	57.5	57.5	57.5
67	, e	66	70	66	70	67	66	65	70	70	66	66	66
20	งผ	N	งง	N	N	N	N	ผ	N	N	N	N	N
T42055	B89917	A89853	A82489	E69608	AE0443	T34593	I40390	B84101	AC0324	AB0202	140158	AB1698	AH1326
cold shock protein	major cold shock p	cold-shock protein	cold shock DNA-bin	cold shock protein	major cold shock p	cold-shock domain	major cold shock p	cold-shock protein	cold shock protein	cold shock protein	major cold shock p	major cold-shock p	major cold-shock p

# ALIGNMENTS

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probable cold shock protein [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2004 C;Accession: F86933

R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroy eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F86933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A70564
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:006360; UNIPARC:UPI000012856D; GB:Z95436; GB:AL123456; NID:
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-67 <COL>
A;Status: preliminary
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;Superfamily: cold shock protein, CspA type; cold shock domain homology
;4-64/Domain: cold shock domain homology <CSD>
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100.0%; Pred. No. 3.7e-35;
tive 0; Mismatches 0;
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Holroyd
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A;Molecule type: DNA
A;Residues: 1-70 <HAY's
A;Cross-references: UNIPROT:Q47130; UNIPARC:UPI000012858A; GB:BA000007;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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C;Superi
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D64840

cold shock protein cspG - Escherichia coli (strain K-12)

C; Species: Escherichia coli

C; Species: 17-Sep-1997 #text
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-i
C;Accession: A90772
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yoi
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shi
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Recession: A90772
A;Status: preliminary
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A;Residues: 1-67 <STO>
A;Cross-references: UNIPROT:069550;
C;Genetics:
A;Gene: cspA
C;Superfamily: cold shock protein, C
                                                  A;Status: nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-70 <BLAT>
                                                                                                                                         Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; PMID:9278503
A,Accession: D64840
                                                                                                                                                                                                                                               C;Accession: D64840
R;Blattner, F.R.; Plunkett III,
A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision
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Cross-references: UNIPROT:Q47130;
Experimental source: strain K-12,
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Best Local S
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Best Local (
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97.0%;
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Pred. No. 2.4e-34;
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UNIPARC:UPI000012858A;
substrain MG1655
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                                                                                                              shown;
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                                                                                                                                                                                                                                                                                         C.A.;
                                                                                                                    translation
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                                GB:AE000201;
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                                   GB:U00096;
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C; Superfamily: C; Keywords: DNA F; 7-67/Domain: Superfamily: cold shock protein, CspA type; cold shock domain; Keywords: DNA binding; stress-induced protein; transcription; 7-67/Domain: cold shock domain homology <CSD> homology

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Matches
                                                                                              Query Match
Best Local
67
                   64 VRSL 67
                                                                                    l Similarity
42; Conserv
                                          7
                                                              4
TIV.
                                         GLVKWFNADKGFGFITPDDGSKDVFVHFTAIQSNEFRTLNENQKVEFSIEQGQRGPAAAN
                                                        GTVKWFNAEKGFGFIAÞEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSFKGFQATG
                                                                                     Conservative
70
                                                                                              62.1%;
                                                                                     5
                                                                                    Score 223; DB 2;
Pred. No. 3.3e-19;
5; Mismatches 17
                                                                                                        Length 70
                                                                                      Indels
                                                                                     0,
                                                                                    Gaps
                                           66
                                                                 63
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RESULT 5 A;Title: Genome sequence of A;Reference number: A84930; A;Accession: A84987 R;Shigenobu, S.; Watana Nature 407, 81-86, 2000 A; Gene: cspE; ! C; Superfamily: A;Cross-references: UNIPARC:UPI000005E5D4; GB:AP000398; GSPDB:GN00144 A;Experimental source: strain APS A; Molecule type: DNA A; Residues: 1-69 <STO> A;Status: preliminary cold shock-like ¡Species: Buchnera sp.
¡Date: 02-Mar-2001 #sequence\_revision
¡Accession: A84987
¡Shigenobu, S.; Watanabe, H.; Hattori, Matches Query Match Best Local ( Genetics: cspE; BU489 63 65 ഗ w 42; Similarity NVISL GVRSL 67 QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQAT KGNVKWFNESKGFGFITPEDGSKDVFVHFSAIQSNGFKTLAEGQSVEFEITEGAKGPSAA cold shock protein cspE [imported] - Buchnera Conservative 61.8%; protein, the endocellular bacterial symbiont of aphids Buchnera MUID:20445173; PMID:10993077 Hattori, Score 222; DB 2; Pred. No. 4.3e-19 Pred. No. 4.30 4; Mismatches CspA type; cold shock domain 02-Mar-2001 M.; Sakaki, ·ф #text\_change 31-Dec-2004 ¥.; Length Indels (strain 69 homology 0 Gaps 62 64 0

cold shock-like protein cspE [imported] - Salmonella enterica subsp. enterica (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 31-Dec-2004 C;Accession: AH0579 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-69 <PAR: A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608 , S.; Moule, S.; O'Gaora, Nature 413, 848-852, 2001 R, Parkhill, J.; Dougan, G.; James, th, T.; Connerton, P.; Cronin, A.; A; Accession: AH0579 <PAR> K.D.; 'Davis, Thomson, N.R.; , P.; Davies, R. Pickard, I Skelton, J.; Stevens, Salmonella enterica s D.; Wain, J , L.; White, J.; Churcher e, N.; Farrar serovar Bero.

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A;Gene: C;Superf

STY0678

;Supertamily:

cold

shock

protein,

CspA type;

cold

shock domain homology

A;Cross-references: UNIPARC:UPI000005A176;

GB:AL513382; PIDN:CAD05106.1;

PID:g16501881;

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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
C;Accession: F84967
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki,
Nature 407, 81-86, 2000
""""" farance commence of the endocellular bacter
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                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-70 <STO>
                                                                                                                                                                                                                                                                       A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                       homolog of Salmonella cold shock protein [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
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A; Residues: 1-69 < STO>
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Best Local S
Matches 41
                                                                                                                                                                  ;Cross-references: UNIPARC:UPI0000165753; GB:AE005174; NID:g12514257; PIDN:AAG55537.1;
;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            Accession: E85634
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                                                                                   Query Match
                                                                                                                      Superfamily: cold shock
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Best Local
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GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQATG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVFSL
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                                                     Conservative
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                                                               61.6%;
67.2%;
                                                                                                                    protein, CspA type; cold shock domain
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Pred. No. 5.6e-
4; Mismatches
                                                     4
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                                                                   Score 221; DB 2;
Pred. No. 5.7e-19;
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Pred. No. 4.3e-19;
7; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CspA type;
                                                     Mismatches
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                                                     16;
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                                                                                   Length
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                                                     Indels
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                                                                                                                      homology
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Potamousis,
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A;Gene: cspB; msmC; gicA
C;Superfamily: cold shock protein, CspA type; cold
C;Keywords: DNA binding; transcription regulation
P;6-66/Domain: cold shock domain homology <CSD>
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P36997; UNIPARC:UPI000000023B; EMBL:D28497; NID:g460700; A;Experimental source: strain K-12 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M., A; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cold shock protein homolog cspB - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change C;Accession: S49950; E64796
                                                                                                                           A;Cross-references: UNIPARC:UPI000000023B; GB:AE000167; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-69 < BLAT>
                                                                                                                                                                                                                                                                                                     Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 13, 301-312, 1994
A;Title: Cloning, sequencing, and characterization of multicopy
A;Reference number: $49048; MUID:95075315; PMID:7984109
A;Accession: $49050
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C;Superfamily: cold shock protein,
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                                                                                                                                                                                                                                                      A; Accession: E64796
                                                                                                                                                                                                                                                                           A; Reference number: A64720; MUID: 97426617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-69 < YAM>
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A; Residues: 1-69 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: B85562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,Yamanaka, K.; Mitani, T.; Ogura, T.; Niki, H.; Hiraga,
ol. Microbiol. 13, 301-312, 1994
                                                                                                      Genetics:
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63.1%;
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Pred. No. 7.4e-19;
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                                                                                                                                                                                                                              shown; translation not
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                                                                                                                                                                                                                                                                                PMID: 9278503
                                                    cold
                                                    shock domain homology
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Potamousis,
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K.; Apodaca
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C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C;Accession: P90711
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: P90711
A;Status: preliminary
A;Accession: P90711
A;Status: preliminary
A;Geneis: 1-69 <HAY>
A;Gross-references: UNIPROT:P36997; UNIPARC:UPI00000023B; GB:BA000007; PIDN:BAB34085.1;
A;Gene: EC80662
C;Superfamily: cold shock protein, CspA type; cold shock domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
AD0755
                                                                                                                                                                                                                                              , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                         cold shock protein [imported] - Salmonella enterica subsp. enterica serovar ()Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also seen called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 31-Dec-2004 C;Accession: AD0755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cold shock protein [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Decies: Bs-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004 C;Accession: F90711
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                                                                                                                                                                                                      A;Accession: AD0755
A;Status: prelimina
                                                                                                                                                                                                                                                                                                                                                            R; Parkhill, J.; Dougan, G.; James, th, T.; Connerton, P.; Cronin, A.;
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Best Local S
Matches 41
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Best Local S
Matches 41
Query Match
Best Local Similarity
                                                                                                                                    Cross-references: UNIPARC:UPI0000059C99; GB:AL513382; PIDN:CAD05743.1; PID:g16503235;
                                                                                                                                                         Molecule type: DNA
Residues: 1-70 <PAR>
                                                                    Superfamily:
                                                                                                                                                                                                      Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVRSL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGNVKWFNESKGFGFITPEDGSKDVFVHFSAIQTNGFKTLAEGQRVEFEITNGAKGPSAA
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                                                                    cold shock
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61.0%;
64.1%;
                                                                  protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 220; DB 2;
Pred. No. 7.4e-19;
7; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 220; DB 2; I
Pred. No. 7.4e-19;
7; Mismatches 17;
Score 219; DB 2;
Pred. No. 9.8e-19;
                                                                  CapA type;
                                                                                                                                                                                                                                                                                                                                                                 K.D.; Thomson, N.R.; Pickard, |
Davis, P.; Davies, R.M.; Dowd,
                                                                    cold shock domain homology
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                       Length
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Salmonella enterica serov
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3 QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVBFBIGHSPKGPQAT

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cold shock protein 7K homolog [similarity] - Streptomyces clavuligerus (;Species: Streptomyces clavuligerus C;Species: Streptomyces clavuligerus C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004 C;Accession: S26378; S25584 R;Av-Gay, Y.; Aharonowitz, Y.; Cohen, G. Nucleic Acids Res. 20, 5478, 1992 Nucleic Acids Res. 20, 5478, 1992 A;Title: Streptomyces contain a 7.0 kDa cold shock like protein. A;Reference number: S26378; MUID:93065223; PMID:1437568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
S26378
                                                                                                                                                                                                                                                                                                                                                     C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
C;Accession: AI0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: cold shock protein, CspA type; cold C;Keywords: DNA binding; transcription regulation F;4-63/Domain: cold shock domain homology <CSD>
                                                                                                                                                                                                                                                                       R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tragg, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-69 < KUR>
                                                                                                                                                                                                                                    A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A; Residues: 1-66 < AVG>
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A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                  A; Accession: AI0212
                                                                                                                                                                                                                                                                                                                                                                                                                cold shock protein [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                   AI0212
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                Best
                                                                           ;Gene: YPO1746
;Superfamily: (
                                                                                                                                    Cross-references:
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Best Local :
                                    Query Match
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Similarity 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MATGTVKWFNAEKGFGFIAQDGGGPDVFVHYSAINATGFRSLEENQVVNFDVTHG-EGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                             cold shock
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  Conservative
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                                                                                                                                    UNIPROT: Q8ZFG3; UNIPARC: UPI00000CD842;
                  60.4%;
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                                                                           protein, CspA type; cold shock domain
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                    Score 217; DB 2;
Pred. No. 1.7e-18;
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6; Mismatches
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  Mismatches
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  19;
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                                    Length
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                                                                                                                                        GB:AL590842; PIDN:CAC90565.1
                                                                                                                                                                                                                                                         agent of plague
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RESULT 15
(C64910
Cold shock protein homolog cspI - Escherichia coli (strain K-12)
Cold shock protein homolog cspI - Escherichia coli (strain K-12)
Cold shock protein homolog cspI - Escherichia coli (strain K-12)
Colote: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2004
Colote: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2004
Colote: 12-C64910
Rose, D.J.; Mau, B.; Shao, Y.
Science 777, 1433-1462, 1997
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1433-1462, 1997
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
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C;Superfamily: cold shock protein, CspA type; cold shock domain homology
C;Keywords: DNA binding; transcription regulation
F;7-67/Domain: cold shock domain homology <CSD>
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A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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PIR; A70564, A70564.

HSSP; P41016; 1HZC.

TIGR; MT3750.1; -...

Tuberculist; Rv3648c; -...

InterPro; IPR012156; Cold_shock_CspA.

InterPro; IPR012159; CSP_DNA_bd.

InterPro; IPR012340; OB_NA_bd_sub.

Pfam; PF00313; CSD; 1...

PIRSF; PIRSF002599; Cold_shock_A; 1.
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STRAIN-CDC 1551 / Oshkosh;

MEDLINE-22206494; PubMed-12218036;

MEDLINE-22206494; PubMed-12218036;

DOI=10.1128/JB.184.19.5479-5490.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.

Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.

Salzberg S.L., Delcher A., Utterback T.R., Venter J.C.,
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01-NOV-1997 (Rel. 35, Created)
25-OCT-2004 (Rel. 45, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
Probable cold shock protein A.
Name-cspA; OrderedLocusNames=Rv3648c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex. MCBI_TaxID=1773;
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EMBL; AE000516;
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J. Bacteriol. 184:5479-5490(2002)
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-!- SIMILARITY: Contains 1 CSD (cold-shock) domain.
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AAK48111.1; -;
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RESULT 3
Q744B8 WYCPA
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ID 2744B8 WYCPA
ID 2744B8;
AC Q744B8;
AC Q744B8;
AC Q744B8;
DT 05-UUL-2004 (TrEMBLIEL 27,
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DE CEPA, 1.

GN Name-csph; OrderedLocusName,
OC Crynebacterium paratuberculo,
OC Mycobacterium avium complex
OX (CBI_TAXID=1770;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=kl0;
RP NUCLEOTIDE SEQUENCE.
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Matches 67
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InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR011129; CSP.
Pfam; PP00313; CSD; 1.
PIRSF; PIRSF002599; Cold_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
PRINTS; PR000621; Cold_shock; 1.
PRODEM; PD000621; COLD_SHOCK; 1.
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DOMAIN 4 64
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ProDom; PD000621; Cold_shock;
SMART; SM00357; CSP; 1:
PROSITE; PS00352; COLD_SHOCK;
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PROSITE; PS00352; COLD_SHOCK;
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                                                                                                                       MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
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Pred. No. 8.2
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Pred. No. 8.2e-34;
Mismatches 0;
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                                                                                                       Query Match
Best Local :
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GO; GO:0003635; P:regulation of transcription, DN.
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold shock.
InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR012129; CSP.
InterPro; IPR012340; NA-bind_OB_sub.
Pfam; PF00313; CSD; 1.
Pfam; PF00313; CSD; 1.
Pfam; PF00359; Cold_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
Activator; Complete proteome; DNA-binding; Transcription regulation.
                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 CSD (cold-shock)
EMBL; AL023093; CAA18820.1; -; Genomic_DNA.
EMBL; AL583917; CAC29706.1; -; Genomic_DNA.
EMBL; P86933; F86933.
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MEDLINE-93188700; PubMed=8446027;
MEDLINE-93188700; PubMed=8446027;
Biglmeier K., Honore N., Woods S.A.,
"Use of an ordered cosmid library to
of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
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01-AUG-1998 (TrEMBLrel. 07, Last sequence up
01-FBB-2005 (TrEMBLrel. 29, Last annotation
Small cold-shock protein (Putative cold shoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001)
-!- SUBCELLULAR LOCATION: Cytoplasmic (By simi-
-!- SIMILARITY: Contains 1 CSD (cold-shock) dor
                                                                                                                                                                                        Transcription 
SEQUENCE 67
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Parkhill J., Barrell
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Mycobacterium leprae
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(APR-1998)
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e EMBL/GenBank/DDBJ
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                                                                           Score 352; DB Pred. No. 5.3e 2; Mismatches
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    DNA-binding; Transcription;

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01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Putative cold shock protein. OrderedLocusNames=nfa3660;
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Q5Z2Y3;
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PROSITE; PS00352; COLD_SHOCK; 1.

Activator; DNA-binding; Transcription; Transcription
SEQUENCE 67 AA; 7347 MW; 56C116E09EP746EA CRC64;
   NUCLEOTIDE SEQUENCE STRAIN=IFM 10152;
                                                                                                                            Corynebacterineae;
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ProDom; PD000621; Cold_shock; 1.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                        NCBI_TaxID=37329;
                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales
                                                                                                                                                                                             Nocardia farcinica.
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                                                                                                                               Nocardiaceae;
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92.5%;
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Last sequence update)
Last annotation update)
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Pred. No. 1e-31;
1; Mismatches
                                                                                                                                  Nocardia.
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RESULT 7
Q66NJS3_CORDI PRELIMINARY;
AC Q6NJS3_CORDI PRELIMINARY;
AC Q6NJS3;
DT 05-JUL-2004 (TYEMBLrel. 27,
DT 05-JUL-2004 (TYEMBLrel. 27,
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DT 05-JUL-2004 (TYEMBLrel. 27,
DE Cold-shock protein
GN Name=csph; OrderedLocusName
OS Corynebacterium diphtheriae
OC Corynebacterium diphtheriae
OC Gorynebacterium diphtheriae
OC Name=csph; OrderedLocusName
OC Corynebacterium diphtheriae
OC STRAIN=1177;
RN NUCLEOTIDE SEQUENCE.
RN PAILEN M., Bfst.
RA PAILEN M., Bfst.
RA CETdeno-Tarraga A.-M., Efst.
RA CETdeno-Tarraga A.-M., Bfst.
RA Pallen M., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
RA Hamlin N., Holroyd S., Jaget
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RA Hamlin N., Holroyd S., Jaget
RA Hamlin N., Holroyd S., J
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Best Local S
Matches 59
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GO; GO:0006350; P:transcription; IEA.
InterPro; IPR002059; Cold_shock.
InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR011129; CSP.
InterPro; IPR011129; CSP.
Pfam; PF000313; CSD; 1.
PIRSF; PIRSF002599; Cold_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
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Cold-shock protein.
Cold-shock protein.
Name=cspA; OrderedLocusNames=DIP0320;
Name=cspA; OrderedLocusNames=DIP0320;
Corynebacterium diphtheriae.
Corynebacterides; Corynebacterides; Corynebacterium.
                        Nucleic Acids Res. 31:6516-6523(2003).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUMILARITY: Contains 1 CSD (cold-shock) domain.

EMBL; BX248354; CAE488825.1; -; Genomic DNA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-deg
GO; GO:0006359; P:transcription; IEA.
InterPro; IPR010259; Cold shock.
InterPro; IPR011129; CSP.
                                                                                                                                                                                                                                                                                Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.I. Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J.; Whitehead S., Barrell B.G., Parkhill J.; The Complete genome sequence and analysis of Corynebacteriu diphtheriae NCTC13129."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Biotype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nax/gkg874;
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Activator; Complete proteome; DNA-binding; Transcription;
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68 AA; 7338 MW; F961B7CC51D05CE6 CRC64;
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Pred. No. 3.6e-29;
Nigmatches 4;
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RESULT 8
Q4JSS1 CORJK
ID Q4JSS1;
AC Q4JSS1;
AC Q4JSS1;
AC Q4JSS1;
AC Q4JSS1;
AC Q4JSS1;
AC Q4JSS1;
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AC CATPANAS
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Best Local S
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Q4USS1;
Q4USS1;
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Putative cold shock protein.
Putative cold shock protein.
Name=cspA; ORFNames=jk1955;
Corynebacterium jeikeium (strain K411).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Actinobacteridae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                  Linke B., Tauch A.;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR931997; CAIJ8136.1; -; Genomic DNA.
SEQUENCE 67 AA; 7267 MW; D60BAE570600D3A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15968079; DOI-10.1128/JB.187.13.4671-4682.2005; Tauch A., Kaiser O., Hain T., Goesman A., Weisshaar B., Albersmeier A., Bekel T., Bischoff N., Brune I., Chakraborty Kalinowski J., Meyer F., Rupp O., Schneiker S., Viehoever P.,
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PROSITE; PS00352; COLD SHOCK;
Activator; Complete proteome;
Transcription regulation.
SEQUENCE 67 AA; 7347 MW; E
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PRODORS; PD000621; Cold_shock; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nosocomial Pathogen Corynebacterium Bacterium of the Human Skin Flora.";
J. Bacteriol. 187:4671-4682(2005).
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AQNVTAL
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                                                   ATGVRSL 67
                                                                                                       MAQGTVKWFNAEKGFGFIAPDDGSSDVFVHYSEIQGSGFRTLEENQKVEFEIGEGAKGPQ
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
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  67
                                                                                                                                                                                                                                        82.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.1%;
83.6%;
                                                                                                                                                                                                             Score 296; DB
Pred. No. 1.7e
5; Mismatches
                                                                                                                                                                                                               <u>ت</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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Pred.
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    DNA-binding; Transcription;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302; DB 2; I
. No. 3.3e-27;
!smatches 7;
                                                                                                                                                                                                                                     296; DB 2;
No. 1.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 of the Multiresistant
jeikeium K411, a Lipid-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                             60
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RESULT 9
Q8FLY0 COREF
ID Q8FLY0 C
AC Q8FLY0;
DT 01-MAR-2

QBFLY0\_COREF

PRELIMINARY;

PRT;

251

ξ

01-MAR-2003

23,

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RESULT 10

QBNTX7_CORGL PRELIMINARY; PRT; 67 AA.

ID QBNTX7_CORGL PRELIMINARY; PRT; 67 AA.

AC QBNTX7; Q6M813;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 13-SEP-2005 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Cold shock proteins (COLD-SHOCK PROTEIN CSPA).

GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
RN (1)
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
RN (1)
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
RN (1)
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RN (1)
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RN (1)
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
RN (1)
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
RN (1)
GN Name=cspA; OrderedLocusNames=Cq10114, cg0215;
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Best Local S
Matches 54
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InterPro; IPR011129; CSP.
InterPro; IPR0112340; Na-bind_OB_sub.
Pfam; PP00313; CSD; 1.
PF1875; PR00050; COLDSHOCK.
PRINTS; PR00050; COLDSHOCK.
PRODOM; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR !
-!- SIMILARITY: (
EMBL; BA000035; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STKAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00352; COLD_SHOCK; 1.
Activator; Complete proteome, Dan-binding; Hypothetical Transcription; Transcription regulation.
SEQUENCE 251 AA; 27583 MW; OCA3D167507D8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
OrderedLocusNames=CE2729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003
01-OCT-2003
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 13:1572-1579(2003).
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GO:0003677; F:DNA binding; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO:0006350; P:transcription; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
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25, Last
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Pred. No. 4.
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annotation update)
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9;
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                                                                                                                              glutamicum ATCC 13032.";
databases.
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RESULT 11
Q8NTJ9_CORGL
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Best Local (
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InterPro; IPR012156; Cold_shock_CspA.
InterPro; IPR011129; CSP.
InterPro; IPR011129; CSP.
InterPro; IPR0112340; NA-bind_OB_sub.
Pfam; PF00313; CSD; 1.
PIRST; PIRST002599; Cold_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN-ATCC 13032 / I
Nakagawa S.;
"Complete genomic sec
            NUCLEOTIDE SEQUENCE.
STRAIN=ATCC 11932 / DSM 20300 / NCIB 10025;
MEDLINE=22830012; PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
MEDLINE=22830012; PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Kallnowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Elkmanns B.J., Gaigalat L.,
Burkovski A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
                                                                                                                                                                                                                                                     Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                      OBNTU9_CORGL PRELIMINARY; PRT; 67 AA. QBNTU9; Q6M54; Q6N54; 01-OCT-2002 (TTEMBLrel. 22, Created) 01-OCT-2002 (TTEMBLrel. 22, Last sequence update) 13-SEP-2005 (TTEMBLrel. 31, Last annotation update) Cold shock proteins (COLD-SHOCK PROTEIN CSPA). Name=cspA2; OrderedLocusNames=Cg10308, cg0371;
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of trans.
GO; GO:0006350; P:transcription; IEA.
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Tauch
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                                                                                                                                                                                                                                 NCBI_TaxID=1718;
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                                                                                                                                 Submitted
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McHardy A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activator; Complete proteome;
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-!- SIMILARITY: Contains 1 CSD (cold-shock)
EMBL; BA000036; BAB97567.1; -; Genomic_DNA.
EMBL; BX927148; CAF18741.1; -; Genomic_DNA.
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                                                                                                                                   genomic sequence of Corynebacterium (MAY-2002) to the EMBL/GenBank/DDBJ
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Meyer F.,
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77.6%;
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Pred. No. 7e-25;
5; Mismatches
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Kraemer R.,
ferle W., Pu
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                                                                                                                                   glutamicum ATCC 13032."; databases.
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Q8FSS6_COREF
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Best Local S
Matches 52
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GO; GO:000355; P:regulation of transcr
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR012059; Cold shock.
InterPro; IPR012156; Cold shock.
InterPro; IPR011129; CSP.
InterPro; IPR013139; CSP, I.
PERM; PF00313; CSD; 1.
PRINTS; PR00050; COLDSHOCK.
PRODOM; PD00051; COLDSHOCK.
PRODOM; PD00057; COLDSHOCK.
PRODOM; PD00057; COLDSHOCK.
PRODOM; PD00057; COLDSHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Putative cold shock protein.
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GO; GO
GO; GO
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Tauch A.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-|- SIMILARITY: Contains 1 CSD (cold-shock) domain.

EMBL; BA00035; BAC17116.1; -; Genomic_DNA.

HSSP; P32081; 1CSP.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0006357; F:regulation of transcription, DNA-deg
GO; GO:0006350; P:transcription; IEA.

InterPro; IPR002059; Cold_shock.
                                                                                                                                                                                                                                                                                           replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                               Nishio Y., Nakamura Y.,
Sugimoto S., Matsui K.,
Gojobori T.;
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Activator; Complete proteome; DNA-binding; Transcription;
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-!- SIMILARITY: Contains 1 CSD (cold-shock) domain.
EMBL; BA00036; BAB97701.1; -; Genomic_DNA.
EMBL; BX927148; CAF18878.1; -; Genomic_DNA.
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J. Biotechnol. 104:5-25(2003).
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AA; 7290 M
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77.6%;
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Pred. No. 4.5e-24;
4; Mismatches 11
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L-aspartate-derived ami
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                                                                             DNA-dependent; IEA.
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InterPro; IPR012340; NA-bind_OB_sub.
Pfam; PP000313; CSD; 1.
PIRSF; PIRSF002599; Cold_shock_A; 1.
PRINTS; PR00050; COLDSHOCK.
PRINTS; PR000521; Cold_shock; 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
                    PIRSF; PIRSF002599; Cold_shock_A;
PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
                                                                                 US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., G
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation updat)
Cold-shock protein, DNA-binding.
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ACLIVATOR; Complete proteome; DNA-binding; Transcription;
Transcription regulation.
SEQUENCE 67 AA; 7292 MW; BDB92D90D88A8CD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter sp. FB24.
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q4NFR7_9MICC
Q4NFR7;
                                                                                                                                                                                                                        STRAIN=FB24;
US DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=ArthDRAFT_1862;
  SEQUENCE
                                                                             Pfam; PF00313; CSD;
                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=290399;
                                                                                                                                                                                                                                                                                                                                                                     Micrococcineae;
            Activator;
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nilarity 77.6%;
Conservative
 300352; CÓLD SHOCK; 1.
DNA-binding; Transcription;
67 AA; 7267 MW; 850595CD01
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Pred. No. 5.9e
4; Mismatches
   850595CD0EC77CF4
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                                                                                                                       Genomic_DNA.
                                                                                                                                              (By similarity).
   Transcription 
EC77CF4 CRC64;
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Query Match

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Matches
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InterPro; IPR012059; CSP DNA bd.
InterPro; IPR012340; OS NA bd_sub.
Pfam; PP00313; CSD; 1.
PIRSF; PIRSF002599; Cold shock A; 1.
PRINTS; PR00050; COLDSHOCK.
PRODOm; PD000621; Cold shock; 1.
SMART; SM00357; CSP; 1.
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ARTGO
CSP_!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P54584;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                  EMBL; L41167; AAB81323.1; -; Genomic_DNA. HSSP; P15277; 1MJC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Berger P., Morellet N., Menu F., Potier P.;
"Cold shock and cold accilmation proteins in the bacterium Arthrobacter globiformis SI55.";
J. Bacteriol. 178:2999-3007(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter globiformis.
Bacteria; Actinobacteria; Actino
Micrococcineae; Micrococcaceae;
                                                                                                                                                   SEQUENCE
                                                                                                                                                             Activator; DNA-binding; Transcription; Transcription regulation.

CSD.

CSD.
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                                                                                                                                                                                                                                                                                                                                                                                                                               -I- INDUCTION: In response to low temperature.-I- SIMILARITY: Contains 1 CSD (cold-shock) domain.

    -!- SUBCELLULAR LOCATION: Cytoplasmic.
    -!- INDUCTION: In response to low temp

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96236009; PubMed=8655472;
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48; Conservative
                        ATGV 64
                                                             MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ
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                                                 MAQGTVKWFNAEKGFGFITPDDSDGDVFVHYSEIQTGGFKTLDENARVQFEIGQGAKGPQ
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73.4%;
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                                                                                               Score 260; DB 1; 1
Pred. No. 2.5e-22;
6; Mismatches 11;
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                                                                                                                                                  850595CD0EDACBF4 CRC64;
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RESULT

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Search completed: April 14, 2006, 17:32:30 Job time: 26.7208 secs

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Q4NLB1 9MICC
ID QANLB1;
AC QANLB1;
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C -:- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
C -:- SIMILARITY: Contains 1 CSD (cold-shock) domain.
C EMBL; AAHG0100001; EAL98431.1; -; Genomic_DNA.
R InterPro; IPR012126; Cold_shock_CspA.
R InterPro; IPR012129; CSP.
R InterPro; IPR012129; CSP_DNA_bd.
R PIRSP; PIRSP00359; CSP_DNA_bd.
R PIRSP; PIRSP00359; COLd_shock_A; 1.
R PIRSP; PIRSP00359; COLd_shock_A; 1.
R PRINTS; PR00050; COLDSHOCK.
R PRINTS; PR00050; COLDSHOCK.
R PRODOM; PD00061; Cold_shock; 1.
R SMART; SM00357; CSP; 1.
                                                                                                                                                                                                                                           Matches
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Best Local (
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Q4NLE1;
13-SEP-2005 (113-SEP-2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., G
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Arthrobacter
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Cold-shock protein, DNA-binding.
ORFNames=ArthDRAFT_4299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arthrobacter sp. FB24.
Bacteria; Actinobacteria; Actinomicrococcineae; Micrococcaceae;
                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00352; COLD_SHOCK; 1.
Activator; DNA-binding; Transcription; Transcription regulation
SEQUENCE 67 AA; 7250 MW; 8173679D2C37B1D6 CRC64;
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US DOE Joint Genome Institute (PGF-ORNL);
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   ABNIRPL
                                                          ATGVRSL
                                                                                                                  MATGTVKWFNAEKGFGFIAPDDGSADVFAHYSAIATSGYRSLDENQKVEFDVTQGPKGPQ
                                                                                                                                                    MPQGTVKWFNAEKGFGF1APEDGSADVFVHYTE1QGTGFRTLBENQKVEFE1GHSPKGPQ
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9; Mismatches 12
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                Sequence 147, App
Sequence 84, Appl
Sequence 84, Appl
Sequence 817, Appl
Sequence 117, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 9, Appl
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Sequence 1126, A
Sequence 20, Appl
Sequence 6235, App
Sequence 7, Appl
Sequence 7, Appl
Sequence 328, App
Sequence 328, App
Sequence 338, App
Sequence 3351, Ap
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Oy 61 ATGVRSL	Qy 1 MPQGT	Query Match Best Local Similarit Matches 67; Conse	SOFTWARE: F SEQ ID NO 14 LENGTH: 67 TYPE: PRT ORGANISM: S-09-050-739-	EARLIER EARLIER EARLIER EARLIER EARLIER NUMBER O	; CORRENT FILING DATE: ; EARLIER APPLICATION; ; EARLIER APPLICATION; ; EARLIER PILING DATE:	TITLE FILE CURRE	APPLICANT: APPLICANT: APPLICANT:	Patent NO. 6 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT:	0-739-14 ce 147,		199 199 198.5 196.5	39 199 55 40 199 55 41 199 55	199.5	201	205 204 201.5	205 205
SL 67	MPQGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQ 	100.0%; Sc y 100.0%; Pr rvative 0;	in Ve	NUMBER: 60/044, 1997-04-18 NUMBER: 60/070, 1998-01-05 : 173	DATE: 1998-03-30 ATION NUMBER: 0376/97 DATE: 1997-04-02 ATION NUMBER: 1277/97 DATE: 1997-11-10	NUCLEIC ACIDS DERIVED FROM M 001-2002.1 NUMBER: US/09/	NDS, Ida Karin Walter	641814 RWATION: RWATION: ANDERSEN, Peter NIBLSEN, Rikke OETTINGER, Thomas	17 Application US/09050739	ALJ	.4 71 2 US .4 71 2 US .4 71 2 US .3 66 2 US .7 70 2 US	.4 71 2 US	.6 67 2 US	.0 82 2 US	.1 85 2 US- .8 68 2 US- .1 66 2 US-	.1 67 2 US-0
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	IQGTGFRTLEENQKVEFEIGHSPKGPQ 60	Length 67; Indels 0; Gaps 0;				PTIDE FRAGMENTS					547°		2 2 2	e 79	254	16294, 2, App

RESULT 2 US-09-603-208A-82 ; Sequence 82, Application US/09603208A ; Patent No. 6822084

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; ORGANISM: Corynebacterium glutamicum
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Matches 52
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SEQ ID NO 82
LENGTH: 67
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APPLICANT: Pompeju
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PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-07-01
CURRENT APPLICATION NUMBER: US/09/603,208A
               TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS FILE REFERENCE: BGI-124CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haberhauer, Gregor
APPLICANT: Lee, Heung-Shick
APPLICANT: Kim, Hyung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941382.7
PRIOR FILING DATE: 1999-08-31
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PRIOR APPLICATION NUMBER: 60/151214
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930429.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR FILING DATE: 1999-07-08
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                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                             Haberhauer, Grego
Lee, Heung-Shick
Kim, Hyung-Joon
                                                                                                                  Schroder, Hartwig
Zelder, Oskar
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Kroger, Burkhard
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1999-07-08
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77.6%;
                                                                                                    Gregor
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Pred. No. 5.8e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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CURRENT APPLICATION NUMBER: US/09/603,208A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILLING DATE: 1999-06-25
PRIOR PILLING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/151214
PRIOR APPLICATION NUMBER: 60/151214
PRIOR FILLING DATE: 1999-07-01
PRIOR FILLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: DE 19930429.7
PRIOR FILLING DATE: 1999-07-01
PRIOR FILLING DATE: 1999-07-01
PRIOR FILLING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931413.6
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US-09-603-208A-84
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SEQ ID NO 84
LENGTH: 67
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                                                                                                                                                                                                                                                    APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Lee, Heung-Shick
APPLICANT: Lie, Heung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTANICUM GENES E
TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
FILE REFERENCE: BGI-124CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941382.7
PRIOR FILING DATE: 1999-08-31
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PRIOR FILING DATE: 1999-C
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-C
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PRIOR FILING DATE: 1999-08-27
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OR FILING DATE: 199-07-01
OR APPLICATION NUMBER: DE 19931413.6
OR FILING DATE: 199-07-08
OR APPLICATION NUMBER: DE 19931457.8
OR APPLICATION NUMBER: DE 19931541.8
OR APPLICATION NUMBER: DE 19931541.8
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R FILING DATE: 1999-07
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APPLICATION NUMBER: DE 19932914.1
FILING DATE: 1999-07-14
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FILING DATE: 1999-06-25
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FILING DATE:
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| 52; Conserva
                                                                                                                                                                                                Application US/09603208A
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Pred. No. 5.8e-30;
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RESULT 6
US-09-489-039A-13476
US-09-489-039A-13476
; Sequence 13476, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
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US-09-134-000C-4171
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Best Local S
Matches 44
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APPLICANT: LYIND DOUGETGE-Stamm et al
APPLICANT: LYIND DOUGETGE-STAMM AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 037796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4171
LENGTH: 88
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Best Local (
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 APPLICANT:
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PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
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ORGANISM: Corynebacterium glutamicum
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APPLICATION NUMBER:
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Gary Breton et.
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IMBER: DE 19931541.8
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                                                                                                                                                                                                                                                                                                      63.4%;
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77.6%;
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Pred. No. 1.4e-22;
7; Mismatches 12;
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Pred. No. 4.9e-29;
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FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13476

LENGTH: 131

TYPE: PRT

ORGANISM: Klebsiella pneumoniae
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US-08-203-806B-11
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
                                                                                                                                                Sequence 11, Application US/08203806B Patent No. 5714575
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APPLICANT: Mang, Nan
APPLICANT: Mang, Nan
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF,
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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CURRENT APPLICATION NUMBER: US/09/516,667
CURRENT FILING DATE: 2001-08-01
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                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIBLLA TITLE OF INVENTION: PUBUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 70
TYPE: PRT
                                                      APPLICANT:
APPLICANT:
APPLICANT: Pollitt, APPLICANT: Goldstei TITLE OF INVENTION:
                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                          67 VVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09516667
                                                                                                                                                                                                                                                                                                                                                                                                 61.6%;
milarity 64.1%;
Conservative
             Weining, Jian
Pollitt, N. Stephen
Goldstein, Joel
                                                                       Jones, Pamela
Etchegaray, Jean-Pierre
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                                                                                                           Inouye,
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                                                                                                                                                                                                                                                          70
                                                                                                             Masayori
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Nucleic Acid Sequences, Stress-induced
                                                                                                                                                                                                                                                                                                                                                                                                   Score 221; DB 2;
Pred. No. 7.7e-22;
6; Mismatches 17;
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Pred. No. 1.3e-21;
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Query Match
Best Local Similarity
Marches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-203-806B-11
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Patent No. 6333191
GENERAL INFORMATION:
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.5998P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8393
TELEPAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acide
TYPE: amino acide
TOPOLOGY: lin-
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Proteins and Uses Thereof NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 230 South CITY: Philadelphia
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                                                                                                                                                                                                     NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: SCHNADER, I
STREET: 1600 Market Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Street Str
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: INOUYE, MASAYORI
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                                                                                                                                         STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PA
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                                                                                                             19103
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Pred. No. 1.5e-21;
6; Mismatches 15;
                                                                                                                                                                                                                                        Street, Suite 3600
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GENERAL INFORMATION:

APPLICANT: INGUYE, MASSYORI

APPLICANT: Wang, Nan

APPLICANT: Wang, Nan

APPLICANT: Yamanaka, Kunitoshi

TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: 1053-00

CURRENT APPLICATION NUMBER: US/09/516,667

CURRENT FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 87

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 79

LENGTH: 70

CORGANISM: E. Coli

US-09-516-667-79
RESULT 11
US-09-902-540-12349
; Sequence 12349, Application US/09902540
; Patent No. 6833447
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Best Local Similarity
Watches 42; Conserve
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NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 1113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-751-2427
TELEPHONE: 215-751-2658
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Matches
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SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,754A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79, Application US/09516667
o. 6610533
                                                                                                         67 VVAL 70
                                                                                                                                        64 VRSL 67
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                                                                                                                                                                                                                                                                  Similarity
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                              60.48;
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Pred. No. 1.5e-21;
6; Mismatches 15;
                                                                                                                                                                                                                                                Score 217; DB 2;
Pred. No. 2.6e-21;
7; Mismatches 16
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                                                                                                                                                                                                                                                                                  Length 70;
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US-08-203-806B-4
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US-09-902-540-12349
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
IITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4,
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TELEX: 834809 WEISTAK INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman,
APPLICANT: Hinkle,
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                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPERM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEB: Welser & Associates
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                           REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.5998P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goldstein, Joel
TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced
TITLE OF INVENTION: Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                         TELEPHONE: Z15 - 8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 60.2%;
Local Similarity 62.1%;
hes 41; Conservative
                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/203,806B FILING DATE: 01-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                   19102
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PA
69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pollitt, N. St. Goldstein, Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones, Pamela
Etchegaray, Jean-Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inouye,
                                                                                                  215-875-8383
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Pred. No. 3.3e-21;
6; Mismatches 19
                                                                                                                                                                                                                                                                                                  Version #1.25
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US-08-203-806B-9
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                                                                                                                                       US-08-203-806B-9
                                                                                   Best Local
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Applic Patent No. 5714575
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                  MOLECULE TYPE: F
ORIGINAL SOURCE:
ORGANISM: Esch
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Sequences, Stress-induced TITLE OF INVENTION: Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pollitt, N. Stephen APPLICANT: Goldstein, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Bolo-
                                                                                                                                                                                                                                                                                             TELEPHONE: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/203,806B FILING DATE: 01-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                           TYPE:
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                                                                                   Similarity
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KGQVKWFNESKGFGFITPADGSKDVFVHFSAIQGNGFKTLAEGQNVEFEIQDGQKGPAAV
                              QGTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFEIGHSPKGPQAT 62
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230 South Fifteenth Street, Suite 500
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Etchegaray, Jean-Pierre
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                                                                  60.2%; Score 216; DB 1; Length 69; 61.5%; Pred. No. 3.5e-21; tive 6; Mismatches 19; Indels
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RESULT 14
US-09-017-754A-4
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US-09-017-754A-9
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Best Local Similarity
Matches 40; Conservat
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                                                                                            Sequence 9, Application US/09017754A Patent No. 6333191
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 215-751-2658
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 1113-cip2-div-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-751-2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,754A
FILING DATE: 03-Feb-1998
ATTORNEY/AGENT INFORMATION:
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COUNTRY: USA
COUNTRY: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHAADER, HARRISON, SEGAL & LEWIS, LLP
STREET: 1600 Market Street, Suite 3600
APPLICANT: INOUYE, MASAYORI
JONES, PAMELA
ETCHEGARAY, JEAN-PIERRE
WEINING, JIANG
POLITT, N. STEPHEN
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WEINING, JIANG
WEINING, JIANG
POLITT, N. STEPHEN
GOLDSTEIN, JOEL
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED
PROTEINS AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
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61.5%;
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Search completed: April 14, 2006, 17:37:59
Job time : 6.19531 secs
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Best Local Similarity 61.5%;
Matches 40; Conservative
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,754A
PILING DATE: 03-Feb-1998
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 1113-cip2-div-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-751-2427
TELEPHONE: 215-751-2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHNADER, HARRISON, SEGAL & LEWIS, LLP
STREET: 1600 Market Street, Suite 3600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOLDSTEIN, JOEL
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES, STRESS-INDUCED
PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                          65 NVTAI 69
                                                                                                                  63 GVRSL 67
                                                                                                                                                  TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                Score 216; DB 2;
Pred. No. 3.5e-21;
6; Mismatches 19
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Result
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Maximum
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Maximum Match 100%
Listing first 45 s
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seq length: 2000000000
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Match
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     Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration
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US-09-738-626-3695
US-10-953-856-51
US-09-738-626-3845
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US-10-156-761-1354
US-10-156-761-3364
US-10-156-761-3364
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US-09-912-020-328
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US-10-282-122A-73080
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US-11-067-337-2
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Sequence 147, App Sequence 147, App Sequence 147, App Sequence 147, App Sequence 147, App Sequence 3695, App Sequence 62113, A Sequence 62113, A Sequence 11466, A Sequence 19, App Sequence 5731, App Sequence 5731, App Sequence 5731, App Sequence 57316, A Sequence 57316, A Sequence 59825, A Sequence 59825, A Sequence 79459, A Sequence 75459, A Sequence 75459, A Sequence 63, App Sequence 63, App Sequence 63, App Sequence 63, App Sequence 63, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App Sequence 57, App 
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QY I MEQGIVAMENAEKGEGELAEBUSSADVEVHYTELQGIGERTLEENQKVEEELGHSEKGEQ 60	Query Match 100.0%; Score 359; DB 3; Length 67; Best Local Similarity 100.0%; Pred. No. 1.6e-38; Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps	PRIOR APPLICATION NUMBER: 60/070,488 PRIOR FILING DATE: 1998-01-05 NUMBER OF SEQ ID NOS: 173 SOPTWARE: PATENTIN VET. 2.0 SEQ ID NO 147 LENGTH: 67 TYPE: PRT ORGANISM: Mycobacterium tuberculosis US-09-791-171-147	CURRENT APPLICATION NUMBER: US/09/791,171  CURRENT FILING DATE: 2001-02-20  PRIOR APPLICATION NUMBER: 09/050,739  PRIOR PILING DATE: 1998-03-30  PRIOR PILING DATE: 1998-03-30  PRIOR PILING DATE: 1997-04-02  PRIOR PILING DATE: 1997-11-10  PRIOR PILING DATE: 1997-11-10  PRIOR PILING DATE: 1997-11-10  PRIOR PILING DATE: 1997-11-10  PRIOR PILING DATE: 1997-11-10	PAREPLY NO. US2002094336A1  GENERAL INFORMATION: APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke APPLICANT: COTTINGER, Thomas APPLICANT: RASMUSSEN, Peter Birk APPLICANT: ROSENKRANDS, Ida APPLICANT: WELDINGH, Karin APPLICANT: WELDINGH, Karin APPLICANT: FLORIO, WALTER TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS	00.5 55.8 79 5 US-10-953-856-59 Sequence ALIGNMENTS 147 Application HS/00781171	201.5 56.1 67 4 US-10-282-122A-45991 Sequence 4599 201 56.0 67 4 US-10-156-761-11688 Sequence 1169 201 56.0 70 4 US-10-282-122A-68525 Sequence 6159 200.5 55.8 66 5 US-10-953-856-45 Sequence 65, 200.5 55.8 67 5 US-10-953-856-91 Sequence 65, 200.5 55.8 67 5 US-10-953-856-61 Sequence 61, 200.5 55.8 71 5 US-10-953-856-61 Sequence 61, 200.5 55.8 79 4 US-10-724-972A-4120 Sequence 61, 200.5 55.8 79 5 US-10-734-856-59 Sequence 61, 200.5 55.	.5 67 4 US-10-156-761-11981 Sequence 11981, .2 70 4 US-10-282-122A-56326 Sequence 56326, .1 66 4 US-10-282-122A-57510 Sequence 57510, .8 66 4 US-10-282-122A-60873 Sequence 60873, .8 66 5 US-10-894-438-4 Sequence 4, Appl4 67 4 US-10-156-761-12310 Sequence 12310, .8 67 4 US-10-156-761-8431 Sequence 4931, Appl4 65 5 US-10-953-856-95 Sequence 95, Appl.
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RESULT 2 US-09-804-980-147 맑

61 ATGVRSL

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APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 147
LENGTH: 67
TYPE: PRT
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Sequence 147, Application US/10620246
Publication No. US20040115211A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR PELICATION NUMBER: 03/6/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
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APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
                                          SOPTWARE: PatentIn
SEQ ID NO 147
LENGTH: 67
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, KARIN
APPLICANT: PLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
                                                                                                                     PRIOR APPLICATION NUMBER: 1281/98
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                        NUMBER OF SEQ ID NOS: 173
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                          APPLICATION NUMBER: 09/415,884 FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/791,171 FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 10/138,473 FILING DATE: 2002-05-02
                                                                                                                                                                  FILING DATE: 1999-01-21
                                                                                                                                                                                     APPLICATION NUMBER: 60/116,673
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/070,488
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RASMUSSEN, Peter Birk
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Pred. No. 1.6e-38;
; Mismatches 0;
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3695
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US-10-953-856-51
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Sequence 51, Application US/10953856
publication No. US20050097640A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology
TITLE OF INVENTION: compositions thereof
FILE REFERENCE: Docket number (38-21)51768C
CURRENT FILING APPLICATION NUMBER: US/10/953,856
CURRENT FILING APPLICATION NUMBER: US/10/953,856
NUMBER OF SEQ ID NOS: 95
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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77.6%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 282; DB 3;
Pred. No. 1.4e-28;
5; Mismatches 10
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RESULT 7
US-10-282-122A-62113
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APPLICANT: SENCH, MACKO
APPLICANT: SENCH, MACATO
APPLICANT: SENCH, MACATO
APPLICANT: SENCH, MACATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
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Matches
Sequence 62113, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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SEQ ID NO 51
LENGTH: 67
TYPE: PRT
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Best Local (
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LENGTH: 67
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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52; Conserv
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Similarity 77.6%;
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                                                                                                                                                  AQAVRAI 67
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELLTRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
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US-10-156-761-12354
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JF 2001-204089
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                                                                                                                                                                                                        Sequence 12354, Application US/10156761
publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWLEA, SAYOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62113
LENGTH: 67
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Matches
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APPLICANT:
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PRIOR FILING DATE: 2001-02-16
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
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Forsyth, R.
Xu, H.
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Trawick, John
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Zyskind, Judith
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Sequence 19, Application US/10953856
Publication No. US20050097640A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology
TITLE OF INVENTION: Methods for enhancing abiotic stress tolerance
TITLE OF INVENTION: compositions thereof
FILE REFERENCE: Docket number (38-21)51768C
CURRENT APPLICATION NUMBER: US/10/953,856
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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SEQ ID NO 11466
LENGTH: 68
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Best Local (
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SEQ ID NO 12354
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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nes 44; Conservative
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70.8%;
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Pred. No. 1.7e-22;
5; Mismatches 18;
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Pred. No. 6.8e-22;
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GENERAL INFORMATION:

APPLICANT: INFORMATION:

APPLICANT: INFORMATION:

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: HARTORI, WASHIYAKI

APPLICANT: HARTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR PILING DATE: 2001-08-02
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US-10-156-761-8364
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                                                                                                                                                                                                               RESULT 12
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US-10-156-761-8364
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US-10-953-856-19
GENERAL INFORMATION:

APPLICANT: Monsanto Technology
APPLICANT: Monsanto Technology
TITLE OF INVENTION: Methods for enhancing abiotic stress tolerance in plants
TITLE OF INVENTION: compositions thereof
FILE REFERENCE: Docket number (38-21)51768C
CURRENT APPLICATION UNMERR. US/10/953,856
CURRENT FILING DATE: 2004-09-29
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 19
                                                                                                                                               Sequence 13, Application US/10953856 Publication No. US20050097640A1
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SEQ ID NO 8364
LENGTH: 67
TYPE: PRT
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Best Local Similarity 65.6%;
Matches 42; Conservative
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TYPE: PRT
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Pred. No. 1.1e-20;
4; Mismatches 19
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Pred. No. 6.6e-21;
5; Mismatches 17
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PatentIn version 3.2

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; ORGANISM: Escherichia coli
US-10-953-856-13
                                                      ; ORGANISM: Enterococcus faecalis US-10-282-122A-57331
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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SOPTWARE: PatentIn versionsEQ ID NO 13
Best Local Similarity
                                                                                                                               SEQ ID NO 57331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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APPLICANT:
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                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
                                                                                                                                                                                                                           APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                    FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/230,347
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Zyskind, Jud
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59.5%;
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Score 213.5; DB Pred. No. 1e-19;
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               Length
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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US-10-282-122A-42639
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US-09-912-020-328
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Best Local Similarity
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APPLICANT:
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CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER: 0777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

TITLE OF INVENTION: ESCHERICHIA COLI

FILE REFERENCE: ELITRA, 001DV1
TITLE OF INVENTION: Identification FILE REFERENCE: BLITRA.034A
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John
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ORGANISM: E. Coli
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Forsyth, R. Allyn
Froelich, Jamie M.
Carr, Grant J.
                                                 Yamamoto, R. Forsyth, R.
                                                                                                     Trawick, John
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Pred. No. 2.3e-19;
8; Mismatches 17; Indels
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                  of Essential Genes in Microorganisms
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42639
LENGTH: 70
TYPE: PRT
ROANISM: Escherichia coli
US-10-282-122A-42639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
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Search completed: April 14, 2006, 18:40:40 Job time : 24.612 secs
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Best Local Similarity 60.9%;
Matches 39; Conservative
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Result
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Perfect score:
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seq length: 2000000000
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1: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

2: /SIDSS/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /SIDSS/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

6: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

7: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

8: /SIDSS/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
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Sequence 8, Appli
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Sequence 9, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 302, Appl
Sequence 3184, Ap
Sequence 316, Ap
Sequence 7165, Ap
Sequence 1048, Ap
Sequence 11534, Ap
Sequence 5316, Ap
Sequence 2523, Ap
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	16630, A	16521, A	10981, A	5412, Ap	27878, A	27879, A	27880, A	30604, A	26, Appl	10907, A	1224, Ap	15364, A	13172, A	10851, A	4166, Ap	17481, A	•	ç	6359, Ap	/0/2/ AP

## ALIGNMENTS

RESULT 1 US-10-506-192-6

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APPLICANT: INOUTE, MASSYORI
APPLICANT: XIA, Bing
APPLICANT: Qing, Guoliang
APPLICANT: Qing, Guoliang
APPLICANT: KE, Haiping
TITLE OF INVENTION: COLD SHOCK INDUCTBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: COLD SHOCK INDUCTBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: DOLYPEPTIDES
TILE REFERENCE: INOUTE-2.1 PCT
CURRENT APPLICATION NUMBER: US/10/506,192
CURRENT APPLICATION NUMBER: 60/402,921
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/402,921
PRIOR APPLICATION NUMBER: 60/402,921
PRIOR APPLICATION NUMBER: 60/402,921
PRIOR RILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 50
SOPTWARE: Patentin version 3.3
SEQ ID NO 6
LENGTH: 70
TYPE: PRIOR EXCEPTION: SOUTHABLE: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE INFORMATION: COTTABE
RESULT 2
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; Sequence 2, Application US/10506192
; Publication No. US20050272924A1
; GENERAL INFORMATION:
; APPLICANT: INOUYE, Masayori
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Best Local S
Matches 42
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Publication No. US20050272924A1
GENERAL INFORMATION:
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5; Mismatches
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Best Local Similarity 60.9
Conservative
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APPLICANT: Feesche, Joerg
APPLICANT: Maurer, Karl-Heinz
APPLICANT: Breves, Roland
APPLICANT: Schweder, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPTWARE: PatentIn version 3.3 SEQ ID NO 18 LENGTH: 70
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Publication No. US20060040279A1
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Best Local (
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TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL

TITLE OF INVENTION IN CHIPS USED FOR BIOPROCESS CONTROL

TITLE OF INVENTION INVENTER: US/11/077,619

CURRENT PILING DATE: 2005-03-11

PRIOR APPLICATION NUMBER: PCT/BP2003/009979

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-01

PRIOR PILING DATE: 2003-09-01
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       67 VTSL
                                                                          64 VRSL 67
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Hecker, Michael
Juergen, Britta
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KE, Haiping
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APPLICANT: Qing, Guollang
APPLICANT: KE, Haiping
FITTLE OF INVENTION: COLD SHOCK INDUCIBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
FITTLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: INOUTS=2.1 PCT
FULRENT APPLICATION NUMBER: US/10/506,192
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO
CORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: Synthetic
US-10-506-192-8
                                                                                                                   APPLICANT: Schweder, Thomas
APPLICANT: Hecker, Michael
APPLICANT: Hecker, Michael
APPLICANT: Vorgen, Britta
APPLICANT: Vorgen, Britta
APPLICANT: Volgt, Birgit
TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REFERENCE: HENK-0122 / H5692
CURRENT APPLICATION NUMBER: US/11/077,619
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP2003/009979
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2003-09-01
INUMBER OF SEG ID NOS: 130
SOFTWARE: Patentin version 3.3
SEG ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Feesche, Joerg
APPLICANT: Maurer, Karl-He
APPLICANT: Brevves, Roland
APPLICANT: Schweder, Thome
APPLICANT: Hecker, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10506192 Publication No. US20050272924A1
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/11077619 Publication No. US20060040279A1
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Best Local S
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APPLICANT: XIA, Bing
APPLICANT: PHADTARE, Sangi
                                                              LENGTH: 67
TYPE: PRT
ORGANISM: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 VVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VRSL 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GTVKWFNABKGFGFIAPEDGSADVFVHYTEIQGTGFRTLEENQKVEFBIGHSFKGPQATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 59.
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Breves, Roland
Schweder, Thomas
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PHADTARE, Sangita
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    55.6%;
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    Score 199.5;
    DB
      7
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      Length 67;
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US-11-077-619-22
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Best Local Similarity
Matches 38; Conserv
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SEQ ID NO 22
LENGTH: 71
TYPE: PRT
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            APPLICANT: Qing, Guoliang
APPLICANT: KE, Halping
TITLE OF INVENTION: COLD SHOCK INDUCIBLE EXPRESSION AND PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES
TILE REFERENCE: INOUYSE-2.1 PCT
CURRENT APPLICATION NUMBER: US/10/506,192
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR APPLICATION NUMBER: 60/361,069
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VOIGT, Birgit
TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REFERENCE: HENK-0122 / H5692
CURRENT APPLICATION NUMBER: US/11/077,619
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP2003/009979
PRIOR FILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: DET 10242433.0
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-09-11
                                                                                                                                                                                                                                          APPLICANT: INOUYE, Masayori
APPLICANT: XIA, Bing
APPLICANT: PHADTARE, Sangi
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APPLICANT: Maurer, Karl-
NUMBER OF
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SEQ ID NOS: 50
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PHADTARE, Sangita
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Breves, Roland
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Hecker, Michael
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APPLICANT: Juergen, Britta
APPLICANT: Voigt, Birgit
TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REFERENCE: HENK-0122 / H5692
CURRENT APPLICATION NUMBER: US/11/077,619
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/EP2003/009979
PRIOR APPLICATION NUMBER: DET/EP2003/009979
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 130
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 130
                                                       RESULT 9
US-10-467-657-3284
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US-11-077-619-98
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; OTHER INFORMATION: Synthetic
US-10-506-192-4
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Sequence 3284, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 98
LENGTH: 66
TYPE: PRT
ORGANISM: Bacillus licheniformis
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SEQ ID NO 4
LENGTH: 72
TYPE: PRT
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Best Local Similarity
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Publication No.
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APPLICANT: Maurer, Karl-Heinz
APPLICANT: Breves, Roland
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                                                                                                                                                                                                                                                                        40; Conservative
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38; Conservative
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                                                                                                                                                                                                     MLEGKVKWFNSEKGFGFIEVE-GQDDVFVHFCAIQGEGFKTLEEGQSVSFEIVEGNRGPQ 59
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Hecker, Michael
Juergen, Britta
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                                                                                                                                                                                                                                                                                         Score 198.5; DB 7;
Pred. No. 5.5e-18;
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Pred. No. 5.3e-18;
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                                                                                                                                                                                                                                                                          18;
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APPLICANT: CHIRON SPA APPLICANT: FONTANA MARIA Rita APPLICANT: PIZZA MARIAGIRAZI APPLICANT: MASIGNANI Vega APPLICANT: MONACI Blisabetta

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Sequence 302, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Russell, Bric
APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
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US-11-169-041-216
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Publication No. US20060019284A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF

TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE

TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER

TITLE OF INVENTION: CELLS

FILE REFERENCE: 10001 NP

CURRENT APPLICATION NUMBER: US/11/169,041

CURRENT FILING DATE: 2005-06-28

CURRENT FILING DATE: 2005-06-28
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SEQ ID NO 3284
LENGTH: 80
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SEQ ID NO 216
LENGTH: 364
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Best Local Similarity
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Best Local &
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 527
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PRIOR FILING DATE: 2004-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                         156 EATNV 160
                                                                                                                                                                                                                                                                                                                60 QATGV 64
                                                                                                                                                                                                                                                                                                                                                              96 GTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKRNNPRKFLRSVGDGETVEFDVVEGEKGA 155
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                                                                                                                                                                                                                                                                                                                                                                                                 4 GTVKWFNAEKGFGFIAPEDGSADVFVHYTEIQGTG----FRTLEENQKVEFEIGHSPKGP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 138; DB 7; Length 364; Pred. No. 1.7e-09;
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1365
LENGTH: 147
TYPE: PAT
ORGANISM: Homo sapiens
US-10-821-234-1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 302
LENGTH: 67
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
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GENERAL INFORMATION:
APPLICANT: GATY L. BRETON
APPLICANT: GATY L. BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR'
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOO-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1369, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
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TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 5051-694
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Similarity 44.1%;
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Pred. No. 0.00045;
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 6490
SEQ ID NO 6490
TYPE: PRT
CRGANISM: Staphylococcus aureus subsp. aureus Mu50
US-11-087-099-6490
                                                                                                                                                                                                                                                                                RESULT 15
US-11-087-099-6490
; Sequence 6490, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-821-234-1048
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US-10-821-234-1048
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PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1048
LENGTH: 826
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Publication No. US20050255114A1
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Best Local Similarity
Query Match
Best Local Similarity
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APPLICANT: Tang, Y. Tom
TITLE OP INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
PILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILLING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                             222 KBAFGFIERGDVVKBIFFHYSEFKG-DLETLOPGDDVEFTIKDRNGKEVATDVRLL 276
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| :::||| ||:||: | | | : | : | : | | : | : | 10
85 GRIEYFNAAKGYGFVKDADCGEKYFFHISSAPA----TIAEGDRVTFEIERGWRGWNAVR 140
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ilarity 37.5%;
Conservative
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18.1%;
39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 78.5; DB 6;
Pred. No. 0.14;
Score 65; DB 7;
Pred. No. 2.4;
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                     Length 351;
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Search completed: April 14, 2006, 18:42:17 Job time : 3.871 secs